Supplementary Table S1. Breakdown of Desulfuromondales pilin gene clusters and pilin gene clusters from e-pilin harboring species from other bacterial orders. Each pilin gene cluster is shaded in a different color. Genes with GC content +/- 7% of the genome average are highlighted in blue.

A. Pilin gene clusters found in the *Geobacter sulfurreducens* genome. Three different gene clusters were identified and each is highlighted in a different color. Only one gene coding for a horizontal gene transfer protein is present in these gene clusters. Genes from the xap operon and additional glycosyl transferase proteins are located in the vicinity of the e-pilin gene. The overall GC content of *G. sulfurreducens* is 60.94%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Sixteen out of 58 (26%) of the genes have deviant GC values, including *e-pilin, pilA-C, xapA, xapB, xapD, xapH*, and *xapJ.*

|  |  |  |  |
| --- | --- | --- | --- |
|  | |  |  |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| GSU\_RF0073 | GEMM riboswitch |  | 0.58 |
| GSU1061 | aspartate aminotransferase | | 0.64 |
| GSU1062 | cytochrome c, putative | | 0.66 |
| GSU1063 | *pilV* |  | 0.58 |
| GSU1064 | *pilW* |  | 0.62 |
| GSU1065 | *pilX* |  | 0.6 |
| GSU1066 | *pilY1* |  | 0.61 |
| GSU1484 | soluble lytic murein transglycosylase | | 0.62 |
| GSU1485 | RNAse R |  | 0.63 |
| GSU1486 | *tatC* |  | 0.56 |
| GSU1487 | Flavokinase |  | 0.6 |
| GSU1488 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.63 |
| GSU1489 | DUF2723 family transferase activity | | 0.58 |
| GSU1490 | *aroE* |  | 0.61 |
| GSU1491 | *pilB* |  | 0.59 |
| GSU1492 | *pilT* |  | 0.6 |
| GSU1493 | *pilC* |  | 0.55 |
| GSU1494 | *pilS* |  | 0.59 |
| GSU1495 | *pilR* |  | 0.58 |
| **GSU1496** | **e-pilin** |  | **0.49** |
| **GSU1497** | ***pilA*-C** |  | **0.45** |
| **GSU1498** | ***xapA*, Tetratricopeptide-like helical** | | **0.44** |
| **GSU1499** | ***xapB*, ABC-2 family transporter protein** | | **0.49** |
| **GSU1500** | **pili subunit family** |  | **0.51** |
| **GSU1501** | ***xapD*, ABC transporter, ATP-binding protein** | | **0.49** |
| GSU1502 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.54 |
| GSU1503 | *xapF*, glycosyl transferase, group 2 family protein | | 0.56 |
| GSU1504 | *xapG*, ABC-type polysaccharide/polyol phosphate export permease | | 0.56 |
| **GSU1505** | ***xapH*, ABC-type polysaccharide/polyol phosphate transport system, ATPase component** | | **0.53** |
| GSU1506 | *xapI*, methyltransferase, FkbM family | | 0.54 |
| **GSU1507** | ***xapJ*, UDP-Glycosyltransferase/glycogen phosphorylase** | | **0.5** |
| **GSU1508** | **Glycosyltransferase WbsX** | | **0.39** |
| **GSU1509** | **glycosyl transferase, group 2 family protein** | | **0.38** |
| **GSU1510** | **glycosyl transferase, group 2 family protein** | | **0.46** |
| **GSU1511** | **glycosyl transferase, group 1 family protein** | | **0.42** |
| GSU1512 | UDP-galactopyranose mutase | | 0.58 |
| **GSU1513** | **S-adenosyl-L-methionine-dependent methyltransferases** | | **0.51** |
| GSU1514 | ADP-heptose--lipooligosaccharide heptosyltransferase II | | 0.6 |
| GSU2019 | biotin carboxylase |  | 0.57 |
| GSU2020 | biotin carboxyl carrier protein | | 0.6 |
| GSU2021 | xaa-pro dipeptidase |  | 0.6 |
| GSU2022 | *aroQ* |  | 0.59 |
| GSU2023 | Roadblock/LC7 domain | | 0.6 |
| GSU2024 | TPR repeat |  | 0.58 |
| GSU2025 | *aroB* |  | 0.61 |
| GSU2026 | *aroK* |  | 0.61 |
| GSU2027 | *aroC* |  | 0.61 |
| GSU2028 | *pilQ* |  | 0.59 |
| GSU2029 | *pilP* |  | 0.58 |
| GSU2030 | *pilO* |  | 0.54 |
| **GSU2031** | ***pilN*** |  | **0.53** |
| GSU2032 | *pilM* |  | 0.56 |
| **GSU\_RF0082** | **GEMM riboswitch** |  | **0.52** |
| **GSU2033** | **putative horizontal transfer** | **Lambda repressor-like, DNA-binding domain** | **0.45** |
| GSU2036 | *pilV* |  | 0.56 |
| GSU2037 | *fimT* |  | 0.55 |
| GSU2038 | *pilY1* |  | 0.59 |
| GSU2043 | *pilD* |  | 0.59 |

B. Pilin gene clusters found in the *Pelobacter carbinolicus* genome. Two different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. This Desulfuromondales species has 2 long type IVa pilin genes. Genes from the xap operon and other glycosyl transferase genes are not present in the *pilA* gene cluster. The overall GC content of *P.carbinolicus* is 55.11%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Nine out of 50 genes (18%) in pilin gene clusters have deviant GC values; these include *pilQ, pilO, pilN, pilM, pilD, pilI*, and *pilC*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Pcar\_0841 | putative horizontal gene transfer protein | Retron-type reverse transcriptase-like | 0.59 |
| Pcar\_0863 | *pihD*, minor pilin protein |  | 0.59 |
| Pcar\_0865 | *pihP*, minor pilin protein |  | 0.58 |
| **Pcar\_0866** | **pihQ, minor pilin protein** |  | **0.64** |
| Pcar\_0867 | *pilN* |  | 0.6 |
| Pcar\_0868 | *pilO* |  | 0.55 |
| Pcar\_0869 | *pihK*, minor pilin protein |  | 0.51 |
| Pcar\_0870 | *pihL*, minor pilin protein |  | 0.59 |
| Pcar\_0871 | *pihM*, minor pilin protein |  | 0.62 |
| Pcar\_0872 | *pilB* |  | 0.6 |
| Pcar\_0873 | *pilC* |  | 0.59 |
| Pcar\_0876 | *pihA*, minor pilin protein |  | 0.55 |
| Pcar\_0877 | *pihH*, minor pilin protein |  | 0.57 |
| Pcar\_2121 | putative horizontal gene transfer protein | Phage\_integrase | 0.56 |
| Pcar\_2122 | hypothetical protein |  | 0.49 |
| Pcar\_2123 | putative horizontal gene transfer protein | Fic family protein | 0.58 |
| **Pcar\_2124** | **putative horizontal gene transfer protein** | **Transposase IS3/IS911family** | **0.44** |
| Pcar\_R0047 | tRNA-Leu-TAA |  | 0.62 |
| Pcar\_2125 | Chorismate dehydratase | | 0.54 |
| Pcar\_2126 | outer membrane efflux protein | | 0.56 |
| Pcar\_2127 | biotin carboxylase |  | 0.54 |
| Pcar\_2128 | biotin carboxyl carrier protein | | 0.56 |
| Pcar\_2129 | xaa-pro dipeptidase |  | 0.56 |
| Pcar\_2130 | Roadblock/LC7 domain | | 0.49 |
| Pcar\_2131 | Tetratricopeptide repeat | | 0.55 |
| Pcar\_2132 | *aroB* |  | 0.5 |
| Pcar\_2133 | *aroC* |  | 0.56 |
| **Pcar\_2134** | ***pilQ*** |  | **0.47** |
| Pcar\_2135 | *pilP* |  | 0.48 |
| **Pcar\_2136** | ***pilO*** |  | **0.43** |
| **Pcar\_2137** | ***pilN*** |  | **0.44** |
| **Pcar\_2138** | ***pilM*** |  | **0.44** |
| **Pcar\_2139** | ***pilD*** |  | **0.46** |
| **Pcar\_2141** | **pilI** |  | **0.45** |
| Pcar\_2142 | *xapD*, probable ABC transporter ATP-binding protein | | 0.5 |
| Pcar\_2143 | *pilA*-2 |  | 0.5 |
| Pcar\_2144 | *pilA*-1 |  | 0.53 |
| Pcar\_2145 | *pilR* |  | 0.49 |
| Pcar\_2146 | *pilS* |  | 0.48 |
| **Pcar\_2147** | ***pilC*** |  | **0.47** |
| Pcar\_2148 | *pilT* |  | 0.54 |
| Pcar\_2149 | *pilB* |  | 0.54 |
| Pcar\_2150 | *aroE* |  | 0.56 |
| Pcar\_2151 | Flavokinase |  | 0.52 |
| Pcar\_2152 | RNAse R |  | 0.55 |
| Pcar\_2154 | *pilE* |  | 0.49 |
| Pcar\_2155 | *pilY1* |  | 0.5 |
| Pcar\_2156 | *pilX* |  | 0.54 |
| Pcar\_2157 | *pilW* |  | 0.51 |
| Pcar\_2158 | *pilV* |  | 0.51 |
| Pcar\_2159 | *fimT* |  | 0.52 |

C. Pilin gene clusters found in the *Geobacter metallireducens* genome. Three different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. At least 3 different glycosyl transferase genes and xap operon genes are located in the vicinity of the e-pilin gene. The overall GC content of *G. metallireducens* is 59.49%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twelve out of 64 (19%) of these genes have deviant GC values, including *e-pilin, pilA-C, xapA, xapB, xapD, xapE, xapG*, and *xapH*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | | GC content |
| Gmet\_0734 | *pilV* |  | | 0.55 |
| Gmet\_0735 | *pilW* |  | | 0.57 |
| Gmet\_0736 | *pilX* |  | | 0.59 |
| Gmet\_0737 | *pilY1* |  | | 0.57 |
| Gmet\_0738 | protein of unknown function DUF294, nucleotidyltransferase putative | | | 0.61 |
| Gmet\_0739 | transporter, SSS family | | | 0.63 |
| Gmet\_0740 | Uncharacterized membrane protein, DUF485 family | | | 0.55 |
| Gmet\_0741 | transcriptional regulator, IclR family | | | 0.61 |
| Gmet\_0742 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | | 0.59 |
| Gmet\_0743 | Transcriptional and/or translational regulatory protein YebC/TACO1 | | | 0.6 |
| Gmet\_0958 | putative horizontal gene transfer protein | | IS111A transposase | 0.53 |
| Gmet\_0959 | *pilD* | |  | 0.63 |
| Gmet\_0960 | *pilS* | |  | 0.64 |
| Gmet\_0961 | *pilR* | |  | 0.64 |
| Gmet\_0962 | *pilE* | |  | 0.57 |
| Gmet\_0963 | *fimU* | |  | 0.55 |
| Gmet\_0964 | *pilV* | |  | 0.52 |
| Gmet\_0965 | *pilW* | |  | 0.57 |
| Gmet\_0966 | *pilX* | |  | 0.59 |
| Gmet\_0967 | *pilY1* | |  | 0.57 |
| Gmet\_0968 | hypothetical protein | |  | 0.53 |
| **Gmet\_0969** | **hypothetical protein** | |  | **0.51** |
| Gmet\_RF0069 | GEMM\_riboswitch | |  | 0.54 |
| Gmet\_0970 | putative horizontal transfer gene protein | | Lambda repressor-like | 0.52 |
| Gmet\_0971 | *pilM* | |  | 0.58 |
| Gmet\_0972 | *pilN* | |  | 0.58 |
| Gmet\_0973 | *pilO* | |  | 0.54 |
| Gmet\_0974 | *pilP* | |  | 0.58 |
| Gmet\_0975 | *pilQ* | |  | 0.57 |
| Gmet\_0976 | *aroC* | |  | 0.65 |
| Gmet\_0977 | *aroK* | |  | 0.6 |
| Gmet\_0978 | *aroB* | |  | 0.63 |
| Gmet\_0979 | Tetratricopeptide repeat | | | 0.59 |
| Gmet\_0980 | Roadblock/LC7 domain | | | 0.6 |
| Gmet\_0981 | *aroQ* |  | | 0.57 |
| Gmet\_0982 | Xaa-Pro aminopeptidase | | | 0.6 |
| Gmet\_0983 | biotin carboxyl carrier protein | | | 0.61 |
| Gmet\_0984 | biotin carboxylase |  | | 0.6 |
|  |  |  | |  |
|  |  |  | |  |
| Gmet\_1386 | RNAse R |  | | 0.65 |
| Gmet\_1387 | *tatC* |  | | 0.6 |
| Gmet\_1388 | flavokinase |  | | 0.61 |
| Gmet\_1389 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | | 0.63 |
| Gmet\_1391 | DUF2723 domain protein with transferase activity | | | 0.6 |
| Gmet\_1392 | *aroE* |  | | 0.63 |
| Gmet\_1393 | *pilB* |  | | 0.6 |
| Gmet\_1394 | *pilT* |  | | 0.62 |
| Gmet\_1395 | *pilC* |  | | 0.6 |
| Gmet\_1396 | *pilS* |  | | 0.57 |
| Gmet\_1397 | *pilR* |  | | 0.61 |
| Gmet\_1398 | putative horizontal gene transfer protein | IS204/IS1001/IS1096/IS1165 transposase | | 0.54 |
| **Gmet\_1399** | **e-pilin** |  | | **0.45** |
| **Gmet\_1400** | ***pilA*-C** |  | | **0.46** |
| **Gmet\_1401** | ***xapB*, ABC-2 family transporter protein** | | | **0.48** |
| **Gmet\_1402** | **Type II secretion system protein G** | | | **0.49** |
| **Gmet\_1403** | ***xapD*, ABC transporter-related protein** | | | **0.48** |
| **Gmet\_1404** | ***xapA*, Tetratricopeptide-like helical** | | | **0.43** |
| **Gmet\_1405** | ***xapE*, UbiA prenyltransferase family** | | | **0.48** |
| **Gmet\_1406** | ***xapG*, lipopolysaccharide transport system permease protein** | | | **0.39** |
| **Gmet\_1407** | ***xapH*, ABC-type polysaccharide/polyol phosphate transport system, ATPase component** | | | **0.44** |
| **Gmet\_1408** | **Glycosyl transferase, group 1** | | | **0.46** |
| **Gmet\_1409** | **hypothetical protein** |  | | **0.41** |
| Gmet\_1410 | *xapJ*, Glycosyl transferase, family 9 | | | 0.52 |

D. Pilin gene clusters found in the *Pelobacter propionicus* genome. Three different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. While some xap genes were detected in the e-pilin gene cluster, no glycosyl transferase genes were present. The overall GC content of *P. propionicus* is 58.48%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Twelve out of 48 (25%) of these genes have deviant GC values, including *pilA-C, xapA, pilX, pilM, pilO*, and *pilP*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ppro\_0982 | *pilD* |  | 0.58 |
| Ppro\_0983 | *pilS* |  | 0.61 |
| Ppro\_0984 | *pilR* |  | 0.61 |
| Ppro\_0985 | thiol:disulfide interchange protein DsbC | | 0.57 |
| Ppro\_0986 | hypothetical protein |  | 0.55 |
| Ppro\_0987 | *pilY1* |  | 0.56 |
| **Ppro\_0988** | ***fimT*** |  | **0.49** |
| Ppro\_0989 | *pilV* |  | 0.53 |
| Ppro\_0990 | *pilW* |  | 0.54 |
| **Ppro\_0991** | ***pilX*** |  | **0.47** |
| **Ppro\_0992** | ***pilM*** |  | **0.45** |
| **Ppro\_0993** | ***pilN*** |  | **0.45** |
| **Ppro\_0994** | ***pilO*** |  | **0.42** |
| **Ppro\_0995** | ***pilP*** |  | **0.45** |
| Ppro\_0996 | *pilQ* |  | 0.52 |
| Ppro\_0997 | *pilZ* |  | 0.52 |
| Ppro\_0998 | Highly conserved protein containing a thioredoxin domain | | 0.56 |
| Ppro\_0999 | Transcriptional regulator WYL domain | | 0.56 |
| Ppro\_RF0077 | GEMM\_RNA\_motif |  | 0.54 |
| Ppro\_1000 | helicase, putative |  | 0.53 |
| **Ppro\_1001** | **putative horizontal gene transfer protein** | **CRISPR-associated protein Cas1** | **0.37** |
| Ppro\_1649 | putative horizontal gene transfer protein | transposase, IS4 family | 0.56 |
| Ppro\_1650 | Protein of unknown function DUF2905 | | 0.61 |
| Ppro\_1651 | Predicted ATPase, Adenine nucleotide alpha hydrolases | | 0.63 |
| Ppro\_1652 | 3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)/GTP cyclohydrolase II | | 0.61 |
| Ppro\_1653 | hypothetical protein |  | 0.5 |
| Ppro\_1654 | enolase |  | 0.61 |
| Ppro\_1655 | *pilR* |  | 0.59 |
| Ppro\_1656 | e-pilin |  | 0.54 |
| **Ppro\_1657** | ***pilA*-C** |  | **0.42** |
| **Ppro\_1658** | ***xapA*, Tetratricopeptide-like helical** | | **0.44** |
| Ppro\_1659 | *xapB*, ABC-2 family transporter protein | | 0.58 |
| Ppro\_1660 | Tetratricopeptide-like helical | | 0.57 |
| Ppro\_1661 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.62 |
| Ppro\_1662 | methionyl-tRNA synthetase | | 0.62 |
| Ppro\_1663 | Cell fate regulator YaaT, PSP1 superfamily | | 0.64 |
| 16 genes |  |  |  |
| **Ppro\_1679** | ***pilZ*** |  | **0.5** |
| **Ppro\_2500** | **putative horizontal gene transfer protein** | **transposase, IS4 family** | **0.5** |
| 4 genes |  |  |  |
| Ppro\_RF0091 | GEMM\_RNA\_motif |  | 0.56 |
| 6 genes |  |  |  |
| Ppro\_2511 | *pilS* |  | 0.62 |
| Ppro\_2512 | *pilC* |  | 0.59 |
| Ppro\_2513 | *pilT* |  | 0.62 |
| Ppro\_2514 | *pilB* |  | 0.6 |
| Ppro\_2515 | DUF2723 |  | 0.63 |
| Ppro\_2516 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.61 |
| Ppro\_2517 | Flavokinase |  | 0.62 |
| **Ppro\_2518** | **ATP-dependent DNA helicase RecG** | | **0.67** |
| Ppro\_2519 | *pilZ* |  | 0.63 |

E. Pilin gene clusters found in the *Geobacter uraniireducens* genome. Two different gene clusters were identified and each is highlighted in a different color. Fourteen genes coding for horizontal gene transfer proteins were detected in these gene clusters. *G. uraniireducens* has a long type IVa *pilA* gene. Only two homologs from the xap operon (*xapB* and *xapD*) were detected in the *pilA* gene cluster, none of which included glycosyl transferases. The overall GC content of G. uraniireducens is 54.24%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Fifteen out of 80 (19%) of the pilin genes had deviant GC values, including *fimT, pilV, pilM, pilN, pilO*, and *pilP*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Gura\_1800 | *pilD* |  | 0.52 |
| Gura\_1801 | *pilS* |  | 0.54 |
| Gura\_1802 | *pilR* |  | 0.52 |
| Gura\_1803 | Thiol:disulfide interchange protein DsbC | | 0.52 |
| Gura\_1804 | *pilY1* |  | 0.52 |
| **Gura\_1805** | ***fimT*** |  | **0.46** |
| **Gura\_1806** | ***pilV*** |  | **0.42** |
| Gura\_1807 | *pilW* |  | 0.49 |
| Gura\_1808 | *pilX* |  | 0.45 |
| Gura\_RF0078 | GEMM\_RNA\_motif |  | 0.5 |
| **Gura\_1809** | **putative horizontal gene transfer protein** | **Lambda repressor-like, DNA-binding domain** | **0.44** |
| **Gura\_1810** | ***pilM*** |  | **0.43** |
| **Gura\_1811** | ***pilN*** |  | **0.4** |
| **Gura\_1812** | ***pilO*** |  | **0.38** |
| **Gura\_1813** | ***pilP*** |  | **0.42** |
| Gura\_1814 | *pilQ* |  | 0.49 |
| **Gura\_1815** | **hypothetical protein** |  | **0.37** |
| Gura\_1816 | Ig family protein | | 0.5 |
| **Gura\_1817** | **Thiol:disulfide interchange protein DsbC** | | **0.38** |
| Gura\_1818 | *aroC* |  | 0.55 |
| Gura\_1819 | *aroK* |  | 0.5 |
| Gura\_1820 | *aroB* |  | 0.52 |
| Gura\_1821 | Tetratricopeptide TPR\_2 repeat protein | | 0.49 |
| Gura\_1822 | Roadblock/LC7 domain | | 0.5 |
| Gura\_1823 | *aroQ* |  | 0.48 |
| Gura\_1824 | Xaa-Pro aminopeptidase | | 0.52 |
| Gura\_1825 | biotin carboxyl carrier protein | | 0.5 |
| Gura\_1826 | biotin carboxylase |  | 0.51 |
| Gura\_2666 | Protein of unknown function DUF2950 | | 0.58 |
| **Gura\_2667** | **Protein of unknown function DUF3300** | | **0.66** |
| Gura\_2668 | putative exported protein | | 0.58 |
| Gura\_2669 | Protein of unknown function DUF3313 | | 0.57 |
| Gura\_2670 | Antibiotic biosynthesis monooxygenase | | 0.54 |
| Gura\_2671 | transcriptional regulator, NifA subfamily, Fis Family | | 0.57 |
| Gura\_2672 | Lipid-binding SYLF domain | | 0.53 |
| **Gura\_2673** | **hypothetical protein** |  | **0.45** |
| Gura\_2674 | *xapB*, ABC-2 family transporter protein | | 0.48 |
| Gura\_2675 | *xapD*, ABC transporter related | | 0.53 |
| Gura\_2676 | putative horizontal gene transfer protein | transposase, IS4 family | 0.47 |
| Gura\_2677 | *pilA* |  | 0.49 |
| Gura\_2678 | *pilR* |  | 0.56 |
| Gura\_2679 | *pilS* |  | 0.57 |
| Gura\_2680 | *pilC* |  | 0.54 |
| Gura\_2681 | *pilT* |  | 0.52 |
| Gura\_2682 | *pilB* |  | 0.5 |
| Gura\_2683 | *aroE* |  | 0.51 |
| Gura\_2684 | DUF2723 |  | 0.51 |
| Gura\_2685 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.52 |
| Gura\_2686 | Flavokinase |  | 0.5 |
| Gura\_2687 | *tatC* |  | 0.52 |
| Gura\_2697 | *pilR* |  | 0.55 |
| Gura\_2698 | *pilS* |  | 0.53 |
| Gura\_2699 | RNAse R |  | 0.58 |
| Gura\_2700 | Soluble lytic murein transglycosylase | | 0.56 |
| **Gura\_2701** | **ABC transporter related** | | **0.62** |
| Gura\_2702 | nucleotidyltransferase | | 0.58 |
| Gura\_2703 | transcriptional regulator, MarR family | | 0.61 |
| Gura\_2704 | outer membrane efflux protein | | 0.56 |
| Gura\_2705 | secretion protein HlyD family protein | | 0.59 |
| Gura\_2706 | drug resistance transporter, EmrB/QacA subfamily | | 0.59 |
| Gura\_2707 | multi-sensor hybrid histidine kinase | | 0.57 |
| Gura\_2708 | putative two component, sigma-54 specific, transcriptional regulator, Fis family | | 0.6 |
| Gura\_2709 | hypothetical protein |  | 0.53 |
| Gura\_2710 | CheY-like superfamily | | 0.54 |
| Gura\_2711 | hypothetical protein |  | 0.6 |
| Gura\_2712 | Cytochrome c family protein | | 0.6 |
| Gura\_2713 | cytochrome B561 |  | 0.59 |
| **Gura\_2714** | **hypothetical protein** |  | **0.62** |
| Gura\_2715 | putative horizontal gene transfer protein | Programmed cell death antitoxin YdcD | 0.57 |
| Gura\_2716 | putative horizontal gene transfer protein | transcriptional modulator of MazE/toxin, MazF | 0.59 |
| Gura\_2717 | putative horizontal gene transfer protein | Prevent host death protein, Phd antitoxin # D | 0.56 |
| Gura\_2718 | putative horizontal gene transfer protein | addiction module toxin, RelE/StbE family | 0.55 |
| **Gura\_2719** | **putative horizontal gene transfer protein** | **CRISPR-associated protein Cas1]** | **0.63** |
| Gura\_2720 | putative horizontal gene transfer protein | Transposase IS200-like | 0.57 |
| Gura\_2721 | putative horizontal gene transfer protein | CRISPR-associated protein, Cas2 family | 0.49 |
| Gura\_2722 | putative horizontal gene transfer protein | Very-short-patch-repair endonuclease | 0.48 |
| Gura\_2723 | putative horizontal gene transfer protein | CRISPR-associated exonuclease, Cas4 family | 0.58 |
| Gura\_2724 | hypothetical protein |  | 0.58 |
| **Gura\_2725** | **putative horizontal gene transfer protein** | **CRISPR-associated helicase Cas3** | **0.43** |
| Gura\_2726 | putative horizontal gene transfer protein | putative addiction module component, TIGR02574 family | 0.5 |
| Gura\_2727 | putative horizontal gene transfer protein | Death on curing protein, Doc toxin | 0.51 |

F. Pilin gene clusters found in the *Geobacter lovleyi* genome. Two different gene clusters were identified and each is highlighted in a different color. Three genes coding for horizontal gene transfer proteins were detected in these gene clusters. Genes from the xap operon and genes coding for additional glycosyl transferase proteins are present. The overall GC content of *G. lovleyi* is 54.74%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Eighteen out of 39 (46%) of the pilin genes have deviant GC values, including *e-pilin, pilA-C, pilX, xapA, xapB, xapI, pilY1, pilV, pilX, pilM, pilN, pilO, pilP, pilQ*, and *fimT*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| **Glov\_1639** | **putative horizontal gene transfer protein** | **Lambda repressor-like, DNA-binding domain** | **0.47** |
| **Glov\_1640** | ***pilM*** |  | **0.47** |
| **Glov\_1641** | ***pilN*** |  | **0.42** |
| **Glov\_1642** | ***pilO*** |  | **0.42** |
| **Glov\_1643** | ***pilP*** |  | **0.47** |
| **Glov\_1644** | ***pilQ*** |  | **0.47** |
| Glov\_1645 | PS51257 family protein | | 0.45 |
| Glov\_1646 | Aldolase |  | 0.46 |
| Glov\_1647 | chorismate mutase |  | 0.49 |
| Glov\_1648 | L-aspartate oxidase |  | 0.51 |
| Glov\_1649 | Flavokinase |  | 0.51 |
| Glov\_1650 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.55 |
| Glov\_1651 | DUF2723 |  | 0.53 |
| Glov\_1652 | *aroE* |  | 0.54 |
| Glov\_1653 | *pilB* |  | 0.52 |
| Glov\_1654 | *pilT* |  | 0.52 |
| Glov\_1655 | *pilC* |  | 0.5 |
| Glov\_1656 | *pilS* |  | 0.52 |
| Glov\_1657 | *pilR* |  | 0.53 |
| Glov\_2089 | *xapD*, ABC transporter related | | 0.49 |
| **Glov\_2090** | **hypothetical protein** |  | **0.46** |
| **Glov\_2091** | ***xapB*, ABC-2 family transporter protein** | | **0.47** |
| **Glov\_2092** | ***xapI*, Methyltransferase type 11** | | **0.4** |
| **Glov\_2093** | **Glycosyl transferase family 41** | | **0.4** |
| **Glov\_2094** | ***xapA*, Tetratricopeptide-like helical** | | **0.36** |
| **Glov\_2095** | ***pilA*-C** |  | **0.43** |
| **Glov\_2096** | **e-pilin** |  | **0.47** |
| **Glov\_2151** | ***pilX*** |  | **0.45** |
| **Glov\_2152** | ***pilW*** |  | **0.46** |
| **Glov\_2153** | ***pilV*** |  | **0.41** |
| **Glov\_2154** | ***fimT*** |  | **0.41** |
| **Glov\_2155** | ***pilY1*** |  | **0.47** |
| Glov\_2156 | PS51257 membrane lipoprotein lipid attachment site | | 0.49 |
| Glov\_2157 | thiol:disulfide interchange protein DsbC | | 0.53 |
| Glov\_2158 | *pilR* |  | 0.56 |
| Glov\_2159 | *pilS* |  | 0.57 |
| Glov\_2160 | *pilD* |  | 0.57 |
| 19 genes |  |  |  |
| Glov\_2179 | putative horizontal gene transfer protein | Integrase catalytic region | 0.52 |
| Glov\_2180 | putative horizontal gene transfer protein | IstB domain protein ATP-binding protein | 0.51 |

G. Pilin gene clusters found in the *Geobacter bemidjiensis* genome. Two different gene clusters were identified and each is highlighted in a different color. Only one gene coding for a horizontal gene transfer protein was detected in these gene clusters. Genes from the *xap* operon and additional glycosyl transferase genes were detected in the e-pilin gene cluster. The overall GC content of *G. bemidjiensis* is 60.27%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Three out of 61 (5%) genes had deviant GC values.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Gbem\_1532 | *pilD* |  | 0.58 |
| Gbem\_1533 | *pilS* |  | 0.63 |
| Gbem\_1534 | *pilR* |  | 0.64 |
| Gbem\_1535 | Disulphide bond isomerase, DsbC | | 0.61 |
| Gbem\_1536 | *pilY1* |  | 0.63 |
| Gbem\_1537 | *fimU* |  | 0.61 |
| Gbem\_1538 | *pilV* |  | 0.58 |
| Gbem\_1539 | *pilW* |  | 0.61 |
| Gbem\_1540 | *pilX* |  | 0.59 |
| Gbem\_1541 | *fimU* |  | 0.56 |
| Gbem\_1542 | *pilV* |  | 0.6 |
| Gbem\_1543 | *pilW* |  | 0.59 |
| Gbem\_1544 | *pilX* |  | 0.62 |
| Gbem\_1545 | putative horizontal transfer gene protein | Lambda repressor-like, DNA-binding domain | 0.55 |
| Gbem\_1546 | *pilM* |  | 0.59 |
| Gbem\_1547 | *pilN* |  | 0.6 |
| Gbem\_1548 | *pilO* |  | 0.56 |
| Gbem\_1549 | *pilP* |  | 0.63 |
| Gbem\_1550 | *pilQ* |  | 0.62 |
| **Gbem\_1551** | **PS51257 membrane lipoprotein lipid attachment** | | **0.49** |
| Gbem\_1552 | Ig-family protein | | 0.61 |
| **Gbem\_1553** | **Disulphide bond isomerase** | | **0.51** |
| Gbem\_1554 | *aroC* |  | 0.65 |
| Gbem\_1555 | *aroK* |  | 0.61 |
| Gbem\_1556 | *aroB* |  | 0.63 |
| Gbem\_1557 | Tetratricopeptide TPR\_2 repeat protein | | 0.63 |
| Gbem\_1558 | Roadblock/LC7 domain | | 0.59 |
| Gbem\_1559 | *aroQ* |  | 0.61 |
| Gbem\_1560 | Xaa-Pro aminopeptidase | | 0.63 |
| Gbem\_1561 | biotin carboxyl carrier protein | | 0.59 |
| Gbem\_1562 | biotin carboxylase |  | 0.61 |
| Gbem\_2573 | *xapF*, glycosyl transferase family 2 | | 0.58 |
| Gbem\_2574 | glycosyl transferase family 2 | | 0.58 |
| Gbem\_2575 | glycosyl transferase group 1 | | 0.55 |
| Gbem\_2576 | acetyltransferase |  | 0.57 |
| Gbem\_2577 | DegT/DnrJ/EryC1/StrS aminotransferase | | 0.59 |
| **Gbem\_2578** | **hypothetical protein** |  | **0.52** |
| Gbem\_2579 | methyltransferase type 12 | | 0.54 |
| Gbem\_2580 | *xapH*, ABC-type polysaccharide/polyol phosphate transport system, ATPase component | | 0.58 |
| Gbem\_2581 | *xapG*, ABC-type polysaccharide/polyol phosphate export permease | | 0.54 |
| Gbem\_2582 | glycosyl transferase family 2 | | 0.58 |
| Gbem\_2583 | glycosyl transferase family 2 | | 0.61 |
| Gbem\_2584 | *xapE*, UbiA prenyltransferase | | 0.59 |
| Gbem\_2585 | *xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase | | 0.6 |
| Gbem\_2586 | *xapD*, ABC transporter related protein | | 0.59 |
| Gbem\_2587 | Tetratricopeptide-like helical | | 0.57 |
| Gbem\_2588 | *xapB*, ABC-2 family transporter protein | | 0.56 |
| Gbem\_2589 | *pilA*-C |  | 0.6 |
| Gbem\_2590 | e-pilin |  | 0.53 |
| Gbem\_2591 | *pilR* |  | 0.63 |
| Gbem\_2592 | *pilS* |  | 0.61 |
| Gbem\_2593 | *pilC* |  | 0.61 |
| Gbem\_2594 | *pilT* |  | 0.61 |
| Gbem\_2595 | *pilB* |  | 0.61 |
| Gbem\_2596 | *aroE* |  | 0.67 |
| Gbem\_2597 | DUF2723 transferase activity | | 0.63 |
| Gbem\_2598 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.61 |
| Gbem\_2599 | Flavokinase |  | 0.64 |
| Gbem\_2600 | *tatC* |  | 0.58 |
| Gbem\_2601 | RNAse R |  | 0.65 |
| Gbem\_2602 | Soluble lytic murein transglycosylase | | 0.63 |

H. Pilin gene clusters found in the *Geobacter daltonii* genome. Two different gene clusters were identified and each is highlighted in a different color. Nine different genes coding for horizontal gene transfer proteins were detected in these gene clusters. *G. daltonii* does not have an e-pilin gene, rather it has a long type IVa *pilA* gene. No xap or glycosyl transferase genes were detected in the *pilA* gene cluster. The overall GC content of G. daltonii is 53.47%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Eleven out of 67 (16%) of the pilin genes had deviant GC values, including *pilS, pilQ, pilO, pilN*, and *pilM*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Geob\_3056 | biotin carboxylase |  | 0.49 |
| Geob\_3057 | biotin carboxyl carrier protein | | 0.49 |
| Geob\_3058 | Xaa-Pro aminopeptidase | | 0.49 |
| Geob\_3059 | *aroQ* |  | 0.47 |
| Geob\_3060 | Roadblock/LC7 domain | | 0.51 |
| Geob\_3061 | Tetratricopeptide domain protein | | 0.47 |
| Geob\_3062 | *aroB* |  | 0.48 |
| Geob\_3063 | *aroC* |  | 0.54 |
| Geob\_3064 | PS51257 Prokaryotic membrane lipoprotein lipid attachment | | 0.46 |
| Geob\_3065 | PS51257 Prokaryotic membrane lipoprotein lipid attachment | | 0.48 |
| **Geob\_3066** | ***pilQ*** |  | **0.44** |
| Geob\_3067 | *pilP* |  | 0.47 |
| **Geob\_3068** | ***pilO*** |  | **0.4** |
| **Geob\_3069** | ***pilN*** |  | **0.41** |
| **Geob\_3070** | ***pilM*** |  | **0.4** |
| **Geob\_3071** | **putative horizontal transfer gene protein** | **Lambda repressor-like, DNA-binding domain** | **0.41** |
| **Geob\_3072** | **hypothetical protein** |  | **0.39** |
| **Geob\_3073** | ***pilX*** |  | **0.45** |
| Geob\_3074 | *pilW* |  | 0.46 |
| **Geob\_3075** | ***pilV*** |  | **0.45** |
| Geob\_3076 | *fimT* |  | 0.46 |
| Geob\_3077 | *pilY1* |  | 0.5 |
| **Geob\_3078** | **pilL** |  | **0.41** |
| Geob\_3079 | *pilR* |  | 0.47 |
| Geob\_3080 | *pilS* |  | 0.49 |
| Geob\_3081 | *pilD* |  | 0.5 |
| Geob\_3361 | phenylalanyl-tRNA synthetase, alpha subunit | | 0.53 |
| Geob\_3362 | LSU ribosomal protein L20P | | 0.53 |
| Geob\_3363 | LSU ribosomal protein L35P | | 0.48 |
| Geob\_3364 | bacterial translation initiation factor 3 (bIF-3) | | 0.49 |
| Geob\_3365 | threonyl-tRNA synthetase | | 0.53 |
| **Geob\_R0048** | **tRNA-Val** |  | **0.66** |
| Geob\_3366 | hypothetical protein |  | 0.46 |
| Geob\_3367 | ABC-type transport system, putative ATPase subunit | | 0.47 |
| Geob\_3368 | *xapD*, ABC transporter related | | 0.52 |
| Geob\_3369 | *pilA* |  | 0.54 |
| Geob\_3370 | *pilR* |  | 0.49 |
| **Geob\_3371** | ***pilS*** |  | **0.43** |
| Geob\_3372 | *pilC* |  | 0.47 |
| Geob\_3373 | *pilT* |  | 0.51 |
| Geob\_3374 | *pilB* |  | 0.51 |
| Geob\_3375 | *aroE* |  | 0.51 |
| Geob\_3376 | DUF2723 |  | 0.51 |
| Geob\_3377 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.51 |
| Geob\_3378 | Flavokinase |  | 0.51 |
| Geob\_3379 | *tatC* |  | 0.51 |
| Geob\_3380 | response regulator receiver modulated CheB methylesterase | | 0.55 |
| Geob\_3381 | MCP methyltransferase, CheR-type | | 0.5 |
| Geob\_3382 | PBS lyase HEAT domain protein repeat-containing protein | | 0.56 |
| Geob\_3383 | MCP methyltransferase, CheR-type | | 0.51 |
| Geob\_3384 | methyl-accepting chemotaxis sensory transducer | | 0.57 |
| Geob\_3385 | CheW protein |  | 0.56 |
| Geob\_3386 | CheA signal transduction histidine kinase | | 0.55 |
| Geob\_3387 | response regulator CheY | | 0.51 |
| Geob\_3388 | response regulator receiver protein | | 0.52 |
| Geob\_3389 | two component, sigma54 specific, transcriptional regulator, Fis family | | 0.56 |
| Geob\_3390 | PAS/PAC sensor signal transduction histidine kinase | | 0.52 |
| Geob\_3391 | RNAse R |  | 0.57 |
| Geob\_3392 | Soluble lytic murein transglycosylase | | 0.56 |
| 16 genes |  |  |  |
| Geob\_3409 | putative horizontal transfer gene protein | CRISPR-associated protein, Cas2 family | 0.51 |
| Geob\_3410 | putative horizontal transfer gene protein | CRISPR-associated protein, Cas1 family | 0.57 |
| Geob\_3411 | putative horizontal transfer gene protein | CRISPR-associated exonuclease, Cas4 family | 0.57 |
| Geob\_3412 | putative horizontal transfer gene protein | Virulence protein RhuM-like | 0.54 |
| Geob\_3413 | putative horizontal transfer gene protein | CRISPR-associated protein, Csd2 family | 0.53 |
| Geob\_3414 | putative horizontal transfer gene protein | CRISPR-associated protein, Csd1 family | 0.52 |
| Geob\_3415 | putative horizontal transfer gene protein | CRISPR-associated protein, Cas5d family | 0.52 |
| Geob\_3416 | putative horizontal transfer gene protein | CRISPR-associated helicase, Cas3 family | 0.52 |

I. Pilin gene clusters found in the Geobacter sp. M21 genome. Two different gene clusters were identified and each is highlighted in a different color. Two different genes coding for horizontal gene transfer proteins were detected in these gene clusters. Numerous xap and glycosyl transferase genes are found in the e-pilin gene cluster. The overall GC content of strain M21 is 60.47%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Two out of 65 (3%) genes had deviant GC values.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| **GM21\_1602** | **putative horizontal gene transfer protein** | **transposase IS116/IS110/IS902** | **0.51** |
| GM21\_1603 | PS51257 membrane lipoprotein lipid attachment | | 0.55 |
| GM21\_1604 | drug resistance transporter, EmrB/QacA subfamily | | 0.61 |
| GM21\_1605 | secretion protein HlyD family protein | | 0.65 |
| GM21\_1606 | Outer membrane protein TolC | | 0.64 |
| 17 genes |  |  |  |
| GM21\_1624 | Soluble lytic murein transglycosylase | | 0.63 |
| GM21\_1625 | RNAse R |  | 0.64 |
| GM21\_1626 | *tatC* |  | 0.57 |
| GM21\_1627 | Flavokinase |  | 0.65 |
| GM21\_1628 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.63 |
| GM21\_1629 | DUF2723 |  | 0.63 |
| GM21\_1630 | *aroE* |  | 0.67 |
| GM21\_1631 | *pilB* |  | 0.61 |
| GM21\_1632 | *pilT* |  | 0.62 |
| GM21\_1633 | *pilC* |  | 0.61 |
| GM21\_1634 | *pilS* |  | 0.62 |
| GM21\_1635 | *pilR* |  | 0.63 |
| GM21\_1636 | e-pilin |  | 0.55 |
| GM21\_1637 | *pilA*-C |  | 0.58 |
| GM21\_1638 | *xapB*, ABC-2 family transporter protein | | 0.56 |
| GM21\_1639 | Tetratricopeptide-like helical | | 0.56 |
| GM21\_1640 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.59 |
| GM21\_1641 | *xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase | | 0.61 |
| GM21\_1642 | *xapE*, UbiA prenyltransferase | | 0.59 |
| GM21\_1643 | glycosyl transferase family 2 | | 0.6 |
| GM21\_1644 | glycosyl transferase family 3 | | 0.65 |
| GM21\_1645 | *xapF*, glycosyl transferase family 2 | | 0.64 |
| GM21\_1646 | *xapG*, ABC-2 type transporter | | 0.6 |
| GM21\_1647 | *xapH*, ABC transporter related | | 0.56 |
| GM21\_1648 | Radical SAM superfamily enzyme YgiQ, UPF0313 family | | 0.58 |
| GM21\_1649 | glycosyl transferase family 2 | | 0.62 |
| GM21\_1650 | glycosyl transferase family 2 | | 0.61 |
| GM21\_1651 | *xapF*, glycosyl transferase family 2 | | 0.61 |
| GM21\_1652 | Methyltransferase type 11 | | 0.62 |
| GM21\_2654 | biotin carboxylase |  | 0.61 |
| GM21\_2655 | biotin carboxyl carrier protein | | 0.61 |
| GM21\_2656 | Xaa-Pro aminopeptidase | | 0.64 |
| GM21\_2657 | *aroQ* |  | 0.63 |
| GM21\_2658 | Roadblock/LC7 domain | | 0.57 |
| GM21\_2659 | Tetratricopeptide TPR\_2 repeat protein | | 0.63 |
| GM21\_2660 | *aroB* |  | 0.63 |
| GM21\_2661 | *aroK* |  | 0.63 |
| GM21\_2662 | *aroC* |  | 0.66 |
| GM21\_2663 | PS51257 membrane lipoprotein lipid attachment | | 0.56 |
| **GM21\_2664** | **PS51257 membrane lipoprotein lipid attachment** | | **0.52** |
| GM21\_2665 | *pilQ* |  | 0.62 |
| GM21\_2666 | *pilP* |  | 0.63 |
| GM21\_2667 | *pilO* |  | 0.57 |
| GM21\_2668 | *pilN* |  | 0.6 |
| GM21\_2669 | *pilM* |  | 0.59 |
| GM21\_2670 | putative horizontal transfer gene protein | Lambda repressor-like, DNA-binding domain | 0.54 |
| GM21\_2671 | *pilX* |  | 0.64 |
| GM21\_2672 | *pilW* |  | 0.59 |
| GM21\_2673 | *pilV* |  | 0.57 |
| GM21\_2674 | *fimT* |  | 0.56 |
| GM21\_2675 | hypothetical protein |  | 0.56 |
| GM21\_2676 | prepilin-type N-terminal cleavage/methylation domain | | 0.57 |
| GM21\_2677 | *pilV* |  | 0.53 |
| GM21\_2678 | *fimT* |  | 0.56 |
| GM21\_2679 | *pilY1* |  | 0.6 |
| GM21\_2680 | hypothetical protein |  | 0.61 |
| GM21\_2681 | Disulphide bond isomerase, DsbC | | 0.61 |
| GM21\_2682 | *pilR* |  | 0.64 |
| GM21\_2683 | *pilS* |  | 0.64 |
| GM21\_2684 | *pilD* |  | 0.59 |

J. Pilin gene clusters found in the Geobacter sp. M18 genome. Two different gene clusters were identified and each is highlighted in a different color. One gene coding for a horizontal gene transfer protein was detected in these gene clusters. Numerous xap and glycosyl transferase genes were found in the e-pilin gene cluster. The overall GC content of strain M18 is 61.18%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Three out of 65 (5%) of the genes have deviant GC values.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal Transfer Gene | GC content |
| GM18\_1367 | *pilD* |  | 0.61 |
| GM18\_1368 | *pilS* |  | 0.61 |
| GM18\_1369 | *pilR* |  | 0.64 |
| GM18\_1370 | Disulphide bond isomerase, DsbC | | 0.6 |
| GM18\_1371 | *pilY1* |  | 0.62 |
| GM18\_1372 | *fimU* |  | 0.58 |
| GM18\_1373 | *pilV* |  | 0.59 |
| GM18\_1374 | *pilW* |  | 0.63 |
| GM18\_1375 | *pilX* |  | 0.62 |
| GM18\_1376 | *fimT* |  | 0.57 |
| GM18\_1377 | *pilV* |  | 0.59 |
| GM18\_1378 | prepilin-type N-terminal cleavage/methylation domain | | 0.63 |
| GM18\_1379 | hypothetical protein |  | 0.68 |
| **GM18\_1380** | **putative horizontal transfer gene protein** | **Lambda repressor-like, DNA-binding domain** | **0.51** |
| GM18\_1381 | *pilM* |  | 0.61 |
| GM18\_1382 | *pilN* |  | 0.6 |
| GM18\_1383 | *pilO* |  | 0.59 |
| GM18\_1384 | *pilP* |  | 0.63 |
| GM18\_1385 | *pilQ* |  | 0.63 |
| GM18\_1386 | PS51257 membrane lipoprotein lipid attachment | | 0.57 |
| GM18\_1387 | Ig-like family protein | | 0.61 |
| **GM18\_1388** | **disulfide bond isomerase, DsbC/G-like protein** | | **0.53** |
| GM18\_1389 | *aroC* |  | 0.67 |
| GM18\_1390 | *aroK* |  | 0.63 |
| GM18\_1391 | *aroB* |  | 0.65 |
| GM18\_1392 | tetratricopeptide repeat-containing protein | | 0.63 |
| GM18\_1393 | Roadblock/LC7 domain | | 0.62 |
| GM18\_1394 | *aroQ* |  | 0.66 |
| GM18\_1395 | Xaa-Pro aminopeptidase | | 0.63 |
| GM18\_1396 | biotin carboxyl carrier protein | | 0.6 |
| GM18\_1397 | biotin carboxylase |  | 0.62 |
| GM18\_2471 | hypothetical protein |  | 0.54 |
| **GM18\_2472** | **family 2 glycosyl transferase** | | **0.5** |
| GM18\_2473 | *xapJ*, glycosyl transferase family 9 | | 0.6 |
| GM18\_2474 | Nucleotide-diphospho-sugar transferases | | 0.62 |
| GM18\_2475 | *xapI*, type 11 methyltransferase | | 0.59 |
| GM18\_2476 | *xapF*, family 2 glycosyl transferase | | 0.58 |
| GM18\_2477 | group 1 glycosyl transferase | | 0.59 |
| GM18\_2478 | group 1 glycosyl transferase | | 0.6 |
| GM18\_2479 | hypothetical protein |  | 0.55 |
| GM18\_2480 | Glycosyl transferases group 1 | | 0.58 |
| GM18\_2481 | *xapH*, ABC transporter-like protein | | 0.59 |
| GM18\_2482 | *xapG*, ABC-2 type transporter | | 0.58 |
| GM18\_2483 | family 2 glycosyl transferase | | 0.62 |
| GM18\_2484 | family 2 glycosyl transferase | | 0.64 |
| GM18\_2485 | family 2 glycosyl transferase | | 0.62 |
| GM18\_2486 | *xapE*, UbiA prenyltransferase | | 0.61 |
| GM18\_2487 | *xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase | | 0.64 |
| GM18\_2488 | *xapD*, ABC transporter-like protein | | 0.61 |
| GM18\_2489 | Tetratricopeptide-like helical | | 0.58 |
| GM18\_2490 | *xapB*, ABC-2 family transporter protein | | 0.59 |
| GM18\_2491 | *pilA*-C |  | 0.61 |
| GM18\_2492 | e-pilin |  | 0.55 |
| GM18\_2493 | *pilR* |  | 0.63 |
| GM18\_2494 | *pilS* |  | 0.61 |
| GM18\_2495 | *pilC* |  | 0.61 |
| GM18\_2496 | *pilT* |  | 0.63 |
| GM18\_2497 | *pilB* |  | 0.62 |
| GM18\_2498 | *aroE* |  | 0.68 |
| GM18\_2499 | DUF2723 |  | 0.62 |
| GM18\_2500 | Lysylphosphatidylglycerol synthetase/glycosyltransferase AglD | | 0.61 |
| GM18\_2501 | Flavokinase |  | 0.65 |
| GM18\_2502 | *tatC* |  | 0.59 |
| GM18\_2503 | RNAse R |  | 0.65 |
| GM18\_2504 | soluble lytic murein transglycosylase | | 0.64 |

K. Pilin gene clusters found in the *Geobacter bremensis* genome. Two different gene clusters were identified and each is highlighted in a different color. One gene coding for a horizontal gene transfer protein was detected in these gene clusters. Numerous xap and glycosyl transferase genes were found in the e-pilin gene cluster. The overall GC content of *G. bremensis* is 60.26%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. One out of 56 (2%) of the genes have deviant GC values.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| K419DRAFT\_00152 | biotin carboxylase |  | 0.61 |
| K419DRAFT\_00153 | biotin carboxyl carrier protein | | 0.6 |
| K419DRAFT\_00154 | Xaa-Pro aminopeptidase | | 0.64 |
| K419DRAFT\_00155 | *aroQ* |  | 0.61 |
| K419DRAFT\_00156 | Roadblock/LC7 domain | | 0.6 |
| K419DRAFT\_00157 | Tetratricopeptide repeat-containing domain | | 0.64 |
| K419DRAFT\_00158 | *aroB* |  | 0.64 |
| K419DRAFT\_00159 | *aroK* |  | 0.62 |
| K419DRAFT\_00160 | *aroC* |  | 0.66 |
| K419DRAFT\_00161 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.53 |
| K419DRAFT\_00162 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.53 |
| K419DRAFT\_00163 | *pilQ* |  | 0.63 |
| K419DRAFT\_00164 | *pilP* |  | 0.65 |
| K419DRAFT\_00165 | *pilO* |  | 0.57 |
| K419DRAFT\_00166 | *pilN* |  | 0.6 |
| K419DRAFT\_00167 | *pilM* |  | 0.6 |
| K419DRAFT\_00168 | putative horizontal transfer gene protein | Lambda repressor-like, DNA-binding domain | 0.54 |
| K419DRAFT\_00169 | hypothetical protein |  | 0.63 |
| K419DRAFT\_00170 | *pilW* |  | 0.59 |
| K419DRAFT\_00171 | *pilV* |  | 0.58 |
| K419DRAFT\_00172 | *fimT* |  | 0.58 |
| K419DRAFT\_00173 | *pilX* |  | 0.6 |
| K419DRAFT\_00174 | *pilW* |  | 0.62 |
| K419DRAFT\_00175 | *pilV* |  | 0.57 |
| K419DRAFT\_00176 | *fimU* |  | 0.61 |
| K419DRAFT\_00177 | *pilY1* |  | 0.63 |
| K419DRAFT\_00178 | Disulphide bond isomerase, DsbC | | 0.61 |
| K419DRAFT\_00179 | *pilR* |  | 0.64 |
| K419DRAFT\_00180 | *pilS* |  | 0.62 |
| K419DRAFT\_00181 | *pilD* |  | 0.59 |
| K419DRAFT\_00788 | radical SAM additional 4Fe4S-binding SPASM domain-containing protein | | 0.62 |
| K419DRAFT\_00789 | methyltransferase, FkbM family | | 0.61 |
| K419DRAFT\_00790 | Methylase involved in ubiquinone/menaquinone biosynthesis | | 0.63 |
| K419DRAFT\_00791 | *xapH*, lipopolysaccharide transport system ATP-binding protein | | 0.61 |
| K419DRAFT\_00792 | *xapG*, lipopolysaccharide transport system permease protein | | 0.57 |
| K419DRAFT\_00793 | Glycosyltransferases involved in cell wall biogenesis | | 0.57 |
| K419DRAFT\_00794 | *xapF*, Glycosyltransferase, GT2 family | | 0.64 |
| K419DRAFT\_00795 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.58 |
| K419DRAFT\_00796 | *xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase | | 0.6 |
| K419DRAFT\_00797 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.58 |
| K419DRAFT\_00798 | hypothetical protein |  | 0.59 |
| K419DRAFT\_00799 | *xapB*, ABC-2 family transporter protein | | 0.58 |
| K419DRAFT\_00800 | *pilA*-C |  | 0.59 |
| K419DRAFT\_00801 | e-pilin |  | 0.53 |
| K419DRAFT\_00802 | *pilR* |  | 0.63 |
| K419DRAFT\_00803 | *pilS* |  | 0.63 |
| K419DRAFT\_00804 | *pilC* |  | 0.61 |
| K419DRAFT\_00805 | *pilT* |  | 0.61 |
| K419DRAFT\_00806 | *pilB* |  | 0.61 |
| **K419DRAFT\_00807** | ***aroE*** |  | **0.68** |
| K419DRAFT\_00808 | 4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family | | 0.63 |
| K419DRAFT\_00809 | Lysylphosphatidylglycerol synthase TM region | | 0.61 |
| K419DRAFT\_00810 | Flavokinase |  | 0.65 |
| K419DRAFT\_00811 | *tatC* |  | 0.58 |
| K419DRAFT\_00812 | RNAse R |  | 0.65 |
| K419DRAFT\_00813 | lytic murein transglycosylase | | 0.63 |

L. Pilin gene clusters found in the *Desulfuromonas sp. TF* genome. Only one pilin gene cluster was identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in this gene cluster. Numerous xap and glycosyl transferase genes were found in the e-pilin gene cluster. The overall GC content of strain TF is 58.66%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Nine out of 62 (15%) of the genes have deviant GC values, including *pilP*, *xapG, pilN*, and *pilO*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| DTFDRAFT\_03587 | *aroC* |  | 0.61 |
| DTFDRAFT\_03588 | *pilQ* |  | 0.55 |
| **DTFDRAFT\_03589** | ***pilP*** |  | **0.48** |
| **DTFDRAFT\_03590** | ***pilO*** |  | **0.45** |
| **DTFDRAFT\_03591** | ***pilN*** |  | **0.46** |
| DTFDRAFT\_03592 | *pilM* |  | 0.54 |
| DTFDRAFT\_03593 | putative horizontal transfer gene protein | Lambda repressor-like, DNA-binding domain | 0.57 |
| DTFDRAFT\_03594 | *pilD* |  | 0.58 |
| **DTFDRAFT\_03595** | **lipopolysaccharide heptosyltransferase II** | | **0.48** |
| **DTFDRAFT\_03596** | **hypothetical protein** | | **0.42** |
| DTFDRAFT\_03597 | Glycosyltransferase involved in cell wall bisynthesis | | 0.53 |
| **DTFDRAFT\_03598** | **Methyltransferase domain-containing protein** | | **0.51** |
| DTFDRAFT\_03599 | Nucleotide-diphospho-sugar transferases | | 0.55 |
| DTFDRAFT\_03600 | Methyltransferase domain-containing protein | | 0.51 |
| DTFDRAFT\_03601 | Glycosyltransferase involved in cell wall bisynthesis | | 0.54 |
| DTFDRAFT\_03602 | Glycosyltransferase involved in cell wall bisynthesis | | 0.56 |
| DTFDRAFT\_03603 | Glycosyl transferase family 11 | | 0.59 |
| DTFDRAFT\_03604 | Glycosyl transferase family 2 | | 0.59 |
| DTFDRAFT\_03605 | UDP-Glycosyltransferase/glycogen phosphorylase | | 0.63 |
| DTFDRAFT\_03606 | Glycosyltransferase involved in cell wall bisynthesis | | 0.63 |
| DTFDRAFT\_03607 | Glycosyl transferase family 2 | | 0.63 |
| DTFDRAFT\_03608 | Methyltransferase domain-containing protein | | 0.61 |
| DTFDRAFT\_03609 | Glycosyltransferase involved in cell wall bisynthesis | | 0.55 |
| DTFDRAFT\_03610 | Glycosyltransferase, GT2 family | | 0.59 |
| DTFDRAFT\_03611 | Glycosyltransferase involved in cell wall bisynthesis | | 0.53 |
| DTFDRAFT\_03612 | UDP-Glycosyltransferase/glycogen phosphorylase | | 0.58 |
| **DTFDRAFT\_03613** | **HAD-superfamily phosphatase, subfamily IIIC/FkbH-like domain-containing protein** | | **0.4** |
| DTFDRAFT\_03614 | N-acylneuraminate cytidylyltransferase | | 0.6 |
| DTFDRAFT\_03615 | perosamine synthetase | | 0.59 |
| DTFDRAFT\_03616 | Sugar phosphate isomerase/epimerase | | 0.58 |
| DTFDRAFT\_03617 | Protein N-acetyltransferase, RimJ/RimL family | | 0.58 |
| DTFDRAFT\_03618 | N-acetylneuraminate synthase | | 0.63 |
| DTFDRAFT\_03619 | *xapH*, lipopolysaccharide transport system ATP-binding protein | | 0.6 |
| **DTFDRAFT\_03620** | ***xapG*, lipopolysaccharide transport system permease protein** | | **0.51** |
| DTFDRAFT\_03621 | Glycosyltransferase involved in cell wall bisynthesis | | 0.56 |
| DTFDRAFT\_03622 | Glycosyl transferase family 2 | | 0.53 |
| DTFDRAFT\_03623 | *xapF*, Glycosyltransferase, GT2 family | | 0.54 |
| DTFDRAFT\_03624 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.52 |
| DTFDRAFT\_03625 | *xapA*, glycosyltransferase protein |  | 0.55 |
| DTFDRAFT\_03626 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.59 |
| DTFDRAFT\_03627 | hypothetical protein |  | 0.54 |
| DTFDRAFT\_03628 | *xapB*, ABC-2 family transporter protein | | 0.55 |
| DTFDRAFT\_03629 | *pilA*-C |  | 0.58 |
| DTFDRAFT\_03630 | e-pilin |  | 0.54 |
| DTFDRAFT\_03631 | *pilR* |  | 0.59 |
| DTFDRAFT\_03632 | *pilS* |  | 0.55 |
| DTFDRAFT\_03633 | *pilC* |  | 0.56 |
| DTFDRAFT\_03634 | *pilT* |  | 0.59 |
| DTFDRAFT\_03635 | *pilB* |  | 0.58 |
| DTFDRAFT\_03636 | Flavokinase |  | 0.56 |
| DTFDRAFT\_03637 | RNAse R |  | 0.59 |
| DTFDRAFT\_03638 | putative horizontal transfer gene protein | plasmid segregation protein ParM | 0.59 |
| DTFDRAFT\_03639 | Uncharacterized conserved protein, DUF1015 family | | 0.57 |
| **DTFDRAFT\_03640** | **hypothetical protein** |  | **0.51** |
| DTFDRAFT\_03641 | *fimT* |  | 0.52 |
| DTFDRAFT\_03642 | PS51257 membrane lipoprotein lipid attachment | | 0.56 |
| DTFDRAFT\_03643 | *pilY1* |  | 0.56 |
| DTFDRAFT\_03644 | *pilX* |  | 0.56 |
| DTFDRAFT\_03645 | *pilW* |  | 0.57 |
| DTFDRAFT\_03646 | *pilV* |  | 0.54 |
| DTFDRAFT\_03647 | *pilR* |  | 0.59 |
| DTFDRAFT\_03648 | *pilS* |  | 0.55 |

M. Pilin gene clusters found in the *Pelobacter seleniigenes* genome. Two pilin gene clusters were identified in this genome. Fourteen genes coding for horizontal gene transfer proteins were detected in these clusters. This genome is incomplete, however, genes for xap and glycosyl transferase proteins were found in the e-pilin gene cluster. The overall GC content of P. seleniigenes is 54.19%. Genes with GC content +/- 7% of this value are highlighted in bold blue. Thirty-three out of 55 (60%) genes in these clusters have deviant GC values, including *e-pilin, pilA-C, pilR, pilS, pilD, pilN, pilO,xapD, xapB, pilP*, and *pilQ*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| **N909DRAFT\_0002** | ***xapB*, ABC-2 family transporter protein** |  | **0.31** |
| **N909DRAFT\_0003** | ***xapD*, ABC-2 type transport system ATP-binding protein** | | **0.39** |
| **N909DRAFT\_0004** | **O-antigen ligase like membrane protein** | | **0.33** |
| **N909DRAFT\_0005** | ***pilA*-C** |  | **0.43** |
| **N909DRAFT\_0006** | **e-pilin** |  | **0.38** |
| **N909DRAFT\_0007** | ***pilR*** |  | **0.44** |
| **N909DRAFT\_0008** | ***pilS*** |  | **0.44** |
| N909DRAFT\_0009 | *pilC* |  | 0.47 |
| N909DRAFT\_0010 | *pilT* |  | 0.5 |
| N909DRAFT\_0011 | *pilB* |  | 0.49 |
| **N909DRAFT\_0012** | ***aroE*** |  | **0.46** |
| N909DRAFT\_0013 | Flavokinase |  | 0.48 |
| N909DRAFT\_0014 | *pilY1* |  | 0.49 |
| **N909DRAFT\_0015** | **hypothetical protein** |  | **0.46** |
| N909DRAFT\_0016 | *pilX* |  | 0.48 |
| N909DRAFT\_0017 | *pilV* |  | 0.48 |
| N909DRAFT\_0018 | *pilW* |  | 0.48 |
| N909DRAFT\_0019 | *fimT* |  | 0.47 |
| **N909DRAFT\_4146** | ***pilD*** |  | **0.45** |
| N909DRAFT\_4147 | putative horizontal gene transfer protein | Lambda repressor-like, DNA-binding domain | 0.47 |
| N909DRAFT\_4148 | *pilM* |  | 0.47 |
| **N909DRAFT\_4149** | ***pilN*** |  | **0.42** |
| **N909DRAFT\_4150** | ***pilO*** |  | **0.43** |
| **N909DRAFT\_4151** | ***pilP*** |  | **0.44** |
| **N909DRAFT\_4152** | ***pilQ*** |  | **0.46** |
| **N909DRAFT\_4153** | ***aroB*** |  | **0.46** |
| **N909DRAFT\_4154** | **Flp pilus assembly protein TadD, contains TPR repeats** | | **0.46** |
| **N909DRAFT\_4155** | **Roadblock/LC7 domain** | | **0.43** |
| **N909DRAFT\_4156** | **Xaa-Pro aminopeptidase** | | **0.46** |
| **N909DRAFT\_4157** | **biotin carboxyl carrier protein** | | **0.45** |
| N909DRAFT\_4158 | Biotin carboxylase |  | 0.49 |
| N909DRAFT\_4159 | chorismate dehydratase | | 0.48 |
| **N909DRAFT\_4160** | **PS51257 membrane lipoprotein lipid attachment** | | **0.46** |
| N909DRAFT\_4161 | tRNA\_Leu\_TAA |  | 0.6 |
| **N909DRAFT\_4162** | **hypothetical protein** |  | **0.36** |
| **N909DRAFT\_4163** | **putative horizontal gene transfer protein** | **RepA plasmid replication protein** | **0.45** |
| **N909DRAFT\_4164** | **putative horizontal gene transfer protein** | **mobilisation protein (MobC)** | **0.44** |
| N909DRAFT\_4165 | putative horizontal gene transfer protein | Relaxase/Mobilisation nuclease domain-containing protein | 0.49 |
| **N909DRAFT\_4166** | **hypothetical protein** |  | **0.46** |
| **N909DRAFT\_4167** | **hypothetical protein** |  | **0.46** |
| **N909DRAFT\_4168** | **putative horizontal gene transfer protein** | **P-type conjugative transfer protein TrbJ** | **0.43** |
| N909DRAFT\_4169 | putative horizontal gene transfer protein | P-type conjugative transfer protein TrbL | 0.47 |
| N909DRAFT\_4170 | putative horizontal gene transfer protein | RNA(fMet)-specific endonuclease VapC | 0.47 |
| **N909DRAFT\_4171** | **putative horizontal gene transfer protein** | **antitoxin VapB** | **0.44** |
| N909DRAFT\_4172 | hypothetical protein |  | 0.56 |
| **N909DRAFT\_4173** | **hypothetical protein** |  | **0.3** |
| **N909DRAFT\_4174** | **putative horizontal gene transfer protein** | **HTH-type transcriptional regulator / antitoxin HigA** | **0.44** |
| **N909DRAFT\_4175** | **Predicted nucleic-acid-binding protein, contains PIN domain** | | **0.45** |
| N909DRAFT\_4176 | putative horizontal gene transfer protein | Antidote-toxin recognition MazE | 0.5 |
| N909DRAFT\_4177 | putative horizontal gene transfer protein | KfrA\_N replication region DNA-binding N-term | 0.52 |
| N909DRAFT\_4178 | putative horizontal gene transfer protein | putative transposase | 0.53 |
| **N909DRAFT\_4179** | **hypothetical protein** |  | **0.35** |
| **N909DRAFT\_4180** | **hypothetical protein** |  | **0.37** |
| **N909DRAFT\_4181** | **putative horizontal gene transfer protein** | **HNH endonuclease** | **0.44** |
| N909DRAFT\_4182 | putative horizontal gene transfer protein | Site-specific recombinase XerC | 0.48 |

N. Pilin gene clusters found in the *Geobacter argillaceus* genome. Two pilin gene clusters were identified in this genome. One gene coding for a horizontal gene transfer protein was detected in these clusters. Numerous genes for xap and glycosyl transferase proteins were detected in the e-pilin gene cluster. The overall GC content of *G. argillaceus* is 58.2%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Seven out of 51 genes (14%) in these clusters have deviant GC values, including *pilM, pilN, xapB, pilO*, and *pilP*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0052872\_00748 | *aroQ* |  | 0.56 |
| Ga0052872\_00749 | Roadblock/LC7 domain | | 0.53 |
| Ga0052872\_00750 | Tetratricopeptide repeat-containing protein | | 0.57 |
| Ga0052872\_00751 | *aroB* |  | 0.61 |
| Ga0052872\_00752 | *aroC* |  | 0.61 |
| **Ga0052872\_00753** | **hypothetical protein** |  | **0.43** |
| Ga0052872\_00754 | *pilQ* |  | 0.55 |
| **Ga0052872\_00755** | ***pilP*** |  | **0.49** |
| **Ga0052872\_00756** | ***pilO*** |  | **0.49** |
| **Ga0052872\_00757** | ***pilN*** |  | **0.47** |
| **Ga0052872\_00758** | ***pilM*** |  | **0.47** |
| **Ga0052872\_00759** | **putative horizontal gene transfer** | **Lambda repressor-like, DNA-binding domain** | **0.48** |
| Ga0052872\_00761 | *pilW* |  | 0.54 |
| Ga0052872\_00762 | *pilV* |  | 0.52 |
| Ga0052872\_00763 | *fimU* |  | 0.54 |
| Ga0052872\_00764 | *pilY1* |  | 0.56 |
| Ga0052872\_00765 | *pilR* |  | 0.57 |
| Ga0052872\_00766 | *pilS* |  | 0.61 |
| Ga0052872\_00767 | *pilD* |  | 0.59 |
| Ga0052872\_01782 | Glycosyltransferase involved in cell wall bisynthesis | ccc | 0.61 |
| Ga0052872\_01783 | Nucleotide-diphospho-sugar transferases | | 0.56 |
| Ga0052872\_01784 | Glycosyltransferase involved in cell wall bisynthesis | | 0.6 |
| Ga0052872\_01785 | Methyltransferase domain-containing protein | | 0.58 |
| Ga0052872\_01786 | Glycosyltransferase involved in cell wall bisynthesis | | 0.57 |
| Ga0052872\_01787 | *xapF*, Glycosyltransferase involved in cell wall bisynthesis | | 0.57 |
| Ga0052872\_01788 | Nucleotide-diphospho-sugar transferases | | 0.57 |
| Ga0052872\_01789 | S-adenosyl-L-methionine-dependent methyltransferases | | 0.6 |
| Ga0052872\_01790 | *xapH*, lipopolysaccharide transport system ATP-binding protein | | 0.59 |
| Ga0052872\_01791 | *xapG*, lipopolysaccharide transport system permease protein | | 0.57 |
| Ga0052872\_01792 | Glycosyltransferase involved in cell wall bisynthesis | | 0.57 |
| Ga0052872\_01793 | Glycosyltransferase, GT2 family | | 0.56 |
| Ga0052872\_01794 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.56 |
| Ga0052872\_01795 | *xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase | | 0.58 |
| Ga0052872\_01796 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.57 |
| Ga0052872\_01797 | Pili subunit family protein | | 0.54 |
| **Ga0052872\_01798** | ***xapB*, ABC-2 family transporter protein** | | **0.44** |
| Ga0052872\_01799 | *pilA*-C |  | 0.55 |
| Ga0052872\_01800 | e-pilin |  | 0.56 |
| Ga0052872\_01801 | *pilA*-C |  | 0.57 |
| Ga0052872\_01802 | e-pilin |  | 0.56 |
| Ga0052872\_02385 | *pilR* |  | 0.61 |
| Ga0052872\_02386 | *pilS* |  | 0.59 |
| Ga0052872\_02387 | *pilC* |  | 0.57 |
| Ga0052872\_02388 | *pilT* |  | 0.61 |
| Ga0052872\_02389 | *pilB* |  | 0.58 |
| Ga0052872\_02390 | DUF2723 |  | 0.58 |
| Ga0052872\_02391 | Lysylphosphatidylglycerol synthase TM region | | 0.6 |
| Ga0052872\_02392 | Flavokinase |  | 0.61 |
| Ga0052872\_02393 | *tatC* |  | 0.56 |
| Ga0052872\_02394 | RNAse R |  | 0.66 |
| Ga0052872\_02395 | soluble lytic murein transglycosylase | | 0.61 |

O. Pilin gene clusters found in the *Desulfuromusa kysingii* genome. Two pilin gene clusters were identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in these clusters. This genome is incomplete and the e-pilin gene was located near the end of a contig, however, xap genes and glycosyltransferase genes were detected in the e-pilin gene cluster. The overall GC content of *D. kysingii* is 46.43%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Six out of 50 genes (12%) in these clusters had GC content that was > 7% from the overall average, but only one pilin gene (*pilA-C*) had a deviant GC value.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0056096\_02700 | e-pilin |  | 0.42 |
| **Ga0056096\_02701** | ***pilA*-C** |  | **0.38** |
| Ga0056096\_02702 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.46 |
| Ga0056096\_02703 | *xapB*, ABC-type transport system, permease component | | 0.42 |
| Ga0056096\_02704 | hypothetical protein |  | 0.44 |
| Ga0056096\_02705 | *xapA*, Dolichyl-phosphate-mannose-protein mannosyltransferase | | 0.44 |
| Ga0056096\_02706 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.44 |
| Ga0056096\_02707 | ABC transporter |  | 0.49 |
| Ga0056096\_02708 | hypothetical protein |  | 0.46 |
| Ga0056096\_02709 | hypothetical protein |  | 0.39 |
| **Ga0056096\_02710** | **putative horizontal gene transfer protein** | **putative addiction module component, TIGR02574 family** | **0.38** |
| **Ga0056096\_02711** | **CDP-alcohol phosphatidyltransferase** | | **0.35** |
| Ga0056096\_02712 | phosphoenolpyruvate mutase | | 0.41 |
| Ga0056096\_02713 | phosphonopyruvate decarboxylase | | 0.39 |
| **Ga0056096\_02714** | **phosphonate metabolism-associated iron-containing alcohol dehydrogenase** | | **0.36** |
| Ga0056096\_02715 | CDP-alcohol phosphatidyltransferase | | 0.42 |
| **Ga0056096\_02716** | **hypothetical protein** |  | **0.35** |
| Ga0056096\_02717 | *xapJ*, lipopolysaccharide heptosyltransferase II | | 0.46 |
| Ga0056096\_02718 | phosphoheptose isomerase | | 0.44 |
| Ga0056096\_02719 | D-alpha,beta-D-heptose 7-phosphate 1-kinase | | 0.47 |
| Ga0056096\_02720 | D-alpha,beta-D-heptose 1,7-bisphosphate phosphatase | | 0.42 |
| Ga0056096\_02721 | *pilD* |  | 0.45 |
| Ga0056096\_02722 | putative horizontal gene transfer | Lambda repressor-like, DNA-binding domain | 0.46 |
| Ga0056096\_02723 | *pilM* |  | 0.44 |
| Ga0056096\_02724 | *pilN* |  | 0.41 |
| Ga0056096\_02725 | *pilO* |  | 0.41 |
| Ga0056096\_02726 | *pilP* |  | 0.44 |
| Ga0056096\_02727 | *pilQ* |  | 0.42 |
| Ga0056096\_02728 | *aroB* |  | 0.4 |
| Ga0056096\_02729 | Tetratricopeptide repeat-containing protein | | 0.45 |
| Ga0056096\_02730 | Roadblock/LC7 domain | | 0.41 |
| Ga0056096\_02731 | *aroQ* |  | 0.46 |
| Ga0056096\_02732 | Xaa-Pro aminopeptidase | | 0.44 |
| Ga0056096\_02733 | biotin carboxyl carrier protein | | 0.43 |
| Ga0056096\_02734 | biotin carboxylase |  | 0.44 |
| Ga0056096\_03266 | *pilR* |  | 0.43 |
| Ga0056096\_03267 | *pilS* |  | 0.45 |
| Ga0056096\_03268 | *pilC* |  | 0.44 |
| Ga0056096\_03269 | *pilT* |  | 0.45 |
| Ga0056096\_03270 | *pilB* |  | 0.45 |
| Ga0056096\_03271 | *aroE* |  | 0.47 |
| Ga0056096\_03272 | Flavokinase |  | 0.48 |
| Ga0056096\_03273 | *fimT* |  | 0.44 |
| Ga0056096\_03274 | pilE |  | 0.47 |
| Ga0056096\_03275 | *pilY1* |  | 0.46 |
| **Ga0056096\_03276** | **hypothetical** |  | **0.35** |
| Ga0056096\_03277 | *pilX* |  | 0.46 |
| Ga0056096\_03278 | *pilW* |  | 0.47 |
| Ga0056096\_03279 | *pilV* |  | 0.47 |
| Ga0056096\_03280 | *fimT* |  | 0.46 |

P. Pilin gene clusters found in the *Desulfuromonas thiophila* genome. Three pilin gene clusters were identified in this genome. One gene coding for a horizontal gene transfer protein was detected in these clusters. Genes coding for *xap* and glycosyltransferase proteins were detected in the e-pilin gene cluster. The overall GC content of *D. thiophila* is 60.71%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Twenty out of 59 genes (34%) in these clusters had GC content that was > 7% from the overall average, including *pilQ, pilO, pilN, pilM, pilC, pilR, xapF, xapD, xapA, e-pilin*, and *pilA-C*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0056074\_101100 | *pihD*, minor pilin protein |  | 0.64 |
| Ga0056074\_101103 | *pihP*, minor pilin protein |  | 0.58 |
| Ga0056074\_101105 | pihQ, minor pilin protein |  | 0.67 |
| Ga0056074\_101107 | *pilO*, minor pilin protein |  | 0.64 |
| Ga0056074\_101115 | pihA, minor pilin protein |  | 0.61 |
| Ga0056074\_101116 | pihH, minor pilin protein |  | 0.6 |
| Ga0056074\_104180 | biotin carboxylase |  | 0.54 |
| **Ga0056074\_104181** | **biotin carboxyl carrier protein** | | **0.52** |
| Ga0056074\_104182 | Xaa-Pro aminopeptidase | | 0.59 |
| Ga0056074\_104183 | *aroQ* |  | 0.55 |
| Ga0056074\_104184 | Roadblock/LC7 domain | | 0.55 |
| Ga0056074\_104185 | Tetratricopeptide repeat-containing protein | | 0.58 |
| Ga0056074\_104186 | *aroB* |  | 0.55 |
| Ga0056074\_104187 | *aroK* |  | 0.54 |
| **Ga0056074\_104188** | ***pilQ*** |  | **0.52** |
| Ga0056074\_104189 | *pilP* |  | 0.58 |
| **Ga0056074\_104190** | ***pilO*** |  | **0.49** |
| **Ga0056074\_104191** | ***pilN*** |  | **0.49** |
| **Ga0056074\_104192** | ***pilM*** |  | **0.52** |
| Ga0056074\_104193 | *pilD* |  | 0.55 |
| Ga0056074\_104194 | Peroxiredoxin |  | 0.57 |
| Ga0056074\_104195 | [LSU ribosomal protein L11P]-lysine N-methyltransferase | | 0.55 |
| Ga0056074\_104196 | *pilR* |  | 0.58 |
| Ga0056074\_104197 | *pilS* |  | 0.57 |
| **Ga0056074\_104198** | ***pilC*** |  | **0.53** |
| Ga0056074\_104199 | *pilT* |  | 0.55 |
| Ga0056074\_104200 | *pilB* |  | 0.56 |
| Ga0056074\_104201 | *aroE* |  | 0.63 |
| Ga0056074\_104202 | Flavokinase |  | 0.61 |
| Ga0056074\_104203 | RNAse R |  | 0.62 |
| Ga0056074\_104204 | DUF1015 family |  | 0.62 |
| Ga0056074\_104219 | putative horizontal gene transfer protein | Integrase core domain-containing protein | 0.54 |
| Ga0056074\_11717 | *pilS* |  | 0.68 |
| **Ga0056074\_11718** | ***pilR*** |  | **0.7** |
| Ga0056074\_11719 | diguanylate cyclase (GGDEF) domain-containing protein | | 0.66 |
| **Ga0056074\_11720** | **4'-phosphopantetheinyl transferase** | | **0.7** |
| Ga0056074\_11721 | *fimT* |  | 0.54 |
| Ga0056074\_11722 | *pilW* |  | 0.57 |
| **Ga0056074\_11723** | ***pilV*** |  | **0.52** |
| **Ga0056074\_11724** | ***pilX*** |  | **0.51** |
| Ga0056074\_11725 | *pilY1* |  | 0.54 |
| Ga0056074\_1236 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.61 |
| **Ga0056074\_1237** | ***xapA*, glycosyltransferase** | | **0.44** |
| **Ga0056074\_1238** | ***xapD*, ABC-2 type transport system ATP-binding protein** | | **0.53** |
| Ga0056074\_1239 | Pili subunit family protein | | 0.55 |
| Ga0056074\_12310 | *xapB*, ABC-2 family transporter protein | | 0.54 |
| **Ga0056074\_12311** | ***pilA*-C** |  | **0.43** |
| **Ga0056074\_12312** | **e-pilin** |  | **0.49** |
| Ga0056074\_12313 | PD-(D/E)XK nuclease superfamily protein | | 0.58 |
| Ga0056074\_12314 | Putative *xapG*, ABC-type multidrug transport system, ATPase and permease component | | 0.64 |
| Ga0056074\_12315 | glucose-1-phosphate thymidylyltransferase | | 0.6 |
| Ga0056074\_12316 | lipopolysaccharide heptosyltransferase II | | 0.63 |
| Ga0056074\_12317 | CDP-alcohol phosphatidyltransferase | | 0.54 |
| **Ga0056074\_12318** | **2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase** | | **0.49** |
| **Ga0056074\_12319** | **CDP-alcohol phosphatidyltransferase** | | **0.46** |
| **Ga0056074\_12320** | ***xapF*, Glycosyltransferase, GT2 family** | | **0.44** |
| **Ga0056074\_12321** | **Glycosyltransferase involved in cell wall biosynthesis** | | **0.42** |
| **Ga0056074\_12322** | **Glycosyltransferase involved in cell wall bisynthesis** | | **0.4** |
| **Ga0056074\_12323** | **S-adenosyl-L-methionine-dependent methyltransferases** | | **0.35** |

Q. Pilin gene clusters found in the *Geobacter pickeringii* genome. Two pilin gene clusters were identified in this genome. Seven genes coding for horizontal gene transfer proteins were detected in these clusters. Genes coding for *xap* and glycosyltransferase proteins were detected in the e-pilin gene cluster. The overall GC content of *G. pickeringii* is 62.27%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Sixteen out of 56 genes (13%) in these clusters had GC content that was > 7% from the overall average, including *pilO, pilN, pilM, e-pilin*, *xapA, xapB, xapD, xapE*, and *pilA-C*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0069007\_111117 | *pilD* |  | 0.63 |
| Ga0069007\_111118 | *pilS* |  | 0.67 |
| Ga0069007\_111119 | *pilR* |  | 0.63 |
| Ga0069007\_111120 | *fimT* |  | 0.56 |
| Ga0069007\_111121 | *pilV* |  | 0.58 |
| Ga0069007\_111122 | *pilW* |  | 0.57 |
| Ga0069007\_111123 | *pilX* |  | 0.59 |
| Ga0069007\_111124 | *pilY1* |  | 0.6 |
| Ga0069007\_111125 | PS51257 |  | 0.58 |
| **Ga0069007\_111126** | ***fimT*** |  | **0.43** |
| Ga0069007\_111127 | GEMM cis-regulatory element | | 0.6 |
| **Ga0069007\_111128** | **putative horizontal gene transfer protein** | **Lambda repressor-like, DNA-binding domain** | **0.48** |
| **Ga0069007\_111129** | ***pilM*** |  | **0.5** |
| **Ga0069007\_111130** | ***pilN*** |  | **0.52** |
| **Ga0069007\_111131** | ***pilO*** |  | **0.5** |
| **Ga0069007\_111132** | ***pilP*** |  | **0.54** |
| Ga0069007\_111133 | *pilQ* |  | 0.57 |
| Ga0069007\_111134 | *aroC* |  | 0.6 |
| Ga0069007\_111135 | *aroK* |  | 0.6 |
| Ga0069007\_111136 | *aroB* |  | 0.63 |
| Ga0069007\_111137 | TPR-like |  | 0.6 |
| Ga0069007\_111138 | Roadblock/LC7 domain | | 0.58 |
| Ga0069007\_111139 | *aroQ* |  | 0.57 |
| Ga0069007\_111140 | Peptidase\_M24 |  | 0.59 |
| Ga0069007\_111142 | biotin carboxylase |  | 0.59 |
| Ga0069007\_111141 | biotin carboxyl carrier protein | | 0.6 |
| **Ga0069007\_111751** | **UDP-galactopyranose mutase** | | **0.54** |
| Ga0069007\_111752 | Glycosyltransferase involved in cell wall bisynthesis | | 0.56 |
| **Ga0069007\_111753** | **Glycosyltransferase involved in cell wall bisynthesis** | | **0.51** |
| Ga0069007\_111754 | Glycosyltransferase involved in cell wall bisynthesis | | 0.55 |
| **Ga0069007\_111755** | ***xapF*, Glycosyl transferase family 2** | | **0.54** |
| **Ga0069007\_111756** | ***xapE*, 4-hydroxybenzoate polyprenyltransferase** | | **0.46** |
| **Ga0069007\_111757** | ***xapD*, ABC-2 type transport system ATP-binding protein** | | **0.47** |
| **Ga0069007\_111758** | **hypothetical protein** |  | **0.45** |
| **Ga0069007\_111759** | ***xapB*, ABC-2 family transporter protein** | | **0.44** |
| **Ga0069007\_111760** | ***xapA*, Tetratricopeptide repeat-containing domain** | | **0.43** |
| **Ga0069007\_111761** | ***pilA*-C** |  | **0.52** |
| **Ga0069007\_111762** | **e-pilin** |  | **0.48** |
| Ga0069007\_111763 | *pilR* |  | 0.57 |
| Ga0069007\_111764 | *pilS* |  | 0.55 |
| Ga0069007\_111765 | *pilC* |  | 0.55 |
| Ga0069007\_111766 | *pilT* |  | 0.58 |
| Ga0069007\_111767 | *pilB* |  | 0.57 |
| Ga0069007\_111768 | *aroE* |  | 0.62 |
| Ga0069007\_111769 | DUF2723 |  | 0.59 |
| Ga0069007\_111771 | UPF0104 family |  | 0.62 |
| Ga0069007\_111772 | Flavokinase |  | 0.61 |
| Ga0069007\_111773 | *tatC* |  | 0.58 |
| Ga0069007\_111774 | RNAse R |  | 0.61 |
| Ga0069007\_111775 | lytic transglycosylase | | 0.61 |
| Ga0069007\_111798 | putative horizontal gene transfer protein | phage integrase | 0.6 |
| Ga0069007\_111799 | putative horizontal gene transfer protein | phage related Site-specific DNA recombinase | 0.57 |
| Ga0069007\_111802 | putative horizontal gene transfer protein | phage related transcriptional regulator, AlpA family | 0.58 |
| Ga0069007\_111804 | putative horizontal gene transfer protein | phage/plasmid primase | 0.61 |
| Ga0069007\_111806 | putative horizontal gene transfer protein | putative transposase | 0.6 |
| Ga0069007\_111807 | putative horizontal gene transfer protein | transposase | 0.58 |

R. Pilin gene clusters found in the *Geoalkalibacter ferrihydriticus* genome. One pilin gene cluster was identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in these clusters. Genes from the *xap* operon and proteins involved in LPS biosynthesis were detected in the e-pilin gene cluster. The overall GC content of *G. ferrihydriticus* is 57.87%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Zero out of 40 genes (0%) in these clusters had GC content that was > 7% from the overall average.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0056053\_00633 | *pilS* |  | 0.6 |
| Ga0056053\_00634 | *pilR* |  | 0.62 |
| Ga0056053\_00635 | *pilV* |  | 0.56 |
| Ga0056053\_00636 | *pilW* |  | 0.6 |
| Ga0056053\_00642 | *pilV* |  | 0.6 |
| Ga0056053\_00643 | *pilW* |  | 0.58 |
| Ga0056053\_00644 | *pilX* |  | 0.6 |
| Ga0056053\_00645 | *pilY1* |  | 0.58 |
| Ga0056053\_00646 | hypothetical protein |  | 0.65 |
| Ga0056053\_00647 | DUF1015 |  | 0.56 |
| Ga0056053\_00648 | putative horizontal transfer gene protein | plasmid segregation protein ParM | 0.58 |
| Ga0056053\_00649 | RNAse R |  | 0.6 |
| Ga0056053\_00650 | Flavokinase |  | 0.59 |
| Ga0056053\_00651 | *aroE* |  | 0.61 |
| Ga0056053\_00652 | *pilB* |  | 0.57 |
| Ga0056053\_00653 | *pilT* |  | 0.58 |
| Ga0056053\_00654 | *pilC* |  | 0.6 |
| Ga0056053\_00655 | *pilS* |  | 0.58 |
| Ga0056053\_00656 | *pilR* |  | 0.58 |
| Ga0056053\_00657 | e-pilin |  | 0.53 |
| Ga0056053\_00658 | *pilA*-C |  | 0.51 |
| Ga0056053\_00659 | 0-antigen ligase |  | 0.55 |
| Ga0056053\_00660 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.6 |
| Ga0056053\_00661 | *xapB*, ABC-2 family transporter protein | | 0.57 |
| Ga0056053\_00662 | Type II secretion system (T2SS), protein G | | 0.61 |
| Ga0056053\_00663 | putative horizontal gene transfer protein | REP element-mobilizing transposase RayT | 0.51 |
| Ga0056053\_00664 | *pilD* |  | 0.58 |
| Ga0056053\_00665 | *pilM* |  | 0.53 |
| Ga0056053\_00666 | *pilN* |  | 0.55 |
| Ga0056053\_00667 | *pilO* |  | 0.54 |
| Ga0056053\_00668 | *pilP* |  | 0.58 |
| Ga0056053\_00669 | *pilQ* |  | 0.6 |
| Ga0056053\_00670 | *aroK* |  | 0.59 |
| Ga0056053\_00671 | *aroB* |  | 0.59 |
| Ga0056053\_00672 | TPR-like |  | 0.6 |
| Ga0056053\_00673 | Roadblock/LC7 domain | | 0.57 |
| Ga0056053\_00674 | *aroQ* |  | 0.58 |
| Ga0056053\_00675 | Peptidase\_M24 |  | 0.59 |
| Ga0056053\_00676 | biotin carboxyl carrier protein | | 0.54 |
| Ga0056053\_00677 | biotin carboxylase |  | 0.57 |

S. Pilin gene clusters found in the *Geopsychrobacter electrodiphilus* genome. Two pilin gene clusters were identified in this genome. Two genes coding for horizontal gene transfer proteins were detected in these clusters. Genes coding for xap and glycosyltransferase proteins were detected in the e-pilin gene cluster. The overall GC content of *G. electrodiphilus* is 53.2%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty-four out of 62 genes (39%) in these clusters had GC content that was > 7% from the overall average, including *pilA-C, pilF, pilN, pilO, pilP, xapA, xapB, xapD*, and *xapF*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| D888DRAFT\_0269 | *pilV* |  | 0.56 |
| D888DRAFT\_0270 | *pilW* |  | 0.53 |
| D888DRAFT\_0271 | *pilX* |  | 0.58 |
| D888DRAFT\_0272 | *pilY1* |  | 0.58 |
| D888DRAFT\_0273 | type II secretion system protein H | | 0.58 |
| D888DRAFT\_0274 | HAMP domain-containing protein | | 0.51 |
| D888DRAFT\_0275 | *fimT* |  | 0.56 |
| D888DRAFT\_0276 | *pilV* |  | 0.54 |
| D888DRAFT\_0277 | *pilW* |  | 0.52 |
| D888DRAFT\_0278 | *pilX* |  | 0.56 |
| D888DRAFT\_0279 | *pilY1* |  | 0.53 |
| D888DRAFT\_0280 | pilE |  | 0.47 |
| **D888DRAFT\_1999** | **polysaccharide chain length determinant protein** | | **0.45** |
| D888DRAFT\_2000 | polysaccharide export outer membrane protein | | 0.47 |
| D888DRAFT\_2001 | sugar transferase |  | 0.46 |
| D888DRAFT\_2002 | Tetratricopeptide repeat-containing domain, FimV | | 0.48 |
| D888DRAFT\_2003 | *pilZ* |  | 0.48 |
| **D888DRAFT\_2004** | **LuxR family transcriptional regulator** | | **0.43** |
| **D888DRAFT\_2005** | **CAAX prenyl protease-related protein** | | **0.45** |
| **D888DRAFT\_2006** | **PEP-CTERM protein-sorting domain** | | **0.4** |
| D888DRAFT\_2007 | horizontal gene transfer | transposase, IS4 family | 0.55 |
| **D888DRAFT\_2008** | **PEP-CTERM protein-sorting domain** | | **0.41** |
| D888DRAFT\_2009 | tRNA\_Leu\_TAA |  | 0.6 |
| D888DRAFT\_2010 | chorismate dehydratase | | 0.47 |
| D888DRAFT\_2011 | biotin carboxylase |  | 0.49 |
| **D888DRAFT\_2012** | **biotin carboxyl carrier protein** | | **0.44** |
| D888DRAFT\_2013 | Xaa-Pro aminopeptidase | | 0.47 |
| **D888DRAFT\_2014** | ***aroQ*** |  | **0.44** |
| **D888DRAFT\_2015** | **Roadblock/LC7 domain** | | **0.42** |
| **D888DRAFT\_2016** | **pilF** |  | **0.45** |
| **D888DRAFT\_2017** | ***aroB*** |  | **0.43** |
| D888DRAFT\_2018 | *pilQ* |  | 0.47 |
| **D888DRAFT\_2019** | ***pilP*** |  | **0.43** |
| **D888DRAFT\_2020** | ***pilO*** |  | **0.45** |
| **D888DRAFT\_2021** | ***pilN*** |  | **0.41** |
| D888DRAFT\_2022 | *pilM* |  | 0.46 |
| D888DRAFT\_2023 | Predicted transcriptional regulator with C-terminal CBS domains | | 0.49 |
| D888DRAFT\_2024 | *pilD* |  | 0.48 |
| D888DRAFT\_2025 | lipopolysaccharide heptosyltransferase II | | 0.5 |
| **D888DRAFT\_2026** | **Glycosyltransferases, probably involved in cell wall biogenesis** | | **0.36** |
| D888DRAFT\_2027 | putative horizontal gene transfer protein | transposase, IS4 family | 0.48 |
| **D888DRAFT\_2028** | **polysaccharide transporter, PST family** | | **0.44** |
| D888DRAFT\_2029 | dTDP-4-amino-4,6-dideoxygalactose transaminase | | 0.52 |
| **D888DRAFT\_2030** | **Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase** | | **0.37** |
| **D888DRAFT\_2031** | **Glycosyltransferase, GT2 family** | | **0.39** |
| **D888DRAFT\_2032** | **rhamnosyltransferase** | | **0.39** |
| **D888DRAFT\_2033** | **Glycosyltransferase, GT2 family** | | **0.38** |
| D888DRAFT\_2034 | *xapF*, Glycosyltransferase, GT2 family | | 0.49 |
| D888DRAFT\_2035 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.49 |
| **D888DRAFT\_2036** | **Dolichyl-phosphate-mannose-protein mannosyltransferase** | | **0.4** |
| D888DRAFT\_2037 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.46 |
| **D888DRAFT\_2038** | **pili subunit superfamily** | | **0.42** |
| **D888DRAFT\_2039** | ***xapB*, ABC-2 family transporter protein** | | **0.42** |
| **D888DRAFT\_2040** | ***xapA*, TPR-like** |  | **0.45** |
| **D888DRAFT\_2041** | ***pilA*-C** |  | **0.43** |
| D888DRAFT\_2042 | e-pilin |  | 0.46 |
| D888DRAFT\_2043 | *pilR* |  | 0.54 |
| D888DRAFT\_2044 | *pilS* |  | 0.52 |
| D888DRAFT\_2045 | *pilC* |  | 0.51 |
| D888DRAFT\_2046 | *pilT* |  | 0.49 |
| D888DRAFT\_2047 | *pilB* |  | 0.5 |
| D888DRAFT\_2048 | *aroE* |  | 0.53 |

T. Pilin gene clusters found in the *Desulfuromonas soudanensis* genome. One pilin gene cluster was identified in this genome. Two genes coding for horizontal gene transfer proteins were present in this cluster. A short e-pilin gene is not present in this Desulfuromondales species but a long type IVa *pilA* gene was detected. Only a couple of putative xap operon genes (*xapB* and *xapD*) were detected in the *pilA* gene cluster. The overall GC content of *D. soudanensis* is 61.19%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Seven out of 49 genes (14%) in these clusters have GC content that is > 7% from the overall average, including *pilC, pilM, pilN, pilO*, and *pilP*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0069009\_112132 | GEMM cis-regulatory |  | 0.55 |
| Ga0069009\_112133 | tRNA\_Leu\_TAA |  | 0.62 |
| Ga0069009\_112134 | chorismate dehydratase | | 0.63 |
| Ga0069009\_112135 | Outer membrane protein TolC | | 0.65 |
| Ga0069009\_112136 | hypothetical protein |  | 0.59 |
| Ga0069009\_112137 | Lipoate--protein ligase | | 0.67 |
| Ga0069009\_112138 | biotin carboxylase |  | 0.62 |
| Ga0069009\_112139 | biotin carboxyl carrier protein |  | 0.58 |
| Ga0069009\_112140 | Xaa-Pro aminopeptidase | | 0.65 |
| Ga0069009\_112141 | *aroQ* |  | 0.63 |
| Ga0069009\_112142 | Roadblock/LC7/MglB family | | 0.56 |
| Ga0069009\_112143 | Tetratricopeptide repeat-containing protein | | 0.64 |
| Ga0069009\_112144 | *aroB* |  | 0.63 |
| Ga0069009\_112145 | *aroK* |  | 0.64 |
| Ga0069009\_112146 | *aroC* |  | 0.65 |
| Ga0069009\_112147 | *pilQ* |  | 0.57 |
| **Ga0069009\_112148** | ***pilP*** |  | **0.53** |
| **Ga0069009\_112149** | ***pilO*** |  | **0.49** |
| **Ga0069009\_112150** | ***pilN*** |  | **0.47** |
| **Ga0069009\_112151** | ***pilM*** |  | **0.46** |
| **Ga0069009\_112152** | **putative horizontal transfer gene protein** | **Lambda repressor-like, DNA-binding domain** | **0.53** |
| Ga0069009\_112153 | *pilD* |  | 0.6 |
| Ga0069009\_112154 | pili subunit family protein | | 0.55 |
| Ga0069009\_112155 | *xapB*, ABC-2 family transporter protein | | 0.56 |
| Ga0069009\_112156 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.6 |
| Ga0069009\_112157 | *pilA* |  | 0.59 |
| Ga0069009\_112158 | *pilR* |  | 0.59 |
| Ga0069009\_112159 | *pilS* |  | 0.6 |
| **Ga0069009\_112160** | ***pilC*** |  | **0.53** |
| Ga0069009\_112161 | *pilT* |  | 0.61 |
| Ga0069009\_112162 | *pilB* |  | 0.6 |
| Ga0069009\_112163 | *aroE* |  | 0.64 |
| Ga0069009\_112164 | flavokinase |  | 0.61 |
| Ga0069009\_112165 | RNAse R |  | 0.63 |
| Ga0069009\_112166 | *pilY1* |  | 0.54 |
| Ga0069009\_112167 | *pilX* |  | 0.56 |
| Ga0069009\_112168 | *pilW* |  | 0.56 |
| Ga0069009\_112169 | *fimT* |  | 0.56 |
| Ga0069009\_112170 | *pilR* |  | 0.65 |
| Ga0069009\_112171 | *pilS* |  | 0.62 |
| Ga0069009\_112172 | ferredoxin |  | 0.64 |
| Ga0069009\_112173 | Predicted arabinose efflux permease, MFS family | | 0.66 |
| Ga0069009\_112174 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.62 |
| Ga0069009\_112175 | heavy metal efflux pump, CzcA family | | 0.62 |
| Ga0069009\_112176 | membrane fusion protein, multidrug efflux system | | 0.66 |
| Ga0069009\_112177 | transcriptional regulator, TetR family | | 0.65 |
| Ga0069009\_112178 | uncharacterized protein | | 0.66 |
| **Ga0069009\_112179** | **putative horizontal transfer gene protein** | **IS4 transposase** | **0.53** |
| Ga0069009\_112180 | Undecaprenyl-diphosphate phosphatase | | 0.65 |

U. Pilin gene clusters found in the *Desulfuromonas subbituminosa* genome. One pilin gene cluster was identified in this genome. No genes coding for horizontal gene transfer proteins were present in this cluster. A short e-pilin gene is not present in this Desulfuromondales species but a long type IVa *pilA* gene was detected. Only a couple of putative xap operon genes (*xapB* and *xapD*) were detected in the *pilA* gene cluster. The overall GC content of *D. subbituminosa* is 60.27%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Three out of 40 genes (8%) in these clusters have GC content that is > 7% from the overall average, including *pilW*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Ga0064601\_106184 | *pilS* |  | 0.66 |
| Ga0064601\_106185 | *pilR* |  | 0.63 |
| Ga0064601\_106186 | *fimT* |  | 0.63 |
| Ga0064601\_106187 | *fimT* |  | 0.56 |
| Ga0064601\_106188 | *pilV* |  | 0.6 |
| **Ga0064601\_106189** | ***pilW*** |  | **0.52** |
| Ga0064601\_106190 | *pilX* |  | 0.53 |
| **Ga0064601\_106191** | **hypothetical protein** |  | **0.34** |
| Ga0064601\_106192 | *pilY1* |  | 0.55 |
| Ga0064601\_106193 | pilE |  | 0.6 |
| Ga0064601\_106194 | Uncharacterized conserved protein, DUF1015 family | | 0.55 |
| Ga0064601\_106195 | RNAse R |  | 0.62 |
| Ga0064601\_106196 | flavokinase |  | 0.58 |
| Ga0064601\_106197 | *aroE* |  | 0.64 |
| Ga0064601\_106198 | *pilB* |  | 0.59 |
| Ga0064601\_106199 | *pilT* |  | 0.62 |
| Ga0064601\_106200 | *pilC* |  | 0.59 |
| Ga0064601\_106201 | *pilS* |  | 0.62 |
| Ga0064601\_106202 | *pilR* |  | 0.62 |
| Ga0064601\_106203 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.57 |
| Ga0064601\_106204 | *xapB*, ABC-type transport system, permease component | | 0.6 |
| Ga0064601\_106205 | pili subunit family |  | 0.59 |
| Ga0064601\_106206 | *pilD* |  | 0.61 |
| Ga0064601\_106207 | *pilM* |  | 0.57 |
| Ga0064601\_106208 | *pilN* |  | 0.58 |
| Ga0064601\_106209 | *pilO* |  | 0.56 |
| Ga0064601\_106210 | *pilP* |  | 0.58 |
| Ga0064601\_106211 | *pilQ* |  | 0.61 |
| Ga0064601\_106212 | *aroC* |  | 0.64 |
| Ga0064601\_106213 | *aroB* |  | 0.6 |
| Ga0064601\_106214 | Tetratricopeptide repeat-containing protein | | 0.63 |
| Ga0064601\_106215 | Roadblock/LC7 |  | 0.59 |
| Ga0064601\_106216 | *aroQ* |  | 0.59 |
| Ga0064601\_106217 | Xaa-Pro aminopeptidase | | 0.63 |
| Ga0064601\_106218 | biotin carboxyl carrier protein | | 0.6 |
| Ga0064601\_106219 | biotin carboxylase |  | 0.6 |
| Ga0064601\_106220 | Outer membrane protein TolC | | 0.65 |
| Ga0064601\_106221 | Chorismate dehydratase | | 0.61 |
| **Ga0064601\_106222** | **tRNA\_Leu\_TAA** |  | **0.71** |
| Ga0064601\_106223 | hypothetical protein |  | 0.58 |

V. Pilin gene clusters found in the *Desulfobacterium autotrophicum* genome. Six pilin gene clusters were identified in this genome. Twenty-three genes coding for horizontal gene transfer proteins were present in this cluster. Several *xap* operon genes (*xapA, xapB*, and *xapD*) and O-antigen ligase, which is involved in LPS biosynthesis, are present in the e-pilin gene cluster. The overall GC content of *D. autotrophicum* is 48.76%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Eleven out of 158 (7%) genes in these clusters have GC content that is > 7% from the overall average, none of which included pilin genes.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| HRM2\_04990 | *pilT* |  | 0.53 |
| HRM2\_05000 | *pilT* |  | 0.51 |
| HRM2\_05010 | CheY-like superfamily |  | 0.49 |
| HRM2\_05020 | putative 4-hydroxybutyrate CoA-transferase | | 0.54 |
| HRM2\_05030 | pantothenate kinase |  | 0.52 |
| HRM2\_05040 | YbbR-like |  | 0.51 |
| HRM2\_05050 | Dihydropteroate synthase | | 0.54 |
| HRM2\_05060 | membrane protease FtsH | | 0.53 |
| HRM2\_05070 | tRNA(Ile)-lysidine synthetase-like protein | | 0.55 |
| HRM2\_05080 | DHH phosphoesterases |  | 0.51 |
| HRM2\_05090 | carbohydrate ABC transporter ATP-binding protein, UgpC | | 0.52 |
| HRM2\_05100 | carbohydrate ABC transporter substrate-binding protein, UgpB | | 0.51 |
| HRM2\_05110 | carbohydrate ABC transporter membrane protein, UgpA | | 0.5 |
| HRM2\_05120 | carbohydrate ABC transporter membrane protein, UgpE | | 0.52 |
| HRM2\_05130 | putative MlaD protein |  | 0.5 |
| HRM2\_05140 | DUF1178 |  | 0.5 |
| HRM2\_05150 | Na / Phosphate-cotransporter family | | 0.52 |
| HRM2\_05160 | putative methyltransferase | | 0.53 |
| HRM2\_05170 | putative horizontal gene transfer protein | phage like HTH domain protein | 0.53 |
| **HRM2\_05180** | **methylthioribose-1-phosphate isomerase** | | **0.57** |
| HRM2\_05190 | 5'-methylthioadenosine phosphorylase | | 0.54 |
| HRM2\_05200 | adenine phosphoribosyltransferase | | 0.49 |
| HRM2\_05210 | Drug/metabolite transporter | | 0.53 |
| HRM2\_05220 | glutamate racemase |  | 0.56 |
| HRM2\_05230 | erythrose 4-phosphate dehydrogenase | | 0.54 |
| HRM2\_05240 | putative horizontal gene transfer protein | phage-like Winged helix-turn-helix transcription repressor | 0.49 |
| HRM2\_05250 | putative horizontal gene transfer protein | phage-like Winged helix-turn-helix transcription repressor | 0.56 |
| HRM2\_05260 | Small-conductance mechanosensitive channel | | 0.55 |
| HRM2\_05270 | Aldehyde ferredoxin oxidoreductase | | 0.56 |
| HRM2\_05280 | cytoplasmic protein RtcB | | 0.54 |
| HRM2\_05290 | putative 2'-5' RNA ligase | | 0.53 |
| HRM2\_05300 | DUF342 |  | 0.53 |
| HRM2\_05310 | YehS, DUF1456 family |  | 0.5 |
| HRM2\_05320 | uracil permease UraA |  | 0.53 |
| HRM2\_05330 | uracil phosphoribosyltransferase | | 0.53 |
| HRM2\_05340 | putative horizontal gene transfer protein | replication restart DNA helicase PriA | 0.54 |
| HRM2\_05350 | hypothetical protein |  | 0.5 |
| HRM2\_05360 | sigma-54 dependent DNA-binding response regulator | | 0.52 |
| HRM2\_05370 | Cys-tRNA(Pro) deacylase, prolyl-tRNA editing enzyme YbaK/EbsC | | 0.55 |
| HRM2\_05380 | succinyl-CoA synthetase, beta subunit SucC2 | | 0.55 |
| HRM2\_05390 | L-glutamine ABC transporter ATP-binding protein | | 0.5 |
| HRM2\_05400 | amino acid ABC transporter membrane protein 2 | | 0.55 |
| HRM2\_05410 | amino acid ABC transporter membrane protein 1 | | 0.51 |
| HRM2\_05420 | Extracellular solute-binding protein, family 3 | | 0.5 |
| HRM2\_05430 | Extracellular solute-binding protein, family 3 | | 0.52 |
| HRM2\_05440 | putative horizontal gene transfer protein | phage-like HTH-transcription repressor | 0.43 |
| HRM2\_05450 | putative horizontal gene transfer protein | CRISPR-associated protein, Cas1 family | 0.44 |
| HRM2\_05460 | putative horizontal gene transfer protein | CRISPR-associated protein, Cas2 family | 0.44 |
| HRM2\_05470 | putative DNA repair protein | | 0.45 |
| **HRM2\_05480** | **putative horizontal gene transfer protein** | **csh1 CRISPR-associated protein Csh1** | **0.41** |
| **HRM2\_05490** | **hypothetical protein** |  | **0.38** |
| HRM2\_05500 | putative horizontal gene transfer protein | CRISPR-associated protein, Csh2 family | 0.42 |
| **HRM2\_05510** | **putative horizontal gene transfer protein** | **putative CRISPR-associated protein Cas5** | **0.4** |
| **HRM2\_05520** | **putative horizontal gene transfer protein** | **CRISPR-associated helicase, Cas3 family** | **0.37** |
| **HRM2\_05530** | **putative horizontal gene transfer protein** | **CRISPR-associated exonuclease, Cas4 family** | **0.33** |
| HRM2\_10740 | putative horizontal gene transfer protein | phage-like transcriptional regulator, XRE family | 0.49 |
| HRM2\_10750 | Branched-chain-amino-acid transaminase | | 0.52 |
| HRM2\_10760 | hypothetical protein |  | 0.51 |
| HRM2\_10770 | putative horizontal gene transfer protein | HNH endonuclease | 0.52 |
| HRM2\_10780 | GTP-binding protein Era | | 0.51 |
| HRM2\_10790 | Probable GTP-binding protein EngB | | 0.49 |
| HRM2\_10800 | aspartate aminotransferase AspC | | 0.5 |
| HRM2\_10810 | ATP phosphoribosyltransferase | | 0.52 |
| HRM2\_10820 | phosphoribosyl-AMP cyclohydrolase | | 0.47 |
| HRM2\_10830 | Membrane carboxypeptidase | | 0.51 |
| HRM2\_10840 | radical SAM domain family protein | | 0.52 |
| HRM2\_10850 | metal-dependent phosphoesterase / ribonuclease III | | 0.52 |
| HRM2\_10860 | putative horizontal gene transfer protein | phage-like transcriptional regulator | 0.47 |
| HRM2\_10870 | glutamyl-tRNA reductase | | 0.51 |
| HRM2\_10880 | cytochrome c assembly protein CcmC | | 0.53 |
| HRM2\_10890 | precorrin-2 dehydrogenase | | 0.53 |
| HRM2\_10900 | putative metal-dependent hydrolase | | 0.51 |
| HRM2\_10910 | dihydrouridine synthase family protein | | 0.56 |
| HRM2\_10920 | ferric uptake regulation protein | | 0.54 |
| HRM2\_10930 | Fe2+ transport system protein FeoB | | 0.52 |
| HRM2\_10940 | DUF1058 |  | 0.5 |
| HRM2\_10950 | Tetratricopeptide-like helical | | 0.49 |
| HRM2\_10960 | hypothetical protein |  | 0.46 |
| HRM2\_10970 | *pilR* |  | 0.51 |
| HRM2\_10980 | *pilS* |  | 0.46 |
| HRM2\_10990 | *PilM* |  | 0.48 |
| HRM2\_11000 | *pilN* |  | 0.43 |
| HRM2\_11010 | *pilO* |  | 0.44 |
| HRM2\_11020 | *pilP* |  | 0.52 |
| HRM2\_11030 | *pilQ* |  | 0.48 |
| HRM2\_11040 | pilF |  | 0.48 |
| HRM2\_11050 | hypothetical protein |  | 0.49 |
| HRM2\_11060 | L-threonine synthase |  | 0.51 |
| HRM2\_11070 | seryl-tRNA synthetase |  | 0.5 |
| HRM2\_11080 | 5-formyltetrahydrofolate cyclo-ligase | | 0.45 |
| HRM2\_11090 | potassium channel protein | | 0.5 |
| HRM2\_11100 | protein-L-isoaspartate O-methyltransferase | | 0.52 |
| HRM2\_11110 | Uncharacterized membrane protein YqaA | | 0.49 |
| HRM2\_11120 | Fe-S-cluster containining protein | | 0.5 |
| HRM2\_11130 | putative horizontal gene transfer protein | phage-like Winged helix-turn-helix transcription repressor | 0.52 |
| HRM2\_11140 | Phosphopantetheine adenylyltransferase | | 0.46 |
| HRM2\_11150 | putative small methyltransferase | | 0.48 |
| HRM2\_11160 | transcriptional regulator (FIS family protein) | | 0.49 |
| HRM2\_11170 | PAS/PAC sensor signal transduction histidine kinase | | 0.5 |
| HRM2\_11180 | DUF4390 |  | 0.47 |
| HRM2\_11190 | UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase | | 0.53 |
| HRM2\_11200 | Mg chelatase-related protein | | 0.55 |
| HRM2\_11210 | homolog of heat shock protein 33 | | 0.52 |
| HRM2\_11220 | hypothetical protein |  | 0.46 |
| HRM2\_11230 | indolepyruvate:ferredoxin oxidoreductase, alpha subunit IorA1 | | 0.53 |
| HRM2\_11240 | indolepyruvate ferredoxin oxidoreductase, subunit iorB | | 0.56 |
| HRM2\_11250 | general secretion pathway protein F | | 0.52 |
| HRM2\_11260 | Zinc finger, SWIM-type |  | 0.49 |
| HRM2\_11270 | putative horizontal gene transfer protein | phage-like helicase | 0.51 |
| HRM2\_27610 | putative horizontal gene transfer protein | phage-like site-specific recombinase XerD | 0.54 |
| HRM2\_27620 | putative horizontal gene transfer protein | predicted phage SPO1 DNA polymerase-related protein | 0.52 |
| HRM2\_27630 | CoaBC |  | 0.53 |
| HRM2\_27640 | putative lipoprotein |  | 0.48 |
| HRM2\_27650 | *pilY1* |  | 0.45 |
| HRM2\_27660 | *pilX* |  | 0.48 |
| HRM2\_27670 | *pilV* |  | 0.44 |
| HRM2\_27680 | *pilW* |  | 0.45 |
| **HRM2\_27690** | ***fimT*** |  | **0.4** |
| HRM2\_27700 | e-pilin |  | 0.46 |
| HRM2\_27710 | *pilA*-C |  | 0.45 |
| HRM2\_27720 | *xapD*, ABC-type transport system, ATP-binding protein | | 0.48 |
| HRM2\_27730 | *xapB*, ABC-type transport system, permease component | | 0.49 |
| HRM2\_27740 | *xapA*, Tetratricopeptide-like helical | | 0.48 |
| **HRM2\_27750** | **O-antigen ligase like membrane protein** | | **0.4** |
| HRM2\_27760 | *pilR* |  | 0.51 |
| HRM2\_22330 | *pilC* |  | 0.46 |
| HRM2\_22340 | *pilS* |  | 0.51 |
| HRM2\_30410 | *pilD* |  | 0.51 |
| HRM2\_30420 | CheX1 |  | 0.5 |
| HRM2\_30430 | Hbp |  | 0.45 |
| HRM2\_30440 | hypothetical protein |  | 0.45 |
| HRM2\_30450 | Exodeoxyribonuclease I subunit C | | 0.49 |
| HRM2\_30460 | SSU ribosomal protein S9P | | 0.51 |
| HRM2\_30470 | LSU ribosomal protein L13P | | 0.44 |
| HRM2\_30490 | hypothetical protein |  | 0.46 |
| HRM2\_30500 | putative ErfK family protein | | 0.5 |
| HRM2\_30510 | putative horizontal gene transfer | Holliday junction ATP-dependent DNA helicase ruvB | 0.54 |
| HRM2\_30520 | putative horizontal gene transfer | ruvA holliday junction DNA helicase RuvA | 0.52 |
| HRM2\_30530 | putative horizontal gene transfer | Holliday junction endonuclease RuvC | 0.53 |
| HRM2\_30540 | putative aspartyl/asparaginyl beta-hydroxylase | | 0.49 |
| HRM2\_30550 | peptidoglycan-associated lipoprotein | | 0.51 |
| HRM2\_30560 | periplasmic component of the TolB complex | | 0.48 |
| HRM2\_30570 | Cell division and transport-associated protein TolA | | 0.52 |
| HRM2\_30580 | Cell division and transport-associated protein TolR | | 0.53 |
| HRM2\_30590 | Cell division and transport-associated protein TolQ | | 0.5 |
| HRM2\_30600 | GroEL |  | 0.5 |
| HRM2\_30610 | GroES |  | 0.47 |
| HRM2\_30620 | putative FmdB family protein | | 0.48 |
| HRM2\_30630 | hypothetical protein |  | 0.45 |
| **HRM2\_30640** | **DUF1713** |  | **0.4** |
| HRM2\_30650 | protease FtsH subunit HflC | | 0.5 |
| HRM2\_30660 | protease FtsH subunit HflK | | 0.49 |
| HRM2\_30670 | putative horizontal gene transfer | transposase (IS4 element) | 0.46 |
| **HRM2\_22780** | **putative horizontal gene transfer** | **integrase (catalytic domain)** | **0.34** |
| HRM2\_22790 | hypothetical protein |  | 0.53 |
| **HRM2\_22800** | **putative horizontal gene transfer** | **transposase for insertion sequences IS116, IS110 and IS902** | **0.39** |
| HRM2\_23080 | *pilB* |  | 0.5 |

W. Pilin gene clusters found in the *Desulfobotulus sapovorans* genome. Six pilin gene clusters were identified in this genome. Ten genes coding for horizontal gene transfer proteins were present in these pilin clusters. Several *xap* operon genes (*xapB* and *xapD*) and O-antigen ligase, which is involved in LPS biosynthesis, are present in the e-pilin gene cluster. The overall GC content of *D. sapovorans* is 53.52%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Six out of 54 genes (11%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin, xapB*, O-antigen ligase, and *pilN*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| **BR04DRAFT\_00387** | **putative horizontal gene transfer protein** | **putative transposase or invertase** | **0.46** |
| BR04DRAFT\_00388 | hypothetical protein | | 0.49 |
| BR04DRAFT\_00389 | Ribosome-binding ATPase YchF, GTP1/OBG family | | 0.54 |
| **BR04DRAFT\_00390** | **Tetratricopeptide-like** | | **0.45** |
| **BR04DRAFT\_00391** | ***xapB*, ABC-2 family transporter protein** | | **0.43** |
| BR04DRAFT\_00392 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.49 |
| **BR04DRAFT\_00393** | **O-antigen ligase** | | **0.43** |
| **BR04DRAFT\_00394** | **e-pilin** |  | **0.45** |
| BR04DRAFT\_00395 | hypothetical protein | | 0.49 |
| BR04DRAFT\_00396 | prolipoprotein diacylglyceryl transferase | | 0.54 |
| BR04DRAFT\_00397 | Nitroreductase | | 0.54 |
| BR04DRAFT\_00398 | homoserine kinase type II | | 0.55 |
| BR04DRAFT\_00399 | methionine aminopeptidase, type I | | 0.53 |
| BR04DRAFT\_00400 | SEC-C motif-containing protein | | 0.57 |
| BR04DRAFT\_00401 | 1,4-dihydroxy-6-naphthoate synthase | | 0.56 |
| BR04DRAFT\_00402 | YHS domain-containing protein | | 0.49 |
| BR04DRAFT\_00403 | putative horizontal gene transfer protein | phage integrase/recombinase XerD | 0.57 |
| BR04DRAFT\_00210 | *pilT* |  | 0.57 |
| BR04DRAFT\_00211 | *pilT* |  | 0.57 |
| BR04DRAFT\_00102 | *pilT* |  | 0.52 |
| BR04DRAFT\_00103 | *pilT* |  | 0.52 |
| BR04DRAFT\_02125 | putative horizontal gene transfer protein | plasmid segregation protein | 0.49 |
| 47 genes |  |  |  |
| BR04DRAFT\_02173 | pilE |  | 0.51 |
| BR04DRAFT\_02174 | *pilY1* |  | 0.52 |
| BR04DRAFT\_02175 | hypothetical protein | | 0.47 |
| BR04DRAFT\_02176 | *pilX* |  | 0.55 |
| BR04DRAFT\_02177 | *pilW* |  | 0.53 |
| BR04DRAFT\_02178 | *pilV* |  | 0.51 |
| BR04DRAFT\_02179 | *pilY1* |  | 0.52 |
| BR04DRAFT\_02180 | *pilX* |  | 0.51 |
| BR04DRAFT\_02181 | prepilin-type N-terminal cleavage/methylation domain-containing protein | | 0.55 |
| BR04DRAFT\_02182 | prepilin-type N-terminal cleavage/methylation domain-containing protein | | 0.52 |
| BR04DRAFT\_02183 | *fimT* |  | 0.5 |
| BR04DRAFT\_02184 | *pilT* |  | 0.57 |
| 7 genes |  |  |  |
| BR04DRAFT\_02192 | *pilC* |  | 0.56 |
| BR04DRAFT\_02193 | *pilB* |  | 0.59 |
| BR04DRAFT\_02194 | Type II secretory pathway, component ExeA | | 0.57 |
| BR04DRAFT\_02195 | putative horizontal gene transfer protein | transposase, IS605 OrfB family, central region | 0.52 |
| **BR04DRAFT\_02578** | **putative horizontal gene transfer protein** | **phage related GEMM cis-regulatory element** | **0.65** |
| 33 genes |  |  |  |
| BR04DRAFT\_02613 | *pilS* |  | 0.55 |
| BR04DRAFT\_02614 | *pilC* |  | 0.51 |
| 6 genes |  |  |  |
| BR04DRAFT\_02621 | putative horizontal gene transfer protein | phage related Site-specific recombinase XerD | 0.47 |
| BR04DRAFT\_02622 | putative horizontal gene transfer protein | phage related HicB\_like antitoxin | 0.51 |
| BR04DRAFT\_02623 | putative horizontal gene transfer protein | phage related Site-specific DNA recombinase | 0.54 |
| 3 genes |  |  |  |
| BR04DRAFT\_02627 | putative horizontal gene transfer protein | Phage integrase family protein | 0.55 |
| BR04DRAFT\_01789 | *pilQ* |  | 0.49 |
| BR04DRAFT\_01790 | *pilP* |  | 0.51 |
| BR04DRAFT\_01791 | *pilO* |  | 0.51 |
| **BR04DRAFT\_01792** | ***pilN*** |  | **0.44** |
| BR04DRAFT\_01793 | *pilM* |  | 0.49 |
| BR04DRAFT\_01794 | *pilS* |  | 0.48 |
| BR04DRAFT\_01795 | *pilR* |  | 0.53 |
| 24 genes |  |  |  |
| BR04DRAFT\_01821 | putative horizontal gene transfer protein | phage-like PIN domain nuclease, toxin-antitoxin system | 0.51 |

X. Pilin gene clusters found in the *Desulfobotulus alkaliphilus* genome. Seven pilin gene clusters were identified in this genome. 18 genes coding for horizontal gene transfer proteins were present in these pilin clusters. Only two *xap* operon genes (*xapB* and *xapD*) are present in the e-pilin gene cluster. The overall GC content of *D. alkaliphilus* is 50.78%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 77 genes (5%) in these clusters have GC content that is > 7% from the overall average.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| **LZ24DRAFT\_00001** | **putative horizontal gene transfer protein** | **PIN domain-like** | **0.37** |
| LZ24DRAFT\_00002 | pili subunit family protein | | 0.49 |
| LZ24DRAFT\_00003 | *xapB*, ABC-2 family transporter protein | | 0.49 |
| LZ24DRAFT\_00004 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.51 |
| LZ24DRAFT\_00005 | *pilA*-C |  | 0.46 |
| LZ24DRAFT\_00006 | e-pilin |  | 0.5 |
| LZ24DRAFT\_00007 | hypothetical protein | | 0.47 |
| LZ24DRAFT\_00008 | Putative transcriptional regulator, AlgH/UPF0301 family | | 0.56 |
| LZ24DRAFT\_00009 | mcp methyl-accepting chemotaxis protein | | 0.53 |
| LZ24DRAFT\_00010 | gspF general secretion pathway protein F | | 0.56 |
| LZ24DRAFT\_00011 | Uncharacterized membrane protein YdjX | | 0.51 |
| LZ24DRAFT\_00012 | hypothetical protein | | 0.49 |
| LZ24DRAFT\_00013 | hypothetical protein | | 0.5 |
| LZ24DRAFT\_00014 | ATP-binding cassette, subfamily B | | 0.54 |
| LZ24DRAFT\_00015 | ATP-binding cassette, subfamily B | | 0.55 |
| LZ24DRAFT\_00016 | putative horizontal gene transfer protein | phage Site-specific recombinase | 0.54 |
| LZ24DRAFT\_00340 | *pilN* |  | 0.56 |
| LZ24DRAFT\_00341 | hypothetical protein | | 0.52 |
| LZ24DRAFT\_00342 | hypothetical protein | | 0.57 |
| LZ24DRAFT\_00343 | hypothetical protein | | 0.51 |
| LZ24DRAFT\_00344 | *pilD* |  | 0.54 |
| LZ24DRAFT\_00345 | *pilT* |  | 0.56 |
| LZ24DRAFT\_00346 | *pilB* |  | 0.56 |
| LZ24DRAFT\_00347 | *pilC* |  | 0.54 |
| LZ24DRAFT\_00348 | PPIC-type PPIASE domain-containing protein | | 0.51 |
| LZ24DRAFT\_00349 | hypothetical protein | | 0.52 |
| LZ24DRAFT\_00350 | hypothetical protein | | 0.49 |
| LZ24DRAFT\_00351 | putative horizontal gene transfer protein | phage related antitoxin RelB | 0.5 |
| LZ24DRAFT\_00352 | putative horizontal gene transfer protein | phage related antitoxin RelB | 0.45 |
| LZ24DRAFT\_00938 | *pilZ* |  | 0.44 |
| LZ24DRAFT\_00939 | *pilB* |  | 0.46 |
| 14 genes |  |  |  |
| LZ24DRAFT\_00955 | *pilZ* |  | 0.5 |
| 8 genes |  |  |  |
| LZ24DRAFT\_00964 | putative horizontal gene transfer protein | phage related Site-specific recombinase XerD | 0.47 |
| LZ24DRAFT\_00965 | hypothetical protein | | 0.5 |
| LZ24DRAFT\_00966 | putative horizontal gene transfer protein | phage Predicted nuclease of the RNAse H fold, HicB family | 0.49 |
| LZ24DRAFT\_00967 | putative horizontal gene transfer protein | phage Site-specific DNA recombinase | 0.52 |
| LZ24DRAFT\_00968 | hypothetical protein | | 0.47 |
| LZ24DRAFT\_00969 | putative horizontal gene transfer protein | Phage integrase family protein | 0.51 |
| **LZ24DRAFT\_01035** | **putative horizontal gene transfer protein** | **addiction module antidote protein, HigA family** | **0.41** |
| 8 genes |  |  |  |
| LZ24DRAFT\_01045 | putative horizontal gene transfer protein | antitoxin YefM | 0.54 |
| 10 genes |  |  |  |
| LZ24DRAFT\_01056 | putative horizontal gene transfer protein | Invasin/intimin cell-adhesion | 0.5 |
| LZ24DRAFT\_01057 | *pilQ* |  | 0.47 |
| LZ24DRAFT\_01058 | *pilP* |  | 0.48 |
| LZ24DRAFT\_01059 | *pilO* |  | 0.52 |
| LZ24DRAFT\_01060 | *pilN* |  | 0.49 |
| LZ24DRAFT\_01061 | *pilM* |  | 0.51 |
| **LZ24DRAFT\_01062** | **hypothetical protein** | | **0.39** |
| LZ24DRAFT\_01063 | *pilS* |  | 0.47 |
| LZ24DRAFT\_01064 | *pilR* |  | 0.54 |
| LZ24DRAFT\_01796 | putative horizontal gene transfer protein | crossover junction endodeoxyribonuclease RuvC | 0.54 |
| LZ24DRAFT\_01797 | tol-pal system protein YbgF | | 0.48 |
| LZ24DRAFT\_01798 | outer membrane protein OmpA | | 0.54 |
| 26 genes |  |  |  |
| LZ24DRAFT\_01825 | putative horizontal gene transfer protein | LysM domain-containing protein | 0.53 |
| LZ24DRAFT\_01826 | *fimT* |  | 0.5 |
| LZ24DRAFT\_01827 | pilE |  | 0.47 |
| LZ24DRAFT\_01828 | *pilY1* |  | 0.45 |
| **LZ24DRAFT\_01829** | **pilY2** |  | **0.36** |
| LZ24DRAFT\_01830 | *pilX* |  | 0.48 |
| LZ24DRAFT\_01831 | *pilW* |  | 0.44 |
| LZ24DRAFT\_01832 | *pilV* |  | 0.49 |
| LZ24DRAFT\_01833 | *pilY1* |  | 0.51 |
| LZ24DRAFT\_01979 | *pilD* |  | 0.5 |
| 7 genes |  |  |  |
| LZ24DRAFT\_01987 | *pilT* |  | 0.52 |
| LZ24DRAFT\_01988 | *pilT* |  | 0.53 |
| LZ24DRAFT\_01989 | TRAP transporter, DctM subunit | | 0.5 |
| LZ24DRAFT\_01990 | hypothetical protein | | 0.48 |
| LZ24DRAFT\_01991 | putative horizontal gene transfer protein | single-stranded-DNA-specific exonuclease | 0.56 |
| 38 genes |  |  |  |
| LZ24DRAFT\_02040 | putative horizontal gene transfer protein | competence protein ComEC | 0.55 |
| 5 genes |  |  |  |
| LZ24DRAFT\_02046 | *pilB* |  | 0.51 |
| LZ24DRAFT\_02700 | *pilT* |  | 0.53 |
| LZ24DRAFT\_02701 | *pilT* |  | 0.53 |
| 96 genes |  |  |  |
| LZ24DRAFT\_02798 | putative horizontal gene transfer protein | LysM domain-containing protein | 0.54 |
| 6 genes |  |  |  |
| LZ24DRAFT\_02805 | *pilB* |  | 0.49 |
| 8 genes |  |  |  |
| LZ24DRAFT\_02814 | putative horizontal gene transfer protein | Phage integrase family protein | 0.52 |
| LZ24DRAFT\_02815 | hypothetical protein | | 0.55 |
| LZ24DRAFT\_02816 | putative horizontal gene transfer protein | phage related KilA-N domain-containing protein | 0.52 |

Y. Pilin gene clusters found in the *Thauera linaloolentis* genome. Seven pilin gene clusters were identified in this genome. Seventeen genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes coding for xap and glycosyltransferase or LPS biosynthesis proteins were not detected in the e-pilin gene cluster. The overall GC content of *T. linaloolentis* is 66.58%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Thirteen out of 64 genes (20%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin, pilE*, a long type IVa *pilA* gene, *pilX, pilV, pilW*, and *pilY1*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| C666\_06255 | putative horizontal transfer | Endonuclease, Uma2 family | 0.63 |
| C666\_06260 | ABC-2 type transport system ATP-binding protein | | 0.67 |
| **C666\_06265** | **Nucleotidyltransferase substrate binding subunit/domain** | | **0.59** |
| C666\_06270 | Nucleotidyltransferase domain | | 0.62 |
| C666\_06275 | hypothetical protein | | 0.69 |
| C666\_06280 | ABC-2 family transporter protein | | 0.62 |
| **C666\_06285** | **e-pilin** |  | **0.48** |
| **C666\_06290** | **putative horizontal transfer gene** | **endonuclease VapC** | **0.59** |
| **C666\_06295** | **putative horizontal transfer gene** | **antitoxin VapB** | **0.58** |
| C666\_06300 | putative horizontal transfer gene | Winged helix" DNA-binding domain | 0.67 |
| C666\_06305 | Glutaredoxin | | 0.62 |
| C666\_06310 | hypothetical protein | | 0.64 |
| C666\_06315 | NADPH-glutathione reductase | | 0.7 |
| C666\_06320 | molybdopterin-guanine dinucleotide biosynthesis protein A | | 0.71 |
| C666\_06325 | diguanylate cyclase (GGDEF) domain-containing protein | | 0.7 |
| C666\_06330 | putative horizontal transfer gene | putative N6-adenine-specific DNA methylase | 0.69 |
| C666\_06335 | pilU |  | 0.64 |
| C666\_06340 | *pilT* |  | 0.65 |
| C666\_06345 | pyridoxal phosphate enzyme, YggS family | | 0.71 |
| C666\_06350 | pyrroline-5-carboxylate reductase | | 0.73 |
| C666\_06355 | YggT family protein | | 0.68 |
| C666\_06360 | putative horizontal transfer gene | Endonuclease, Uma2 family | 0.68 |
| C666\_06365 | dihydroorotase | | 0.69 |
| C666\_06370 | aspartate carbamoyltransferase | | 0.6 |
| C666\_06375 | uracil phosphoribosyltransferase | | 0.69 |
| C666\_06380 | putative horizontal transfer gene | Holliday junction resolvase-like protein | 0.71 |
| C666\_06385 | Putative transcriptional regulator, AlgH/UPF0301 family | | 0.67 |
| C666\_06390 | deoxyribodipyrimidine photo-lyase | | 0.69 |
| C666\_06395 | cystathione beta-lyase | | 0.72 |
| C666\_06400 | Acyl-CoA N-acyltransferase | | 0.64 |
| C666\_06405 | chemosensory pili system protein ChpA | | 0.71 |
| C666\_06410 | pilJ |  | 0.7 |
| **C666\_06415** | **pilI** |  | **0.75** |
| C666\_06420 | pilH |  | 0.65 |
| C666\_06425 | pilG |  | 0.65 |
| **C666\_05425** | **pilE** |  | **0.58** |
| **C666\_05430** | ***fimT*** |  | **0.61** |
| **C666\_05435** | ***pilV*** |  | **0.55** |
| **C666\_05440** | ***pilW*** |  | **0.57** |
| **C666\_05445** | ***pilX*** |  | **0.58** |
| **C666\_05450** | ***pilY1*** |  | **0.57** |
| **C666\_15290** | **long *pilA*** |  | **0.53** |
| C666\_15295 | D-alanyl-D-alanine carboxypeptidase | | 0.67 |
| C666\_15300 | Peptidoglycan/LPS O-acetylase OafA/YrhL, | | 0.66 |
| C666\_15305 | Transketolase | | 0.68 |
| C666\_15310 | putative horizontal transfer gene | Putative restriction endonuclease | 0.68 |
| C666\_15315 | putative horizontal transfer gene | mRNA-degrading endonuclease RelE, toxin component of the RelBE toxin-antitoxin system | 0.6 |
| C666\_15320 | putative horizontal transfer gene | Lambda repressor-like, DNA-binding domain | 0.68 |
| C666\_15325 | putative horizontal transfer gene | plasmid stability protein | 0.6 |
| **C666\_15330** | **putative horizontal transfer gene** | **plasmid stabilization protein** | **0.57** |
| C666\_15335 | putative horizontal transfer gene | LysR family transcriptional regulator, | 0.73 |
| C666\_04815 | putative horizontal transfer gene | phage integrase/recombinase XerD | 0.66 |
| 15 genes |  |  |  |
| C666\_04895 | *pilB* |  | 0.64 |
| C666\_04900 | *pilC* |  | 0.63 |
| C666\_04905 | *pilD* |  | 0.65 |
| C666\_00255 | *pilR* |  | 0.67 |
| C666\_00260 | *pilS* |  | 0.69 |
| 10 genes |  |  |  |
| C666\_00310 | putative horizontal transfer gene | DNA-binding transcriptional regulator, LysR family | 0.68 |
| C666\_08630 | *pilM* |  | 0.65 |
| C666\_08635 | *pilN* |  | 0.63 |
| C666\_08640 | *pilO* |  | 0.63 |
| C666\_08645 | *pilP* |  | 0.64 |
| 17 genes |  |  |  |
| C666\_08730 | putative horizontal transfer gene | DNA-binding transcriptional regulator, LysR family | 0.68 |
| C666\_15955 | *pilQ* |  | 0.7 |

Z. Pilin gene clusters found in the *Thauera terpenica* genome. Five pilin gene clusters were identified in this genome. Thirteen genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes coding for *xap*, glycosyltransferase and LPS biosynthesis proteins were not detected in the e-pilin gene cluster. The overall GC content of *T. terpenica* is 64.3%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Eight out of 55 genes (15%) in these clusters had GC content that was > 7% from the overall average, including *e-pilin*, *pilQ, pilX, pilV, pilW*, and *pilY1*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| M622\_11220 | pilG |  | 0.6 |
| M622\_11225 | pilH |  | 0.62 |
| M622\_11230 | pilI |  | 0.66 |
| M622\_11235 | pilJ |  | 0.67 |
| M622\_11240 | chemosensory pili system protein ChpA | | 0.69 |
| M622\_11245 | cystathione beta-lyase | | 0.69 |
| M622\_11250 | deoxyribodipyrimidine photo-lyase | | 0.65 |
| M622\_11255 | Putative transcriptional regulator, AlgH/UPF0301 family | | 0.65 |
| M622\_11260 | putative horizontal transfer gene | putative transcription antitermination factor YqgF | 0.69 |
| M622\_11265 | uracil phosphoribosyltransferase | | 0.68 |
| M622\_11270 | aspartate carbamoyltransferase | | 0.66 |
| M622\_11275 | dihydroorotase | | 0.68 |
| M622\_11280 | putative horizontal transfer gene | Endonuclease, Uma2 family | 0.67 |
| M622\_11285 | YggT family protein | | 0.65 |
| M622\_11290 | pyrroline-5-carboxylate reductase | | 0.71 |
| M622\_11295 | pyridoxal phosphate enzyme, YggS family | | 0.69 |
| M622\_11300 | *pilT* |  | 0.63 |
| M622\_11305 | pilU |  | 0.63 |
| M622\_11310 | putative horizontal transfer gene | putative N6-adenine-specific DNA methylase | 0.69 |
| M622\_11315 | molybdopterin-guanine dinucleotide biosynthesis protein A | | 0.71 |
| M622\_11320 | NADPH-glutathione reductase | | 0.67 |
| M622\_11325 | hypothetical protein | | 0.63 |
| M622\_11330 | putative horizontal transfer gene | Resolvase, N terminal domain | 0.61 |
| M622\_11335 | putative horizontal transfer gene | prevent-host-death family protein | 0.57 |
| M622\_11340 | *pilT* |  | 0.61 |
| **M622\_11345** | **e-pilin** |  | **0.54** |
| M622\_11350 | hypothetical protein | | 0.58 |
| M622\_11355 | ABC-2 family transporter protein | | 0.67 |
| M622\_11360 | hypothetical protein | | 0.64 |
| M622\_11365 | putative horizontal transfer gene | prevent-host-death family protein | 0.64 |
| M622\_11370 | putative horizontal transfer gene | ParE toxin of type II toxin-antitoxin system, parDE | 0.63 |
| M622\_11375 | *xapD* |  | 0.68 |
| M622\_01585 | long *PilA* |  | 0.58 |
| M622\_01590 | hypothetical protein | | 0.57 |
| **M622\_01595** | ***pilY1*** |  | **0.55** |
| **M622\_01600** | ***pilX*** |  | **0.53** |
| **M622\_01605** | ***pilW*** |  | **0.5** |
| **M622\_01610** | ***pilV*** |  | **0.56** |
| **M622\_01615** | ***fimT*** |  | **0.56** |
| 18 genes |  |  |  |
| M622\_01705 | *pilZ* |  | 0.66 |
| M622\_11650 | putative horizontal transfer gene | Helix-turn-helix domain of transposase family ISL3 | 0.65 |
| M622\_11655 | putative horizontal transfer gene | RES domain-containing protein | 0.6 |
| 17 genes |  |  |  |
| M622\_11740 | *pilB* |  | 0.62 |
| M622\_11745 | *pilC* |  | 0.62 |
| M622\_11750 | *pilD* |  | 0.65 |
| M622\_13925 | *pilR* |  | 0.65 |
| M622\_13930 | *pilS* |  | 0.66 |
| 16 genes |  |  |  |
| M622\_14010 | horizontal gene transfer | excinuclease ABC subunit A | 0.65 |
| **M622\_00030** | ***pilQ*** |  | **0.52** |
| **M622\_00035** | **hypothetical protein** | | **0.42** |
| M622\_00040 | *pilP* |  | 0.59 |
| M622\_00045 | *pilO* |  | 0.6 |
| M622\_00050 | *pilN* |  | 0.63 |
| M622\_00055 | *pilM* |  | 0.63 |
| 37 genes |  |  |  |
| M622\_00240 | horizontal gene transfer | LysR family transcriptional regulator | 0.64 |
| 8 genes |  |  |  |
| M622\_00280 | horizontal gene transfer | TraT complement resistance protein | 0.61 |

AA. Pilin gene clusters found in the *Thauera humireducens* genome. Five pilin gene clusters were identified in this genome. Five genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes coding for *xap*, glycosyltransferase and LPS biosynthesis proteins were not detected in the e-pilin gene cluster. The overall GC content of *T. humireducens* is 66.4%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 28 genes (14%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin*, long type IVa *pilA, pilV*, and *pilY1*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| WP\_048706603.1 | horizontal transfer gene | crossover junction endodeoxyribonuclease RuvA | 0.71 |
| 6 genes |  |  |  |
| WP\_038012416 | pilU |  | 0.64 |
| WP\_048706607.1 | *pilT* |  | 0.64 |
| 14 genes |  |  |  |
| WP\_048706619 | prevent-host-death protein | | 0.63 |
| WP\_048706621 | relE toxin |  | 0.6 |
| 3 genes |  |  |  |
| **WP\_048706629.1** | **epilin** |  | **0.51** |
| WP\_048710114.1 | hypothetical protein | | 0.59 |
| WP\_048706631.1 | hypothetical protein | | 0.66 |
| WP\_048706634 | horizontal gene transfer-prophage | prevent-host-death family protein | 0.61 |
| WP\_004252063.1 | horizontal transfer | phasin family protein | 0.63 |
| 5 genes |  |  |  |
| WP\_004252011.1 | *pilZ* |  | 0.65 |
| 8 genes |  |  |  |
| **WP\_048709378** | **long *pilA*** |  | **0.58** |
| WP\_048709380.1 | *fimT* |  | 0.62 |
| **WP\_048709381.1** | ***pilV*** |  | **0.57** |
| WP\_048709383.1 | *pilW* |  | 0.6 |
| WP\_048710599.1 | *pilX* |  | 0.59 |
| **WP\_048709385.1** | ***pilY1*** |  | **0.58** |
| WP\_048705994 | *pilB* |  | 0.63 |
| WP\_038011757.1 | *pilC* |  | 0.62 |
| WP\_048705996.1 | *pilD* |  | 0.66 |
| WP\_048706143.1 | *pilR* |  | 0.69 |
| WP\_048706145.1 | *pilS* |  | 0.69 |
| 4 genes |  |  |  |
| WP\_048706172.1 | horizontal gene transfer | LysR family transcriptional regulator | 0.7 |
| WP\_004253778 | *pilM* |  | 0.62 |
| WP\_004253781.1 | *pilN* |  | 0.6 |
| WP\_038010918.1 | *pilO* |  | 0.6 |
| WP\_004253787.1 | *pilP* |  | 0.6 |
| WP\_048710322.1 | *pilQ* |  | 0.6 |

AB. Pilin gene clusters found in the *Flexistipes sinusarabici* genome. Four pilin gene clusters were identified in this genome. Thirty-four genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon were not detected, but O-antigen ligase, which is involved in LPS biosynthesis, is present in the e-pilin gene cluster. The overall GC content of *F. sinusarabici* is 38.29%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 89 genes (5%) in these clusters have GC content that is > 7% from the overall average.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Flexsi\_0510 | *pilM* |  | 0.37 |
| Flexsi\_0511 | *pilN* |  | 0.34 |
| Flexsi\_0512 | *pilO* |  | 0.34 |
| Flexsi\_0513 | *pilP* |  | 0.34 |
| Flexsi\_0514 | *pilQ* |  | 0.37 |
| 14 genes |  |  |  |
| Flexsi\_0529 | putative horizontal gene transfer protein | Transposase | 0.39 |
| 21 genes |  |  |  |
| Flexsi\_0551 | putative horizontal gene transfer protein | Transposase | 0.39 |
| Flexsi\_0552 | putative horizontal gene transfer protein | Transposase DDE domain-containing protein | 0.39 |
| **Flexsi\_0553** | **putative horizontal gene transfer protein** | **TraT complement resistance protein** | **0.47** |
| 6 genes |  |  |  |
| Flexsi\_0560 | putative horizontal gene transfer protein | transposase, IS5 family | 0.38 |
| Flexsi\_0561 | putative horizontal gene transfer protein | transposase, IS5 family | 0.38 |
| Flexsi\_0562 | putative horizontal gene transfer protein | Transposase DDE domain group 1 | 0.36 |
| Flexsi\_0563 | PAS domain S-box-containing protein |  | 0.38 |
| Flexsi\_0564 | ABC-2 type transport system ATP-binding protein |  | 0.38 |
| Flexsi\_0565 | Type II secretion system (T2SS), protein G |  | 0.36 |
| Flexsi\_0566 | *xapD* |  | 0.37 |
| Flexsi\_0807 | putative horizontal gene transfer protein | Transposase | 0.39 |
| 7 genes |  |  |  |
| Flexsi\_0814 | putative horizontal gene transfer protein | transposase, IS5 family | 0.38 |
| 7 genes |  |  |  |
| Flexsi\_0822 | putative horizontal gene transfer protein | transposase IS4 family protein | 0.36 |
| Flexsi\_0823 | putative horizontal gene transfer protein | virulence factor lipase N-terminal | 0.4 |
| 4 genes |  |  |  |
| Flexsi\_0828 | putative horizontal gene transfer protein | Transposase | 0.36 |
| Flexsi\_0829 | putative horizontal gene transfer protein | integrase/recombinase XerD | 0.35 |
| Flexsi\_0830 | hypothetical protein | | 0.34 |
| **Flexsi\_0831** | **hypothetical protein** | | **0.25** |
| Flexsi\_0832 | putative horizontal gene transfer protein | Transposase | 0.42 |
| Flexsi\_0833 | putative horizontal gene transfer protein | IstB\_IS21 | 0.44 |
| 4 genes |  |  |  |
| **Flexsi\_0838** | **putative horizontal gene transfer protein** | **CAAX amino terminal protease** | **0.3** |
| 3 genes |  |  |  |
| Flexsi\_0842 | *pilC* |  | 0.39 |
| Flexsi\_0843 | putative horizontal gene transfer protein | Transposase | 0.36 |
| Flexsi\_0844 | two component transcriptional regulator, winged helix family | | 0.39 |
| Flexsi\_0845 | ATP-binding region ATPase domain protein | | 0.35 |
| **Flexsi\_0846** | **hypothetical protein** | | **0.25** |
| Flexsi\_0847 | *pilY1* |  | 0.37 |
| Flexsi\_0848 | prepilin-type N-terminal cleavage/methylation domain-containing protein | | 0.35 |
| Flexsi\_0849 | *pilV* |  | 0.32 |
| Flexsi\_0850 | *pilW* |  | 0.33 |
| Flexsi\_0851 | *pilX* |  | 0.36 |
| Flexsi\_0852 | hypothetical protein | | 0.33 |
| Flexsi\_0853 | putative horizontal gene transfer protein | IstB domain protein ATP-binding protein | 0.41 |
| Flexsi\_0854 | putative horizontal gene transfer protein | Transposase | 0.41 |
| Flexsi\_0855 | putative horizontal gene transfer protein | transposase, IS5 family | 0.4 |
| 4 genes |  |  |  |
| Flexsi\_0860 | putative horizontal gene transfer protein | integrase/recombinase XerD | 0.37 |
| 8 genes |  |  |  |
| Flexsi\_0869 | putative horizontal gene transfer protein | transposase, IS5 family | 0.37 |
| Flexsi\_1189 | putative horizontal gene transfer protein | DNA-binding protein HU-beta | 0.38 |
| Flexsi\_1190 | putative horizontal gene transfer protein | transcriptional regulator, XRE family | 0.36 |
| 23 genes |  |  |  |
| Flexsi\_1214 | *pilS* |  | 0.32 |
| Flexsi\_1215 | *pilR* |  | 0.35 |
| Flexsi\_1216 | dihydroorotate oxidase B, catalytic subunit | | 0.38 |
| Flexsi\_1217 | dihydroorotate dehydrogenase electron transfer subunit | | 0.39 |
| Flexsi\_1218 | carbamoyl-phosphate synthase large subunit | | 0.4 |
| Flexsi\_1219 | *pilS* |  | 0.35 |
| Flexsi\_1220 | *pilC* |  | 0.42 |
| Flexsi\_1221 | *pilT* |  | 0.42 |
| Flexsi\_1222 | *pilB* |  | 0.4 |
| Flexsi\_1223 | *aroE* |  | 0.35 |
| Flexsi\_2256 | putative horizontal gene transfer protein | Retron-type reverse transcriptase | 0.38 |
| Flexsi\_2257 | putative horizontal gene transfer protein | Transposase | 0.36 |
| 6 genes |  |  |  |
| Flexsi\_2264 | putative horizontal gene transfer protein | Transposase | 0.42 |
| Flexsi\_2265 | putative horizontal gene transfer protein | IstB-like ATP binding protein | 0.41 |
| Flexsi\_2266 | putative horizontal gene transfer protein | Transposase DDE domain-containing protein | 0.35 |
| Flexsi\_2267 | hypothetical protein | | 0.38 |
| Flexsi\_2268 | putative horizontal gene transfer protein | Transposase DDE domain group 1 | 0.36 |
| Flexsi\_2269 | putative horizontal gene transfer protein | Transposase | 0.38 |
| Flexsi\_2270 | putative horizontal gene transfer protein | transposase, IS4 family protein | 0.35 |
| Flexsi\_2271 | small redox-active disulfide protein 2 | | 0.43 |
| Flexsi\_2272 | Protein of unknown function DUF318, transmembrane | | 0.44 |
| Flexsi\_2273 | arsenite transporter, ACR3 family | | 0.39 |
| Flexsi\_2274 | arsenate reductase | | 0.38 |
| Flexsi\_2275 | sulfoxide reductase catalytic subunit YedY | | 0.4 |
| Flexsi\_2276 | GCN5-related N-acetyltransferase | | 0.43 |
| Flexsi\_2277 | pyridoxamine 5'-phosphate oxidase-related FMN-binding | | 0.35 |
| Flexsi\_2278 | transcriptional regulator, GntR family with aminotransferase domain | | 0.38 |
| Flexsi\_2279 | Predicted arabinose efflux permease, MFS family | | 0.36 |
| Flexsi\_2280 | putative horizontal gene transfer protein | transposase, IS4 family protein | 0.35 |
| Flexsi\_2281 | putative horizontal gene transfer protein | Transposase | 0.38 |
| Flexsi\_2282 | enoyl-CoA hydratase | | 0.41 |
| Flexsi\_2283 | 2-aminoadipate transaminase | | 0.36 |
| Flexsi\_2284 | DinB family protein | | 0.33 |
| Flexsi\_2285 | Threonine/homoserine efflux transporter RhtA | | 0.41 |
| Flexsi\_2286 | PAS domain S-box-containing protein | | 0.41 |
| Flexsi\_2287 | two-component system, NtrC family, sensor histidine kinase HydH | | 0.41 |
| Flexsi\_2288 | e-pilin |  | 0.42 |
| Flexsi\_2289 | *pilA*-C |  | 0.33 |
| Flexsi\_2290 | O-antigen ligase | | 0.31 |
| Flexsi\_2291 | e-pilin |  | 0.4 |
| Flexsi\_2292 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.33 |
| Flexsi\_R0054 | tRNA\_SeC |  | 0.68 |
| Flexsi\_2293 | ribulose-5-phosphate 3-epimerase | | 0.41 |
| Flexsi\_2294 | DUF1858 |  | 0.39 |
| Flexsi\_2295 | NAD(P)-dependent dehydrogenase, short-chain alcohol | | 0.38 |
| Flexsi\_2296 | hypothetical protein | | 0.4 |
| Flexsi\_2297 | putative horizontal gene transfer protein | membrane-bound lytic murein transglycosylase F | 0.39 |
| Flexsi\_2298 | putative horizontal gene transfer protein | Transposase | 0.36 |

AC. Pilin gene clusters found in the *Hippea maritima* genome. Three pilin gene clusters were identified in this genome. Twenty-nine genes coding for horizontal gene transfer proteins were present in these pilin clusters. Two xap operon genes (*xapB* and *xapD*) and O-antigen ligase can be found in the e-pilin gene cluster. The overall GC content of *H. maritima* is 37.47%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Fifteen out of 134 genes (11%) in these clusters have GC content that is > 7% from the overall average, including *pilV* and *pilT*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| Hipma\_0474 | *pilC* |  | 0.38 |
| Hipma\_0475 | *pilT* |  | 0.4 |
| Hipma\_0476 | *pilB* |  | 0.36 |
| Hipma\_0477 | *aroE* |  | 0.35 |
| Hipma\_0610 | *pilD* |  | 0.36 |
|  | 20 genes |  |  |
| Hipma\_0631 | putative horizontal gene transfer protein | conjugal transfer mating pair stabilization protein TraN | 0.43 |
| Hipma\_0632 | putative horizontal gene transfer protein | Possible phage DNA methylase | 0.41 |
| Hipma\_0633 | hypothetical protein | | 0.4 |
| Hipma\_0634 | putative horizontal gene transfer protein | phage M3 protein | 0.42 |
| **Hipma\_0635** | **hypothetical protein** | | **0.46** |
| Hipma\_0636 | putative horizontal gene transfer protein | Type IV conjugative transfer system, protein TraL | 0.37 |
| Hipma\_0637 | putative horizontal gene transfer protein | conjugal transfer pilus assembly protein TraE | 0.39 |
| Hipma\_0638 | putative horizontal gene transfer protein | TraK protein | 0.39 |
| **Hipma\_0639** | **putative horizontal gene transfer protein** | **conjugal transfer pilus assembly protein TraB** | **0.45** |
| Hipma\_0640 | putative horizontal gene transfer protein | conjugal transfer pilus assembly protein TraV | 0.36 |
| Hipma\_0641 | Thiol:disulfide interchange protein DsbC | | 0.41 |
| Hipma\_0642 | hypothetical protein | | 0.39 |
| Hipma\_0643 | hypothetical protein | | 0.4 |
| Hipma\_0644 | hypothetical protein | | 0.4 |
| Hipma\_0645 | OmpA family protein | | 0.36 |
| Hipma\_0646 | putative horizontal gene transfer protein | conjugative transfer signal peptidase TraF | 0.35 |
| Hipma\_0647 | putative horizontal gene transfer protein | conjugal transfer pilus assembly protein TraF | 0.38 |
| **Hipma\_0648** | **putative cytoplasmic protein** | | **0.47** |
| Hipma\_0649 | putative horizontal gene transfer protein | conjugal transfer pilus assembly protein TraW | 0.39 |
| Hipma\_0650 | putative horizontal gene transfer protein | conjugal transfer pilus assembly protein TraU | 0.44 |
| Hipma\_0651 | putative horizontal gene transfer protein | type-F conjugative transfer system pilin assembly protein TrbC | 0.35 |
| Hipma\_0652 | trichohyalin |  | 0.33 |
| Hipma\_0653 | hypothetical protein | | 0.39 |
| Hipma\_0654 | putative horizontal gene transfer protein | CRISPR-associated exonuclease Cas4 | 0.38 |
| Hipma\_0655 | hypothetical protein | | 0.36 |
| Hipma\_0656 | hypothetical protein | | 0.31 |
| Hipma\_0657 | hypothetical protein | | 0.37 |
| Hipma\_0658 | putative horizontal gene transfer protein | exodeoxyribonuclease V alpha subunit | 0.43 |
| Hipma\_0665 | putative horizontal gene transfer protein | DNA-binding protein HU/Integration host factor | 0.38 |
| Hipma\_0667 | putative horizontal gene transfer protein | conjugal transfer mating pair stabilization protein TraG | 0.43 |
| Hipma\_0669 | putative horizontal gene transfer protein | conjugative transfer pilus assembly protein TraH | 0.42 |
| **Hipma\_0670** | **putative horizontal gene transfer protein** | **putative transposase** | **0.29** |
| **Hipma\_0671** | **putative horizontal gene transfer protein** | **putative transposase** | **0.28** |
| **Hipma\_0675** | **putative horizontal gene transfer protein** | **TraT complement resistance protein** | **0.45** |
| **Hipma\_0676** | **hypothetical protein** | | **0.47** |
| Hipma\_0677 | P-loop containing nucleoside triphosphate hydrolases | | 0.35 |
| Hipma\_0678 | hypothetical protein | | 0.38 |
| Hipma\_0679 | putative horizontal gene transfer protein | plasmid segregation protein ParM | 0.41 |
| **Hipma\_0680** | **putative horizontal gene transfer protein** | **single stranded DNA-binding protein** | **0.45** |
| **Hipma\_0681** | **hypothetical protein** | | **0.5** |
| Hipma\_0682 | hypothetical protein | | 0.38 |
| Hipma\_0683 | hypothetical protein | | 0.44 |
| Hipma\_0684 | putative horizontal gene transfer protein | conjugal transfer ATP-binding protein TraC | 0.4 |
| Hipma\_0685 | hypothetical protein | | 0.34 |
| Hipma\_0686 | putative horizontal gene transfer protein | Replicative DNA helicase | 0.41 |
| Hipma\_0687 | hypothetical protein | | 0.38 |
| Hipma\_0688 | hypothetical protein | | 0.43 |
| Hipma\_0690 | putative horizontal gene transfer protein | Helix-turn-helix domain-containing protein | 0.39 |
| Hipma\_0695 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.39 |
| Hipma\_0696 | 2-dehydropantoate 2-reductase | | 0.33 |
| Hipma\_0697 | Enoyl-CoA hydratase/carnithine racemase | | 0.42 |
| **Hipma\_R0026** | **tRNA\_Pro** |  | **0.73** |
| Hipma\_0698 | Xaa-Pro aminopeptidase | | 0.37 |
| Hipma\_0699 | diguanylate cyclase (GGDEF) domain | | 0.33 |
| Hipma\_0700 | Signal transduction histidine kinase | | 0.34 |
| Hipma\_0701 | tryptophanyl-tRNA synthetase | | 0.39 |
| Hipma\_0702 | GGDEF domain-containing protein, diguanylate cyclase | | 0.33 |
| Hipma\_0703 | biotin carboxylase | | 0.42 |
| Hipma\_0704 | biotin carboxyl carrier protein | | 0.39 |
| Hipma\_0705 | PAS domain S-box-containing protein/diguanylate cyclase (GGDEF) domain | | 0.32 |
| Hipma\_0706 | DUF763 |  | 0.4 |
| Hipma\_0707 | acetolactate synthase, large subunit | | 0.4 |
| Hipma\_0708 | acetolactate synthase, small subunit | | 0.35 |
| Hipma\_0709 | ketol-acid reductoisomerase | | 0.41 |
| Hipma\_0710 | phosphatidylserine decarboxylase | | 0.37 |
| Hipma\_0711 | CDP-diacylglycerol---serine O-phosphatidyltransferase | | 0.36 |
| Hipma\_0712 | 2-isopropylmalate synthase | | 0.39 |
| Hipma\_0713 | hypothetical protein | | 0.33 |
| Hipma\_0714 | DisA checkpoint controller nucleotide-binding | | 0.36 |
| Hipma\_0715 | methylenetetrahydrofolate dehydrogenase (NADP+) | | 0.38 |
| Hipma\_0716 | ribosome maturation factor RimP | | 0.38 |
| Hipma\_0717 | putative horizontal gene transfer protein | NusA antitermination factor | 0.39 |
| Hipma\_0718 | translation initiation factor IF-2 | | 0.39 |
| Hipma\_0719 | DUF503 |  | 0.34 |
| Hipma\_0720 | ribosome-binding factor A | | 0.34 |
| Hipma\_0721 | phosphoesterase RecJ domain-containing protein | | 0.38 |
| Hipma\_0722 | tRNA pseudouridine55 synthase | | 0.34 |
| Hipma\_0723 | poly-beta-hydroxybutyrate-responsive repressor | | 0.36 |
| Hipma\_0724 | HD-GYP domain, c-di-GMP phosphodiesterase class II | | 0.36 |
| Hipma\_0725 | 2-octaprenylphenol hydroxylase | | 0.36 |
| Hipma\_0726 | 4-hydroxy-3-polyprenylbenzoate decarboxylase | | 0.36 |
| Hipma\_0727 | flagella basal body P-ring formation protein FlgA | | 0.33 |
| **Hipma\_0728** | **flagellar basal-body rod protein FlgG** | | **0.45** |
| Hipma\_0729 | flagellar basal-body rod protein FlgG | | 0.36 |
| Hipma\_0730 | *xapB*, ABC-2 family transporter protein | | 0.34 |
| Hipma\_0731 | hypothetical protein | | 0.35 |
| Hipma\_0732 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.37 |
| **Hipma\_0733** | **hypothetical protein** | | **0.28** |
| **Hipma\_0734** | ***pilT*** |  | **0.28** |
| Hipma\_0735 | O-antigen ligase |  | 0.3 |
| Hipma\_0736 | *pilA*-C |  | 0.38 |
| Hipma\_0737 | e-pilin |  | 0.37 |
| Hipma\_0738 | OmpA family protein | | 0.34 |
| Hipma\_0739 | hypothetical protein | | 0.34 |
| Hipma\_0740 | osmoprotectant transport system permease protein | | 0.39 |
| Hipma\_0741 | osmoprotectant transport system ATP-binding protein | | 0.36 |
| Hipma\_0742 | osmoprotectant transport system permease protein | | 0.34 |
| Hipma\_0743 | osmoprotectant transport system substrate-binding protein | | 0.35 |
| Hipma\_0744 | Multimeric flavodoxin WrbA | | 0.4 |
| Hipma\_0745 | copper-translocating P-type ATPase | | 0.38 |
| Hipma\_0746 | DNA-binding transcriptional regulator, FrmR family | | 0.33 |
| Hipma\_0747 | hypothetical protein | | 0.35 |
| Hipma\_0748 | Protein of unknown function DUF2078, membrane | | 0.3 |
| Hipma\_0749 | cation:H+ antiporter | | 0.34 |
| **Hipma\_R0027** | **tRNA\_Leu** |  | **0.66** |
| Hipma\_0750 | peroxiredoxin |  | 0.4 |
| Hipma\_0751 | LemA family protein | | 0.32 |
| Hipma\_0752 | Protein of unknown function DUF2207, membrane | | 0.34 |
| Hipma\_0753 | Gamma-glutamyl cyclotransferase-like | | 0.31 |
| Hipma\_0754 | hypothetical protein | | 0.38 |
| Hipma\_0755 | diguanylate cyclase (GGDEF) domain-containing protein | | 0.3 |
| Hipma\_0756 | putative horizontal gene transfer protein | Transposase | 0.37 |
| Hipma\_0768 | putative horizontal gene transfer protein | integrase/recombinase XerD | 0.35 |
| Hipma\_1079 | putative horizontal gene transfer protein | Integrase, catalytic core; Helix-turn-helix | 0.38 |
| Hipma\_1080 | pyrroline-5-carboxylate reductase | | 0.42 |
| Hipma\_1081 | heat shock protein HspR | | 0.35 |
| Hipma\_1082 | curved DNA-binding protein | | 0.39 |
| Hipma\_1083 | HSP20 family protein | | 0.41 |
| Hipma\_1084 | ATP-dependent Clp protease ATP-binding subunit ClpB | | 0.42 |
| Hipma\_1085 | hypothetical protein | | 0.34 |
| Hipma\_1086 | *pilW* |  | 0.33 |
| **Hipma\_1087** | ***pilV*** |  | **0.29** |
| Hipma\_1088 | N\_methyl\_3 domain protein | | 0.33 |
| Hipma\_1089 | *pilY1* |  | 0.35 |
| Hipma\_1185 | *pilQ* |  | 0.36 |
| Hipma\_1186 | *pilP* |  | 0.34 |
| Hipma\_1187 | *pilO* |  | 0.31 |
| Hipma\_1188 | *pilN* |  | 0.34 |
| Hipma\_1189 | *pilM* |  | 0.33 |

AD. Pilin gene clusters found in the *Hippea alviniae* genome. Four pilin gene clusters were identified in this genome. Three genes coding for horizontal gene transfer proteins were present in these pilin clusters. The *xap* operon (*xapA-J*) can be found in the e-pilin gene cluster. The overall GC content of *H. alviniae* is 37.03%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Four out of 53 genes (8%) in these clusters have GC content that is > 7% from the overall average.

|  |  |  |  |
| --- | --- | --- | --- |
| Hippea alviniae | GC content is 37.03% | horizontal transfer gene | GC content |
| G415DRAFT\_0150 | flagellar basal-body rod protein FlgB |  | 0.34 |
| G415DRAFT\_0151 | flagellar basal-body rod protein FlgC | | 0.38 |
| G415DRAFT\_0152 | flagellar hook-basal body complex protein FliE | | 0.39 |
| G415DRAFT\_0153 | flagellar M-ring protein FliF | | 0.38 |
| G415DRAFT\_0154 | lagellar motor switch protein FliG | | 0.41 |
| G415DRAFT\_0155 | flagellar assembly protein FliH | | 0.38 |
| G415DRAFT\_0156 | type III secretion system ATPase, FliI/YscN |  | 0.41 |
| G415DRAFT\_0157 | flagellar FliJ protein | | 0.35 |
| G415DRAFT\_0158 | MgtE N-terminal domain-like | | 0.37 |
| G415DRAFT\_0159 | amino acid/amide ABC transporter substrate-binding protein, HAAT family | | 0.4 |
| G415DRAFT\_0160 | Uncharacterized conserved protein, contains tandem ACT domains | | 0.37 |
| G415DRAFT\_0161 | phenylacetate-CoA ligase | | 0.39 |
| G415DRAFT\_0162 | Glutaredoxin-like protein, YruB-family | | 0.39 |
| G415DRAFT\_0163 | L-threonine ammonia-lyase | | 0.37 |
| **G415DRAFT\_0164** | **tRNA\_Ala\_CGC** | | **0.6** |
| G415DRAFT\_0165 | DUF302 |  | 0.38 |
| G415DRAFT\_0166 | methyl-accepting chemotaxis sensory transducer with Cache sensor | | 0.36 |
| G415DRAFT\_0167 | dgcB diguanylate cyclase | | 0.32 |
| G415DRAFT\_0168 | hypothetical protein | | 0.34 |
| G415DRAFT\_0169 | *pilM* |  | 0.34 |
| G415DRAFT\_0170 | *pilN* |  | 0.34 |
| G415DRAFT\_0171 | *pilO* |  | 0.33 |
| G415DRAFT\_0172 | *pilP* |  | 0.32 |
| G415DRAFT\_0173 | *pilQ* |  | 0.34 |
| G415DRAFT\_0790 | *pilW* |  | 0.35 |
| G415DRAFT\_0791 | *pilV* |  | 0.34 |
| G415DRAFT\_0792 | *fimT* |  | 0.33 |
| G415DRAFT\_0793 | *pilY1* |  | 0.35 |
| 20 genes |  |  |  |
| G415DRAFT\_0814 | putative horizontal gene transfer protein | putative transposase or invertase | 0.33 |
| G415DRAFT\_0867 | aspartyl-tRNA synthetase | | 0.4 |
| **G415DRAFT\_0868** | **tRNA\_Val\_CAC** | | **0.62** |
| G415DRAFT\_0869 | P-loop containing nucleoside triphosphate hydrolase | | 0.34 |
| G415DRAFT\_0870 | hypothetical protein | | 0.41 |
| G415DRAFT\_0871 | putative horizontal gene transfer protein | Transposase | 0.36 |
| G415DRAFT\_0872 | e-pilin |  | 0.36 |
| G415DRAFT\_0873 | *pilA*-C |  | 0.38 |
| **G415DRAFT\_0874** | **hypothetical protein** | | **0.25** |
| G415DRAFT\_0875 | *xapA*, Tetratricopeptide repeat-containing protein | | 0.3 |
| G415DRAFT\_0876 | ATPase |  | 0.33 |
| G415DRAFT\_0877 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.33 |
| G415DRAFT\_0878 | CDP-alcohol phosphatidyltransferase | | 0.32 |
| G415DRAFT\_0879 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | | 0.35 |
| **G415DRAFT\_0880** | **CDP-glycerol glycerophosphotransferase** | | **0.26** |
| G415DRAFT\_0881 | *xapH*, lipopolysaccharide transport system ATP-binding protein | | 0.33 |
| G415DRAFT\_0882 | *xapG*, lipopolysaccharide transport system permease protein | | 0.35 |
| G415DRAFT\_0883 | hypothetical protein | | 0.31 |
| G415DRAFT\_0884 | putative horizontal gene transfer protein | prevent-host-death family protein | 0.34 |
| G415DRAFT\_0885 | hypothetical protein | | 0.33 |
| G415DRAFT\_0886 | **ATPase** | | **0.28** |
| G415DRAFT\_0887 | *xapJ* | | 0.35 |
| G415DRAFT\_0888 | *xapH* | | 0.33 |
| G415DRAFT\_0889 | *xapD* | | 0.35 |
| G415DRAFT\_0890 | *xapB* | | 0.33 |
| G415DRAFT\_0936 | *pilC* |  | 0.35 |
| G415DRAFT\_0937 | *pilT* |  | 0.4 |
| G415DRAFT\_0938 | *pilB* |  | 0.36 |
| G415DRAFT\_0939 | *aroE* |  | 0.35 |
| 58 genes |  |  |  |
| G415DRAFT\_0998 | *pilD* |  | 0.36 |

AE. Pilin gene clusters found in the *Deferribacter desulfuricans* genome. Five pilin gene clusters were identified in this genome. Two genes coding for horizontal gene transfer proteins were present in these pilin clusters. Several xap operon genes (*xapA*, *xapB*, and *xapD*) were detected in the e-pilin gene cluster. The overall GC content of D. desulfuricans is 30.31%. Genes that had GC contents +/- 7% of this value are highlighted in bold blue. Two out of 50 genes (4%) in these clusters had GC content that was > 7% from the overall average, including *pilN.*

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horiontal transfer gene | GC content |
| DEFDS\_0111 | Putative chemotaxis protein CheX | | 0.33 |
| DEFDS\_0112 | *pilD* |  | 0.3 |
| DEFDS\_0113 | tyrosyl-tRNA synthetase | | 0.34 |
| DEFDS\_0858 | *pilX* |  | 0.28 |
| DEFDS\_0859 | *pilW* |  | 0.31 |
| DEFDS\_0860 | *pilV* |  | 0.31 |
| DEFDS\_0861 | Type II secretory pathway, pseudopilin PulG | | 0.28 |
| DEFDS\_0862 | *pilY1* |  | 0.3 |
| 9 genes |  |  |  |
| DEFDS\_0873 | putative horizontal gene transfer protein | transposase IS654 family | 0.33 |
| DEFDS\_1090 | putative horizontal gene transfer protein | Exodeoxyribonuclease VII | 0.29 |
| DEFDS\_1091 | transcription elongation factor GreA | | 0.33 |
| DEFDS\_1092 | *pilR* |  | 0.29 |
| 7 genes |  |  |  |
| DEFDS\_1100 | putative horizontal gene transfer protein | NusB antitermination factor | 0.3 |
| 6 genes |  |  |  |
| DEFDS\_1108 | *aroE* |  | 0.25 |
| DEFDS\_1109 | *pilB* |  | 0.35 |
| DEFDS\_1110 | *pilT* |  | 0.35 |
| DEFDS\_1111 | *pilC* |  | 0.34 |
| DEFDS\_1112 | *pilS* |  | 0.23 |
| **DEFDS\_1252** | ***pilN*** |  | **0.21** |
| DEFDS\_1253 | hypothetical protein | | 0.25 |
| DEFDS\_1254 | hypothetical protein | | 0.24 |
| DEFDS\_1255 | *pilQ* |  | 0.3 |
| DEFDS\_1256 | *pilB* |  | 0.33 |
| DEFDS\_1258 | Biotin transporter BioY | | 0.3 |
| DEFDS\_1259 | patatin-like phospholipase family protein | | 0.32 |
| DEFDS\_1260 | NAD-dependent formate dehydrogenase catalytic subunit | | 0.33 |
| DEFDS\_1261 | NADH dehydrogenase I, F subunit | | 0.31 |
| DEFDS\_1262 | S-adenosyl-L-methionine-dependent methyltransferases | | 0.33 |
| DEFDS\_1263 | hypothetical protein | | 0.27 |
| DEFDS\_1264 | biopolymer transport protein, ExbB/TolQ family | | 0.35 |
| DEFDS\_1265 | Tetratricopeptide-like helical | | 0.24 |
| DEFDS\_1266 | Survival protein SurE-like phosphatase/nucleotidase | | 0.36 |
| DEFDS\_1267 | stationary-phase survival protein | | 0.36 |
| **DEFDS\_1268** | **ATP-binding protein, CobQ/CobB/MinD/ParA family** | | **0.38** |
| DEFDS\_1269 | AAA-ATPase\_like | | 0.29 |
| DEFDS\_1270 | e-pilin |  | 0.33 |
| DEFDS\_1271 | *pilA*-C |  | 0.33 |
| DEFDS\_1272 | *xapD*, ABC transporter ATP-binding protein | | 0.31 |
| DEFDS\_1273 | *xapA*, Tetratricopeptide-like helical | | 0.28 |
| DEFDS\_1274 | *xapB*, ATP-binding Cassette (ABC) Superfamily | | 0.25 |
| DEFDS\_1275 | pyruvate carboxylase | | 0.33 |
| DEFDS\_1276 | mechanosensitive ion channel, MscS family | | 0.34 |
| DEFDS\_1277 | Stringent starvation protein B | | 0.28 |
| DEFDS\_1278 | mechanosensitive ion channel, MscS family | | 0.28 |
| DEFDS\_1279 | chorismate dehydratase | | 0.25 |
| DEFDS\_1724 | *pilQ* |  | 0.29 |
| DEFDS\_1725 | *pilP* |  | 0.28 |
| DEFDS\_1726 | *pilO* |  | 0.26 |
| DEFDS\_1727 | *pilN* |  | 0.26 |
| DEFDS\_1728 | *pilM* |  | 0.32 |

AF. Pilin gene clusters found in the *Desulfobacula toluolica* genome. Seven pilin gene clusters were identified in this genome. Seventy-five genes coding for horizontal gene transfer proteins were present in these pilin clusters. Gene from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of *D. toluolica* is 41.45%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty-four out of 187 genes (13%) in these clusters have GC content that is > 7% from the overall average, including *xapG, xapH*, *pilN* and *pilO*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | Horizontal transfer gene | GC content |
| TOL2\_05690 | *pilT* |  | 0.46 |
| TOL2\_05700 | *pilT* |  | 0.43 |
| TOL2\_05710 | CheY-like receiver domain |  | 0.37 |
| TOL2\_05720 | conserved uncharacterized protein | | 0.41 |
| TOL2\_05730 | PbpA: penicillin-binding protein 1A | | 0.45 |
| TOL2\_05740 | Sporulation related domain-containing protein | | 0.36 |
| TOL2\_05750 | selenium metabolism protein YedF | | 0.4 |
| TOL2\_05760 | Fe-S-cluster containining protein | | 0.38 |
| TOL2\_05770 | tRNA-dihydrouridine synthase | | 0.43 |
| TOL2\_05780 | Fur: ferric uptake regulator |  | 0.39 |
| TOL2\_05790 | FeoB: ferrous iron transport protein B | | 0.41 |
| TOL2\_05800 | SH3-like domain-containing protein | | 0.39 |
| TOL2\_05810 | Tetratricopeptide repeat-containing protein | | 0.35 |
| TOL2\_05820 | *pilR* |  | 0.44 |
| TOL2\_05830 | *pilS* |  | 0.38 |
| TOL2\_05840 | *pilM* |  | 0.37 |
| **TOL2\_05850** | ***pilN*** |  | **0.32** |
| **TOL2\_05860** | ***pilO*** |  | **0.33** |
| TOL2\_05870 | *pilP* |  | 0.37 |
| TOL2\_05880 | *pilQ* |  | 0.37 |
| TOL2\_05890 | pilF |  | 0.38 |
| TOL2\_05900 | putative horizontal gene transfer protein | LysM domain protein | 0.35 |
| TOL2\_13280 | putative horizontal gene transfer protein | integration host factor subunit beta | 0.36 |
| TOL2\_13290 | putative horizontal gene transfer protein | Transcription antitermination factor NusG | 0.39 |
| TOL2\_13300 | LPS-assembly protein |  | 0.41 |
| TOL2\_13310 | cysteinyl-tRNA synthetase |  | 0.42 |
| TOL2\_13320 | conserved uncharacterized protein, precursor | | 0.39 |
| TOL2\_13330 | *pilB* |  | 0.42 |
| TOL2\_13340 | putative horizontal gene transfer protein | LysM domain-containing protein | 0.38 |
| TOL2\_13640 | putative horizontal gene transfer protein | Integration host factor (IHF)-like DNA-binding domain | 0.38 |
| TOL2\_13650 | chemotaxis protein CheX |  | 0.39 |
| TOL2\_13660 | *pilD* |  | 0.39 |
| TOL2\_13670 | ATP-dependent Lon protease | | 0.42 |
| TOL2\_13680 | tRNA threonylcarbamoyladenosine biosynthesis protein TsaB | | 0.45 |
| TOL2\_13690 | phosphatidylserine decarboxylase | | 0.41 |
| TOL2\_13700 | CDP-diacylglycerol---serine O-phosphatidyltransferase | | 0.38 |
| TOL2\_13710 | transcription elongation factor GreA | | 0.44 |
| TOL2\_16880 | putative horizontal gene transfer protein | Transposase | 0.47 |
| TOL2\_16900 | conserved uncharacterized protein | | 0.4 |
| TOL2\_16910 | Cytidylate kinase |  | 0.33 |
| TOL2\_16920 | Glycine cleavage system H protein (lipoate-binding) | | 0.47 |
| TOL2\_16930 | archaemetzincin |  | 0.48 |
| TOL2\_16940 | *pilR* |  | 0.46 |
| TOL2\_16950 | *pilS* |  | 0.46 |
| **TOL2\_16960** | **uncharacterized protein** |  | **0.32** |
| TOL2\_16970 | predicted pyridoxamine-phosphate oxidase | | 0.44 |
| TOL2\_16980 | Rhomboid family protein |  | 0.39 |
| TOL2\_16990 | DUF3820 |  | 0.38 |
| TOL2\_17000 | voltage-gated potassium channel | | 0.42 |
| TOL2\_17010 | Heme-degrading monooxygenase HmoA | | 0.37 |
| TOL2\_17020 | protein of unknown function (DUF3786) | | 0.43 |
| TOL2\_17030 | Flavin-binding protein dodecin | | 0.38 |
| TOL2\_17040 | HD-like signal output (HDOD) domain, no enzymatic activity | | 0.41 |
| TOL2\_17050 | conserved uncharacterized protein | | 0.45 |
| TOL2\_17060 | *pilT* |  | 0.48 |
| TOL2\_17070 | hypothetical protein |  | 0.41 |
| **TOL2\_17080** | **putative horizontal gene transfer protein** | **Predicted endonuclease, GIY-YIG superfamily** | **0.33** |
| TOL2\_17090 | putative horizontal gene transfer protein | exodeoxyribonuclease | 0.43 |
| TOL2\_20060 | *pilS* |  | 0.35 |
| TOL2\_20070 | *pilC* |  | 0.4 |
| TOL2\_20080 | tRNA nucleotidyltransferase (CCA-adding enzyme) | | 0.38 |
| TOL2\_20090 | tryptophanyl-tRNA synthetase | | 0.42 |
| TOL2\_20100 | 23S rRNA pseudouridine2605 synthase | | 0.38 |
| TOL2\_20110 | glutamate N-acetyltransferase | | 0.44 |
| TOL2\_20120 | putative horizontal gene transfer protein | integron integrase | 0.43 |
| TOL2\_20130 | putative horizontal gene transfer protein | Predicted nuclease of the RNAse H fold, HicB family | 0.36 |
| TOL2\_20140 | putative horizontal gene transfer protein | Putative abortive phage resistance protein AbiGi, antitoxin | 0.36 |
| TOL2\_20150 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20160 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| **TOL2\_20170** | **uncharacterized protein** |  | **0.54** |
| TOL2\_20180 | Protein of unknown function (DUF3800) | | 0.45 |
| TOL2\_20190 | uncharacterized protein |  | 0.38 |
| TOL2\_20200 | putative horizontal gene transfer protein | Predicted nuclease of the RNAse H fold, HicB family | 0.39 |
| TOL2\_20210 | putative horizontal gene transfer protein | Transposase zinc-binding domain-containing protein | 0.43 |
| TOL2\_20220 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.44 |
| **TOL2\_20230** | **uncharacterized protein** |  | **0.31** |
| **TOL2\_20240** | **orotate phosphoribosyltransferase** | | **0.3** |
| TOL2\_20250 | conserved uncharacterized integral membrane protein, DUF165 | | 0.35 |
| TOL2\_20260 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20270 | uncharacterized protein |  | 0.33 |
| TOL2\_20280 | conserved uncharacterized protein | | 0.37 |
| TOL2\_20290 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20300 | putative horizontal gene transfer protein | transposase, IS801/IS1294 family | 0.43 |
| TOL2\_20310 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.44 |
| TOL2\_20320 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20330 | uncharacterized protein |  | 0.32 |
| TOL2\_20340 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20350 | putative horizontal gene transfer protein | Transposase zinc-binding domain-containing protein | 0.43 |
| TOL2\_20360 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.43 |
| TOL2\_20370 | putative horizontal gene transfer protein | Transposase zinc-binding domain-containing protein | 0.43 |
| TOL2\_20380 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.43 |
| TOL2\_20390 | putative horizontal gene transfer protein | HicA toxin of toxin-antitoxin | 0.41 |
| TOL2\_20400 | putative horizontal gene transfer protein | Predicted nuclease of the RNAse H fold, HicB family | 0.46 |
| TOL2\_20410 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20420 | uncharacterized protein |  | 0.45 |
| TOL2\_20430 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20440 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| **TOL2\_20450** | **uncharacterized protein** |  | **0.6** |
| TOL2\_20460 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| **TOL2\_20470** | **uncharacterized protein** |  | **0.54** |
| TOL2\_20480 | putative horizontal gene transfer protein | antitoxin StbD | 0.44 |
| TOL2\_20490 | putative horizontal gene transfer protein | mRNA interferase RelE/StbE | 0.41 |
| TOL2\_20500 | putative horizontal gene transfer protein | Transposase zinc-binding domain-containing protein | 0.43 |
| TOL2\_20510 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.43 |
| TOL2\_20520 | putative horizontal gene transfer protein | HicA toxin of toxin-antitoxin | 0.35 |
| TOL2\_20530 | putative horizontal gene transfer protein | Predicted nuclease of the RNAse H fold, HicB family | 0.36 |
| TOL2\_20540 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20550 | putative horizontal gene transfer protein | Helix-turn-helix domain-containing protein | 0.37 |
| TOL2\_20560 | putative horizontal gene transfer protein | mRNA interferase RelE/StbE | 0.34 |
| TOL2\_20570 | putative horizontal gene transfer protein | prevent-host-death family protein | 0.4 |
| TOL2\_20580 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| **TOL2\_20590** | **uncharacterized protein** |  | **0.6** |
| TOL2\_20600 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| **TOL2\_20610** | **putative horizontal gene transfer protein** | **prevent-host-death family protein** | **0.31** |
| TOL2\_20620 | putative horizontal gene transfer protein | Predicted nucleic acid-binding protein, contains PIN domain | 0.34 |
| TOL2\_20630 | putative horizontal gene transfer protein | Transposase and inactivated derivatives | 0.4 |
| TOL2\_20640 | putative horizontal gene transfer protein | putative transposase | 0.41 |
| TOL2\_20650 | putative horizontal gene transfer protein | Transposase | 0.45 |
| TOL2\_20660 | conserved uncharacterized protein | | 0.45 |
| TOL2\_20670 | putative horizontal gene transfer protein | transposase, IS66 family Orf2 | 0.42 |
| TOL2\_20680 | putative horizontal gene transfer protein | Transposase | 0.44 |
| **TOL2\_20690** | **uncharacterized protein** |  | **0.27** |
| TOL2\_20700 | conserved uncharacterized protein | | 0.39 |
| TOL2\_20710 | protein of unknown function (DUF4160) | | 0.39 |
| TOL2\_20720 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| TOL2\_20730 | uncharacterized protein |  | 0.47 |
| TOL2\_20740 | conserved uncharacterized protein | | 0.43 |
| TOL2\_20750 | putative horizontal gene transfer protein | transposase, IS66 family Orf2 | 0.47 |
| TOL2\_20760 | putative horizontal gene transfer protein | Transposase IS66 family protein | 0.45 |
| TOL2\_20770 | putative horizontal gene transfer protein | Phage-related protein | 0.39 |
| TOL2\_20780 | putative horizontal gene transfer protein | Lambda repressor-like, DNA-binding domain | 0.41 |
| TOL2\_20790 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.46 |
| TOL2\_20800 | conserved uncharacterized protein | | 0.45 |
| TOL2\_20810 | putative horizontal gene transfer protein | transposase, IS66 family Orf2 | 0.4 |
| TOL2\_20820 | putative horizontal gene transfer protein | Transposase | 0.45 |
| TOL2\_20830 | putative horizontal gene transfer protein | mRNA interferase MazF | 0.34 |
| TOL2\_20840 | putative horizontal gene transfer protein | antitoxin MazE | 0.41 |
| TOL2\_20850 | putative horizontal gene transfer protein | group II intron reverse transcriptase/maturase | 0.45 |
| **TOL2\_20860** | **uncharacterized protein** |  | **0.51** |
| TOL2\_20870 | putative horizontal gene transfer protein | Transposase zinc-binding domain-containing protein | 0.43 |
| TOL2\_20880 | putative horizontal gene transfer protein | Site-specific recombinase XerD | 0.44 |
| TOL2\_20890 | putative horizontal gene transfer protein | phage Homeodomain-like | 0.38 |
| TOL2\_20900 | putative horizontal gene transfer protein | phage Homeodomain-like | 0.42 |
| TOL2\_20910 | putative horizontal gene transfer protein | Transposase DDE domain-containing protein | 0.41 |
| TOL2\_20920 | putative horizontal gene transfer protein | Transposase IS116/IS110/IS902 family protein | 0.4 |
| TOL2\_20930 | putative horizontal gene transfer protein | Transposase | 0.39 |
| 13 genes |  |  |  |
| TOL2\_21080 | putative horizontal gene transfer protein | Transposase IS116/IS110/IS902 family protein | 0.4 |
| TOL2\_21300 | putative lipoprotein |  | 0.4 |
| **TOL2\_21310** | ***xapA*, TPR-like membrane protein** | | **0.32** |
| TOL2\_21320 | pili subunit family |  | 0.35 |
| TOL2\_21330 | *xapB*, ABC-2 family transporter protein | | 0.34 |
| TOL2\_21340 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.39 |
| TOL2\_21350 | e-pilin |  | 0.41 |
| TOL2\_21360 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.4 |
| TOL2\_21370 | ADP-heptose:LPS heptosyltransferase | | 0.38 |
| TOL2\_21380 | *xapF*, Glycosyltransferase, GT2 family | | 0.36 |
| TOL2\_21390 | UDP-galactopyranose mutase | | 0.38 |
| **TOL2\_21400** | **predicted glycosyl transferase, family 2** | | **0.32** |
| **TOL2\_21410** | **Glycosyltransferase, GT2 family** | | **0.31** |
| **TOL2\_21420** | **Iron-sulfur cluster-binding domain-containing protein** | | **0.29** |
| **TOL2\_21430** | **Protein of unknown function DUF115** | | **0.32** |
| **TOL2\_21440** | **N-acylneuraminate cytidylyltransferase** | | **0.3** |
| **TOL2\_21450** | ***xapG*** |  | **0.3** |
| **TOL2\_21460** | ***xapH*, lipopolysaccharide transport system ATP-binding protein** | | **0.31** |
| TOL2\_21470 | ABC-type polysaccharide/polyol phosphate export permease | | 0.35 |
| TOL2\_21480 | Kynurenine formamidase |  | 0.41 |
| TOL2\_21490 | UDP-glucose 4-epimerase |  | 0.38 |
| TOL2\_21500 | 2-dehydro-3-deoxyglucarate aldolase | | 0.39 |
| **TOL2\_21510** | **HAD-superfamily hydrolase, subfamily IA, variant 1** | | **0.3** |
| **TOL2\_21520** | **D-3-phosphoglycerate dehydrogenase** | | **0.33** |
| TOL2\_21530 | *xapG*, predicted O-antigen export system, permease protein | | 0.35 |
| TOL2\_21540 | putative horizontal gene transfer protein | Fic/DOC family protein | 0.4 |
| **TOL2\_21550** | **putative horizontal gene transfer protein** | **nucleoside triphosphate hydrolase** | **0.31** |
| TOL2\_21560 | *fimT* |  | 0.43 |
| TOL2\_21570 | *pilW* |  | 0.42 |
| TOL2\_21580 | *pilV* |  | 0.4 |
| TOL2\_21590 | *pilX* |  | 0.41 |
| TOL2\_21600 | *pilY1* |  | 0.42 |
| 29 genes |  |  |  |
| TOL2\_21900 | *pilR* |  | 0.41 |
| TOL2\_21910 | PyrC: dihydroorotase |  | 0.43 |
| TOL2\_21920 | PyrB: aspartate carbamoyltransferase | | 0.42 |
| TOL2\_21930 | signal peptidase I |  | 0.36 |
| TOL2\_21940 | Uncharacterized conserved protein, DUF39 family | | 0.41 |
| TOL2\_21950 | putative horizontal gene transfer protein | Murein DD-endopeptidase MepM and murein hydrolase activator NlpD, contain LysM domain | 0.37 |
| TOL2\_24450 | *pilB* |  | 0.42 |
| 15 genes |  |  |  |
| TOL2\_24610 | putative horizontal gene transfer protein | integrase/recombinase XerC | 0.4 |
| TOL2\_24620 | putative horizontal gene transfer protein | dpo DNA polymerase bacteriophage-type | 0.37 |

AG. Pilin gene clusters found in the *Desulfobacula phenolica* genome. Seven pilin gene clusters were identified in this genome. 10 genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of *D. phenolica* is 41.33%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Five out of 72 genes (7%) in these clusters have GC content that is > 7% from the overall average, including *xapA, pilN* and *pilO*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus ID | Gene | horizontal transfer gene | GC content |
| Ga0066824\_102262 | pilF |  | 0.38 |
| Ga0066824\_102263 | *pilQ* |  | 0.37 |
| Ga0066824\_102264 | *pilP* |  | 0.37 |
| **Ga0066824\_102265** | ***pilO*** |  | **0.33** |
| **Ga0066824\_102266** | ***pilN*** |  | **0.32** |
| Ga0066824\_102267 | *pilM* |  | 0.37 |
| Ga0066824\_102268 | *pilS* |  | 0.4 |
| Ga0066824\_102269 | *pilR* |  | 0.46 |
| Ga0066824\_102270 | Putative negative regulator of RcsB-dependent stress response | | 0.36 |
| Ga0066824\_102271 | SH3-like domain-containing protein | | 0.41 |
| Ga0066824\_102272 | ferrous iron transport protein B | | 0.41 |
| Ga0066824\_102273 | Fur family transcriptional regulator | | 0.41 |
| Ga0066824\_102274 | tRNA-dihydrouridine synthase | | 0.45 |
| Ga0066824\_102275 | Fe-S-cluster containining protein | | 0.39 |
| Ga0066824\_102276 | hypothetical protein | | 0.42 |
| Ga0066824\_102277 | selenium metabolism protein YedF | | 0.4 |
| Ga0066824\_102278 | Sporulation related domain-containing protein | | 0.37 |
| Ga0066824\_102279 | penicillin-binding protein 1A | | 0.44 |
| Ga0066824\_102280 | hypothetical protein | | 0.41 |
| Ga0066824\_102281 | CheY-like superfamily | | 0.38 |
| Ga0066824\_102282 | *pilT* |  | 0.42 |
| Ga0066824\_102283 | *pilT* |  | 0.45 |
| Ga0066824\_101248 | putative horizontal gene transfer protein | integration host factor subunit beta | 0.36 |
| Ga0066824\_101249 | putative horizontal gene transfer protein | Transcription antitermination factor NusG | 0.41 |
| Ga0066824\_101250 | LPS-assembly protein | | 0.4 |
| Ga0066824\_101251 | cysteinyl-tRNA synthetase | | 0.42 |
| Ga0066824\_101252 | hypothetical protein | | 0.38 |
| Ga0066824\_101253 | 4Fe-4S dicluster domain-containing protein | | 0.41 |
| Ga0066824\_101254 | *pilB* |  | 0.42 |
| Ga0066824\_101296 | *pilZ* |  | 0.36 |
| Ga0066824\_101297 | putative horizontal gene transfer protein | Integration host factor (IHF)-like DNA-binding domain | 0.38 |
| Ga0066824\_101298 | chemotaxis protein CheX | | 0.39 |
| Ga0066824\_101299 | *pilD* |  | 0.39 |
| Ga0066824\_1194 | hypothetical protein | | 0.34 |
| Ga0066824\_1195 | putative horizontal gene transfer protein | Predicted nuclease of the RNAse H fold, HicB family | 0.41 |
| Ga0066824\_1196 | putative horizontal gene transfer protein | YcfA-like protein | 0.4 |
| Ga0066824\_1197 | hypothetical protein | | 0.35 |
| Ga0066824\_1198 | putative horizontal gene transfer protein | integron integrase | 0.45 |
| Ga0066824\_1199 | glutamate N-acetyltransferase | | 0.44 |
| Ga0066824\_11910 | 23S rRNA pseudouridine(2605) synthase | | 0.4 |
| Ga0066824\_11911 | tryptophanyl-tRNA synthetase | | 0.42 |
| Ga0066824\_11912 | tRNA nucleotidyltransferase (CCA-adding enzyme) | | 0.38 |
| Ga0066824\_11913 | *pilC* |  | 0.4 |
| Ga0066824\_11914 | *pilS* |  | 0.36 |
| Ga0066824\_11639 | 4-oxalocrotonate tautomerase | | 0.36 |
| Ga0066824\_11640 | Thioesterase/thiol ester dehydrase-isomerase | | 0.38 |
| Ga0066824\_11641 | phosphopantothenoylcysteine decarboxylase | | 0.42 |
| Ga0066824\_11642 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.4 |
| **Ga0066824\_11643** | ***xapA*, TPR-like membrane protein** | | **0.32** |
| **Ga0066824\_11644** | **Pili subunit family** |  | **0.33** |
| Ga0066824\_11645 | *xapB*, ABC-2 family transporter protein | | 0.34 |
| Ga0066824\_11646 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.43 |
| Ga0066824\_11647 | *pilA*-C |  | 0.47 |
| Ga0066824\_11648 | epilin |  | 0.38 |
| Ga0066824\_11649 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.39 |
| Ga0066824\_11650 | *xapJ*, ADP-heptose:LPS heptosyltransferase | | 0.38 |
| Ga0066824\_11651 | *xapF*, Glycosyltransferase, GT2 family | | 0.37 |
| Ga0066824\_11652 | UDP-galactopyranose mutase | | 0.37 |
| Ga0066824\_11653 | putative horizontal transfer gene protein | DDE superfamily endonuclease | 0.38 |
| Ga0066824\_103400 | *pilR* |  | 0.4 |
| 23 genes |  |  |  |
| Ga0066824\_103424 | *pilY1* |  | 0.42 |
| Ga0066824\_103425 | *pilX* |  | 0.4 |
| Ga0066824\_103426 | *pilV* |  | 0.4 |
| Ga0066824\_103427 | *pilW* |  | 0.42 |
| Ga0066824\_103428 | *fimT* |  | 0.43 |
| **Ga0066824\_103429** | **Predicted ATPase, AAA+ superfamily** | | **0.31** |
| Ga0066824\_103430 | putative horizontal gene transfer protein | Fido domain | 0.38 |
| Ga0066824\_103431 | hypothetical protein | | 0.41 |
| Ga0066824\_103432 | *xapG*, lipopolysaccharide transport system permease | | 0.35 |
| Ga0066824\_103433 | putative horizontal gene transfer protein | Integrase core domain-containing protein | 0.4 |
| Ga0066824\_103136 | *pilB* |  | 0.41 |
| 8 genes |  |  |  |
| Ga0066824\_103145 | putative horizontal gene transfer protein | Phage integrase family protein | 0.37 |

AH. Pilin gene clusters found in the *Geobacter soli* genome. Three pilin gene clusters were identified in this genome. Three genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of *G. soli* is 61.76%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty out of 72 genes (28%) in these clusters have GC content that is > 7% from the overall average, including *e-pilin, xapA, xapE, pilV, pilW* and *pilX*.

|  |  |  |  |
| --- | --- | --- | --- |
| Geobacter soli | GC content is 61.76% | horizontal transfer gene | GC content |
| **Ga0077628\_111560** | **Haloacid dehalogenase-like hydrolase** | | **0.54** |
| Ga0077628\_111561 | Glycosyltransferase involved in cell wall bisynthesis | | 0.56 |
| Ga0077628\_111562 | Glycosyltransferase involved in cell wall bisynthesis | | 0.56 |
| Ga0077628\_111563 | Methyltransferase domain-containing protein | | 0.57 |
| Ga0077628\_111564 | perosamine synthetase | | 0.57 |
| **Ga0077628\_111565** | **RmlC-like cupin domain** | | **0.53** |
| **Ga0077628\_111566** | **Glycosyl transferase family 2** | | **0.53** |
| **Ga0077628\_111567** | **Glycosyltransferase involved in cell wall bisynthesis** | | **0.49** |
| **Ga0077628\_111568** | **Glycosyltransferase involved in cell wall bisynthesis** | | **0.5** |
| **Ga0077628\_111569** | **UDP-glucose 4-epimerase** | | **0.49** |
| **Ga0077628\_111570** | **Glycosyl transferases group 1** | | **0.39** |
| **Ga0077628\_111571** | ***xapI*, Methyltransferase domain-containing protein** | | **0.41** |
| **Ga0077628\_111572** | **ABC-type polysaccharide/polyol phosphate transport system, ATPase component** | | **0.47** |
| Ga0077628\_111573 | *xapG*, lipopolysaccharide transport system permease protein | | 0.56 |
| Ga0077628\_111574 | *xapF*, Glycosyl transferase family 2 | | 0.57 |
| **Ga0077628\_111575** | ***xapE*, 4-hydroxybenzoate polyprenyltransferase** | | **0.54** |
| **Ga0077628\_111576** | ***xapD*, ABC-2 type transport system ATP-binding protein** | | **0.47** |
| **Ga0077628\_111577** | **hypothetical protein** |  | **0.45** |
| **Ga0077628\_111578** | ***xapB*, ABC-2 family transporter protein** | | **0.41** |
| **Ga0077628\_111579** | ***xapA*, Tetratricopeptide repeat-containing protein** | | **0.45** |
| **Ga0077628\_111580** | **e-pilin** |  | **0.49** |
| Ga0077628\_111581 | *pilR* |  | 0.59 |
| Ga0077628\_111582 | *pilS* |  | 0.59 |
| Ga0077628\_111583 | *pilC* |  | 0.58 |
| Ga0077628\_111584 | *pilT* |  | 0.61 |
| Ga0077628\_111585 | *pilB* |  | 0.6 |
| Ga0077628\_111586 | *aroE* |  | 0.63 |
| Ga0077628\_111587 | DUF2723 |  | 0.6 |
| Ga0077628\_111588 | Lysylphosphatidylglycerol synthase TM region | | 0.64 |
| Ga0077628\_111589 | flavokinase |  | 0.61 |
| Ga0077628\_111590 | *tatC* |  | 0.56 |
| Ga0077628\_111591 | RNAse R |  | 0.63 |
| Ga0077628\_111592 | soluble lytic murein transglycosylase | | 0.63 |
| Ga0077628\_111593 | DNA-binding transcriptional regulator, MarR family | | 0.59 |
| Ga0077628\_111977 | Putative nucleotidyltransferase substrate binding domain-containing protein | | 0.62 |
| Ga0077628\_111978 | *pilY1* |  | 0.62 |
| Ga0077628\_111979 | *pilX* |  | 0.62 |
| Ga0077628\_111980 | *pilW* |  | 0.62 |
| Ga0077628\_111981 | *pilV* |  | 0.59 |
| Ga0077628\_111982 | hypothetical protein |  | 0.64 |
| Ga0077628\_111983 | aspartate aminotransferase | | 0.65 |
| Ga0077628\_111984 | hypothetical protein |  | 0.61 |
| Ga0077628\_11906 | diguanylate cyclase (GGDEF) domain | | 0.62 |
| Ga0077628\_11907 | *pilD* |  | 0.6 |
| Ga0077628\_11908 | *pilS* |  | 0.65 |
| Ga0077628\_11909 | *pilR* |  | 0.62 |
| Ga0077628\_11910 | prepilin-type N-terminal cleavage/methylation domain-containing protein | | 0.6 |
| Ga0077628\_11911 | *pilY1* |  | 0.55 |
| Ga0077628\_11912 | Pili subunits |  | 0.52 |
| **Ga0077628\_11913** | ***pilV*** |  | **0.53** |
| **Ga0077628\_11914** | ***pilW*** |  | **0.54** |
| **Ga0077628\_11915** | ***pilX*** |  | **0.53** |
| Ga0077628\_11916 | GEMM cis-regulatory element | | 0.52 |
| **Ga0077628\_11917** | **putative horizontal transfer gene protein** | **Lambda repressor-like, DNA-binding domain** | **0.53** |
| Ga0077628\_11918 | *pilM* |  | 0.56 |
| Ga0077628\_11919 | *pilN* |  | 0.57 |
| Ga0077628\_11920 | *pilO* |  | 0.55 |
| Ga0077628\_11921 | *pilP* |  | 0.59 |
| Ga0077628\_11922 | *pilQ* |  | 0.6 |
| **Ga0077628\_11923** | **PS51257  Prokaryotic membrane lipoprotein lipid attachment** | | **0.48** |
| Ga0077628\_11924 | *aroC* |  | 0.63 |
| Ga0077628\_11925 | *aroK* |  | 0.61 |
| Ga0077628\_11926 | *aroB* |  | 0.64 |
| Ga0077628\_11927 | Tetratricopeptide repeat-containing protein | | 0.62 |
| Ga0077628\_11928 | Roadblock/LC7 domain | | 0.61 |
| Ga0077628\_11929 | *aroQ* |  | 0.6 |
| Ga0077628\_11930 | Xaa-Pro aminopeptidase | | 0.61 |
| Ga0077628\_11931 | biotin carboxyl carrier protein | | 0.62 |
| Ga0077628\_11932 | biotin carboxylase |  | 0.6 |
| Ga0077628\_11933 | glycine cleavage system H protein | | 0.59 |
| Ga0077628\_11934 | chorismate dehydratase | | 0.61 |
| Ga0077628\_11935 | diguanylate cyclase (GGDEF) domain | | 0.58 |

AI. Pilin gene clusters found in the *Geobacter sp. OR-1* genome. Three pilin gene clusters were identified in this genome. Four genes coding for horizontal gene transfer proteins were present in these pilin clusters. Genes from the xap operon (*xapA-J*) were detected in the e-pilin gene cluster. The overall GC content of strain OR-1 is 54.18%. Genes with GC contents +/- 7% of this value are highlighted in bold blue. Twenty out of 84 genes (24%) in these clusters have GC content that is > 7% from the overall average, including *pilO, pilN,* and *pilM.*

|  |  |  |  |
| --- | --- | --- | --- |
| Geobacter OR-1 | GC content is 54.18% | Horizontal transfer gene | GC content |
| Ga0098289\_12615 | BioD-like N-terminal domain of phosphotransacetylase | | 0.57 |
| Ga0098289\_12616 | soluble lytic murein transglycosylase | | 0.57 |
| Ga0098289\_12617 | RNAse R |  | 0.61 |
| Ga0098289\_12618 | sec-independent protein translocase protein *TatC* | | 0.53 |
| Ga0098289\_12619 | Flavokinase |  | 0.56 |
| Ga0098289\_12620 | Lysylphosphatidylglycerol synthase TM region | | 0.57 |
| Ga0098289\_12621 | DUF2723 |  | 0.54 |
| Ga0098289\_12622 | *pilB* |  | 0.55 |
| Ga0098289\_12623 | *pilT* |  | 0.56 |
| Ga0098289\_12624 | *pilC* |  | 0.53 |
| Ga0098289\_12625 | *pilS* |  | 0.54 |
| Ga0098289\_12626 | *pilR* |  | 0.55 |
| Ga0098289\_12627 | e-pilin |  | 0.52 |
| Ga0098289\_12628 | *pilA*-C |  | 0.49 |
| Ga0098289\_12629 | hypothetical protein |  | 0.51 |
| Ga0098289\_12630 | *xapA*, TPR-like |  | 0.49 |
| Ga0098289\_12631 | *xapB*, ABC-2 family transporter protein | | 0.53 |
| Ga0098289\_12632 | TPR-like |  | 0.48 |
| Ga0098289\_12633 | *xapD*, ABC-2 type transport system ATP-binding protein | | 0.52 |
| Ga0098289\_12634 | *xapE*, 4-hydroxybenzoate polyprenyltransferase | | 0.5 |
| Ga0098289\_12635 | *xapF*, Glycosyltransferase, GT2 family | | 0.53 |
| Ga0098289\_12636 | *xapG*, lipopolysaccharide transport system permease protein | | 0.53 |
| Ga0098289\_12637 | *xapH*, lipopolysaccharide transport system ATP-binding protein | | 0.48 |
| **Ga0098289\_12638** | **Radical SAM superfamily enzyme, MoaA/NifB/PqqE/SkfB family** | | **0.46** |
| Ga0098289\_12639 | Glycosyl transferases group 1 | | 0.49 |
| **Ga0098289\_12640** | **S-adenosyl-L-methionine-dependent methyltransferases** | | **0.46** |
| **Ga0098289\_12641** | **hypothetical protein** |  | **0.45** |
| **Ga0098289\_12642** | **hypothetical protein** |  | **0.46** |
| **Ga0098289\_12643** | ***xapI*, Methyltransferase small domain-containing protein** | | **0.43** |
| **Ga0098289\_12644** | **Polysaccharide pyruvyl transferase family protein WcaK** | | **0.46** |
| Ga0098289\_12645 | Glycosyltransferase involved in cell wall bisynthesis | | 0.48 |
| Ga0098289\_12646 | Glycosyltransferase involved in cell wall bisynthesis | | 0.47 |
| **Ga0098289\_12647** | **Glycosyltransferase involved in cell wall bisynthesis** | | **0.38** |
| **Ga0098289\_12648** | **Glycosyltransferase, GT2 family** | | **0.41** |
| Ga0098289\_12649 | CDP-alcohol phosphatidyltransferase | | 0.48 |
| Ga0098289\_12650 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | | 0.49 |
| Ga0098289\_10198 | chorismate dehydratase | | 0.5 |
| Ga0098289\_10199 | glycine cleavage system H protein | | 0.51 |
| Ga0098289\_10200 | biotin carboxylase |  | 0.53 |
| Ga0098289\_10201 | biotin carboxyl carrier protein | | 0.52 |
| Ga0098289\_10202 | Xaa-Pro aminopeptidase | | 0.55 |
| Ga0098289\_10203 | *aroQ* |  | 0.49 |
| Ga0098289\_10204 | Roadblock/LC7 domain | | 0.47 |
| Ga0098289\_10205 | Tetratricopeptide repeat-containing protein | | 0.52 |
| Ga0098289\_10206 | *aroB* |  | 0.55 |
| Ga0098289\_10207 | *aroC* |  | 0.55 |
| Ga0098289\_10208 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.5 |
| Ga0098289\_10209 | PS51257  Prokaryotic membrane lipoprotein lipid attachment | | 0.49 |
| Ga0098289\_10210 | *pilQ* |  | 0.5 |
| Ga0098289\_10211 | *pilP* |  | 0.44 |
| **Ga0098289\_10212** | ***pilO*** |  | **0.46** |
| **Ga0098289\_10213** | ***pilN*** |  | **0.43** |
| **Ga0098289\_10214** | ***pilM*** |  | **0.45** |
| **Ga0098289\_10215** | **putative horizontal transfer gene protein** | **Lambda repressor-like, DNA-binding domain** | **0.38** |
| **Ga0098289\_10216** | **putative horizontal transfer gene protein** | **DNA polymerase lambda, fingers domain** | **0.42** |
| Ga0098289\_10217 | *pilX* |  | 0.49 |
| Ga0098289\_10218 | *pilW* |  | 0.5 |
| Ga0098289\_10219 | *pilV* |  | 0.51 |
| Ga0098289\_10220 | pilE |  | 0.48 |
| Ga0098289\_10221 | *pilY1* |  | 0.52 |
| **Ga0098289\_10222** | **hypothetical protein** |  | **0.41** |
| Ga0098289\_10223 | thiol:disulfide interchange protein DsbC | | 0.49 |
| Ga0098289\_10224 | *pilR* |  | 0.51 |
| Ga0098289\_10225 | *pilS* |  | 0.51 |
| Ga0098289\_10226 | *pilD* |  | 0.51 |
| Ga0098289\_101108 | S51257  Prokaryotic membrane lipoprotein lipid attachment |  | 0.5 |
| Ga0098289\_101109 | S51257  Prokaryotic membrane lipoprotein lipid attachment |  | 0.49 |
| Ga0098289\_101110 | *pilQ* |  | 0.5 |
| Ga0098289\_101111 | *pilP* |  | 0.44 |
| Ga0098289\_101112 | *pilO* |  | 0.46 |
| Ga0098289\_101113 | *pilN* |  | 0.43 |
| Ga0098289\_101114 | *pilM* |  | 0.45 |
| Ga0098289\_101115 | putative horizontal transfer gene | Lambda repressor-like, DNA-binding domain | 0.38 |
| Ga0098289\_101116 | putative horizontal transfer gene | DNA polymerase lambda, fingers domain | 0.42 |
| Ga0098289\_101117 | hypothetical protein |  | 0.49 |
| Ga0098289\_101118 | *pilW* |  | 0.5 |
| Ga0098289\_101119 | *pilV* |  | 0.51 |
| Ga0098289\_101120 | *pile* |  | 0.48 |
| Ga0098289\_101121 | *pilY1* |  | 0.52 |
| **Ga0098289\_101122** | **hypothetical protein** |  | **0.41** |
| Ga0098289\_101123 | *pilR* |  | 0.49 |
| Ga0098289\_101124 | *pilS* |  | 0.51 |
| Ga0098289\_101125 | *pilD* |  | 0.51 |
| Ga0098289\_101126 |  |  | 0.51 |