

Table S9 Enzymes and other proteins predicted from the haloarchaeal genomes involved in the main metabolic pathways to be relevant for their ecophysiology. AA similarity obtained by direct protein sequences comparison using the RAST Prokaryotic Genome Annotation Server.

| Primary transport | gene_name | locus HTSR1 | locus HSR6 | AA similarity |
|--|-----------|-------------|------------|---------------|
| Oligopeptide transport ATP-binding protein OppF (TC 3.A.1.5.1) | | HTSR_0046 | HSR6_0046 | 98.53 |
| Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2) | | HTSR_0047 | HSR6_0047 | 98.56 |
| Dipeptide transport system permease protein DppB (TC 3.A.1.5.2) | | HTSR_0048 | HSR6_0048 | 99.12 |
| Dipeptide transport system permease protein DppC (TC 3.A.1.5.2) | | HTSR_0049 | HSR6_0049 | 100 |
| Ferric iron ABC transporter, permease protein | | HTSR_0119 | HSR6_0118 | 99.81 |
| Iron(III) ABC transporter, periplasmic-binding protein | | HTSR_0120 | HSR6_0119 | 100 |
| ABC transporter ATP-binding protein | | HTSR_0121 | HSR6_0120 | 98.41 |
| Amidase clustered with urea ABC transporter and nitrile hydratase functions | | HTSR_0209 | HSR6_1370 | 36.74 |
| ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1) | potD | HTSR_0210 | | |
| Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) | potA | HTSR_0211 | HSR6_2144 | 47.44 |
| Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1) | potB | HTSR_0212 | HSR6_2145 | 26.72 |
| Spermidine Putrescine ABC transporter permease component potC (TC 3.A.1.11.1) | potC | HTSR_0213 | HSR6_1703 | 29.61 |
| Probable transmembrane protein (transporter component) | | HTSR_0371 | HSR6_0356 | 100 |
| Zn-dependent hydroxyacylglutathione hydrolase | | HTSR_0372 | HSR6_0357 | 99.5 |
| ABC-type transport system, permease component | | HTSR_0373 | HSR6_0358 | 100 |
| ABC transporter, ATP-binding protein | | HTSR_0374 | HSR6_0359 | 100 |
| S-layer domain (syalidase) | | HTSR_0375 | HSR6_0360 | 99.03 |
| hypothetical protein | | HTSR_0641 | HSR6_0666 | 100 |
| ATPase component CbiO of energizing module of cobalt ECF transporter | | HTSR_0642 | HSR6_0667 | 100 |
| Transmembrane component CbiQ of energizing module of cobalt ECF transporter | | HTSR_0643 | HSR6_0668 | 99.26 |
| Cobalamin transport operon protein | | HTSR_0644 | HSR6_0669 | 100 |
| Substrate-specific component NikM of nickel ECF transporter | | HTSR_0645 | HSR6_0670 | 100 |
| Vitamin B12 ABC transporter, ATPase component BtuD | | HTSR_0646 | HSR6_0671 | 100 |
| Iron(III) dicitrate transport system permease protein | | HTSR_0647 | HSR6_0672 | 100 |
| iron (III) ABC transporter, ATP-binding protein (hemV-2) | | HTSR_0648 | HSR6_0673 | 100 |
| conserved hypothetical protein (probable surface protein) | | HTSR_0692 | HSR6_0718 | 99.79 |
| Cell division transporter, ATP-binding protein FtsE (TC 3.A.5.1.1) | | HTSR_0693 | HSR6_0719 | 100 |
| Cell division protein FtsX | | HTSR_0694 | HSR6_0720 | 100 |
| Nucleoside ABC transporter, permease protein 2 | rbsC2 | HTSR_0793 | HSR6_0820 | 99.72 |
| Nucleoside ABC transporter, permease protein 1 | rbsC1 | HTSR_0794 | HSR6_0821 | 98.32 |
| ABC transporter ATP-binding protein | | HTSR_0795 | HSR6_0822 | 96.54 |
| Nucleoside ABC transporter, periplasmic nucleoside-binding protein | | HTSR_0796 | HSR6_0823 | 100 |
| Arsenical pump-driving ATPase (EC 3.6.3.16) | arsA | HTSR_0815 | HSR6_0842 | 99.03 |
| Lipid A export ATP-binding/permease protein MsbA | | HTSR_0879 | HSR6_0894 | 99.66 |
| ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | | HTSR_0918 | HSR6_0932 | 92.94 |
| hypothetical protein | | HTSR_0919 | HSR6_0933 | 88.1 |
| ABC-type nitrate/sulfonate/bicarbonate transport system, permease component | | HTSR_0920 | HSR6_0934 | 95.42 |
| ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component | | HTSR_0921 | HSR6_0935 | 99.62 |
| Glutamine ABC transporter, periplasmic glutamine-binding protein (TC 3.A.1.3.2) | glnH | HTSR_1007 | HSR6_1040 | 97.78 |
| Polar amino acid ABC transporter, inner membrane subunit | glnP | HTSR_1008 | HSR6_1041 | 96.51 |
| Glutamine transport ATP-binding protein GlnQ (TC 3.A.1.3.2) | glnQ | HTSR_1009 | HSR6_1042 | 95.63 |
| Putative transport system permease protein (amino acid ABC transporter permease) | | HTSR_1010 | HSR6_1043 | 99.67 |
| Permease of the drug/metabolite transporter (DMT) superfamily | | HTSR_1632 | HSR6_1701 | 100 |
| Tungstate ABC transporter, periplasmic substrate-binding protein WtpA | | HTSR_1633 | HSR6_1702 | 94.75 |
| Tungstate ABC transporter, permease protein WtpB | | HTSR_1634 | HSR6_1703 | 97.83 |
| Ferric iron ABC transporter, ATP-binding protein | cysA | HTSR_1635 | HSR6_1704 | 98.26 |
| Substrate-specific component PdxU2 of predicted pyridoxin-related ECF transporter | | HTSR_1775 | HSR6_1841 | 82.63 |
| Duplicated ATPase component YkoD of energizing module of thiamin-regulated ECF transporter for Hydroxymethylpyrimidine | cbiO1 | HTSR_1776 | HSR6_1842 | 93.12 |
| ATPase component NikO of energizing module of nickel ECF transporter | cbiO2 | HTSR_1777 | HSR6_1843 | 88.93 |
| Transmembrane component STY3231 of energizing module of queuosine-regulated ECF transporter | | HTSR_1778 | HSR6_1844 | 94.09 |
| ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | | HTSR_1851 | HSR6_1920 | 100 |
| ABC-type nitrate/sulfonate/bicarbonate transport system, permease component | | HTSR_1852 | HSR6_1921 | 100 |
| ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component; sulfonate ABC transporter ATP binding protein(EC:3.6.3.25) | | HTSR_1853 | HSR6_1922 | 98.83 |
| ABC-type tungstate transport system, ATP-binding protein | tupc | HTSR_1924 | HSR6_1995 | 65.06 |
| ABC-type tungstate transport system, permease protein | tupA | HTSR_1925 | HSR6_1993 | 70.14 |
| ABC-type tungstate transport system, periplasmic binding protein | tupB | HTSR_1926 | HSR6_1994 | 70.06 |
| DNA-binding domain of ModE / Molybdate-binding domain of ModE | modE | HTSR_1927 | HSR6_1996 | 83.33 |
| Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1) | pstS | HTSR_1928 | HSR6_1997 | 95.67 |
| Phosphate transport system permease protein PstC (TC 3.A.1.7.1) | pstC | HTSR_1929 | HSR6_1998 | 97.53 |
| Phosphate transport system permease protein PstA (TC 3.A.1.7.1) | pstA | HTSR_1930 | HSR6_1999 | 99.06 |
| Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1) | pstB | HTSR_1931 | HSR6_2000 | 100 |
| Signal recognition particle, subunit Ffh SRP54 (TC 3.A.5.1.1) | | HTSR_2039 | HSR6_2115 | 99.78 |
| Mg/Co/Ni transporter MgtE | | HTSR_2040 | HSR6_2116 | 98.49 |
| Mg/Co/Ni transporter MgtE | | HTSR_2041 | HSR6_2117 | 99.47 |
| predicted transporter | | HTSR_2066 | HSR6_2142 | 97.52 |
| Thiamin ABC transporter, substrate-binding component | thiB | HTSR_2067 | HSR6_2143 | 94.55 |
| Thiamin ABC transporter, transmembrane component | thiP | HTSR_2068 | HSR6_2144 | 96.97 |
| Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) | thiQ | HTSR_2069 | HSR6_2145 | 100 |
| ABC transporter permease protein with unknown substrate | | HTSR_1549 | HSR6_1619 | 100 |
| Caffeoyl-CoA O-methyltransferase | | HTSR_1550 | HSR6_1620 | 99.58 |
| ABC transporter substrate-binding protein | | HTSR_1551 | HSR6_1621 | 99.75 |
| ABC-type probable sulfate transporter, ATPase component | | HTSR_1552 | HSR6_1622 | 99.64 |
| Alkanesulfonates transport system permease protein | | HTSR_1553 | HSR6_1623 | 100 |
| Vitamin B12 ABC transporter, permease component BtuC | btuC | HTSR_1674 | HSR6_1742 | 100 |
| Vitamin B12 ABC transporter, ATPase component BtuD | btuD | HTSR_1675 | HSR6_1743 | 99.77 |
| Trimethylamine methyltransferase family protein | | HTSR_1676 | HSR6_1744 | 99.79 |
| Vitamin B12 ABC transporter, B12-binding component BtuF | | HTSR_1758 | HSR6_1824 | 99.43 |
| Substrate-specific component CbiM of cobalt ECF transporter | cbiM | HTSR_1836 | HSR6_1905 | 99.09 |
| Additional substrate-specific component CbiN of cobalt ECF transporter | cbiN | HTSR_1837 | HSR6_1906 | 100 |
| Transmembrane component CbiQ of energizing module of cobalt ECF transporter | cbiQ | HTSR_1838 | HSR6_1907 | 98.76 |
| ATPase component CbiO of energizing module of cobalt ECF transporter | cbiO | HTSR_1839 | HSR6_1908 | 99.57 |
| Potassium channel protein | | HTSR_1155 | HSR6_1190 | 99.81 |
| Transcriptional regulator, AsnC family | | HTSR_1156 | HSR6_1191 | 99.49 |
| Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | copB | HTSR_1157 | HSR6_1192 | 99.3 |
| Mercuric transport protein | | HTSR_1158 | HSR6_1193 | 100 |
| Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4) | | HTSR_0574 | HSR6_0562 | 99.18 |
| Secondary transport | | | | |
| hypothetical protein (Na ⁺ /H ⁺ antiporter (sodium/proton antiporter) | | HTSR_0020 | HSR6_0020 | 100 |
| amino acid transporter | | HTSR_0021 | HSR6_0021 | 98.78 |
| Probable low-affinity inorganic phosphate transporter (PiT) | | HTSR_0025 | HSR6_0025 | 100 |
| Probable low-affinity inorganic phosphate transporter (PiT) | | HTSR_0026 | HSR6_0026 | 100 |

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| cationic amino acid transporter (UspA domain) | uspA2 | HTSR_0027 | HSR6_0027 | 95.59 |
| Magnesium and cobalt efflux protein CorC | | HTSR_0072 | HSR6_0071 | 99.78 |
| Probable low-affinity inorganic phosphate transporter | | HTSR_0073 | HSR6_0072 | 99.23 |
| Probable low-affinity inorganic phosphate transporter | | HTSR_0362 | HSR6_0252 | 53.35 |
| Probable low-affinity inorganic phosphate transporter | | HTSR_0454 | HSR6_0439 | 97.87 |
| Sodium-and chloride-dependent transporter | | HTSR_0253 | HSR6_0240 | 95.99 |
| Trk system potassium uptake protein TrkA (NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporter) | | HTSR_0255 | HSR6_0242 | 99.51 |
| UPF0098 protein MTH_273 Select (phosphatidylethanolamine-binding protein) | | HTSR_0256 | HSR6_0243 | 87.33 |
| Potassium uptake protein TrkH | | HTSR_0357 | HSR6_0342 | 98.28 |
| Trk system potassium uptake protein TrkA | | HTSR_0358 | HSR6_0343 | 94.27 |
| sodium/pantothenate symporter | | HTSR_0394 | HSR6_0379 | 99 |
| Potassium uptake protein TrkH | trkH | HTSR_0461 | HSR6_0446 | 99.81 |
| Trk system potassium uptake protein TrkA | trkA | HTSR_0462 | HSR6_0447 | 97.75 |
| Sodium/calcium exchanger | | HTSR_0573 | HSR6_0561 | 96.79 |
| Trk system potassium uptake protein TrkA | | HTSR_0925 | HSR6_0939 | 100 |
| Sulfate permease, Trk-type | | HTSR_0957 | HSR6_0988 | 99.84 |
| Na ⁺ /H ⁺ antiporter NhaC | | HTSR_0998 | HSR6_1031 | 99.11 |
| Na ⁺ /H ⁺ antiporter | nhaC | HTSR_1314 | HSR6_1387 | 80.08 |
| pH adaptation potassium efflux system protein E; sodium- potassium/hydrogen antiporter subunit E | | HTSR_1024 | HSR6_1057 | 99.73 |
| Multiple resistance and pH regulation protein F precursor | | HTSR_1025 | HSR6_1058 | 100 |
| pH adaptation potassium efflux system protein G; sodium- potassium/hydrogen antiporter subunit G | | HTSR_1026 | HSR6_1059 | 100 |
| pH adaptation potassium efflux system protein B1; sodium- potassium/hydrogen antiporter subunit B1 | | HTSR_1027 | HSR6_1060 | 100 |
| pH adaptation potassium efflux system protein B2; sodium- potassium/hydrogen antiporter subunit B2 | | HTSR_1028 | HSR6_1061 | 100 |
| pH adaptation potassium efflux system protein C; sodium- potassium/hydrogen antiporter subunit C | | HTSR_1029 | HSR6_1062 | 100 |
| pH adaptation potassium efflux system protein D 1 | | HTSR_1030 | HSR6_1063 | 100 |
| pH adaptation potassium efflux system protein D 2 | | HTSR_1031 | HSR6_1064 | 99.82 |
| pH adaptation potassium efflux system protein D 3 | | HTSR_1032 | HSR6_1065 | 100 |
| TRAP transporter solute receptor, unknown substrate 1 (C4-dicarboxylate ABC transporter substrate-binding protein) | | HTSR_0198 | HSR6_0196 | 100 |
| DUF1850 domain-containing protein (C4-dicarboxylate ABC transporter) | | HTSR_0199 | HSR6_0197 | 100 |
| TRAP transporter, 4TM/12TM fusion protein, unknown substrate 1 | | HTSR_0200 | HSR6_0198 | 99.11 |
| Sodium-dependent transporter | | HTSR_1902 | HSR6_1972 | 100 |
| Sodium-dependent transporter | | HTSR_1993 | HSR6_2069 | 100 |
| Glycine betaine transporter OpuD | | HTSR_0234 | HSR6_0221 | 100 |
| Potassium voltage-gated channel subfamily KQT; possible potassium channel, VIC family | | HTSR_0427 | HSR6_0412 | 98.92 |
| Zinc transporter, ZIP family | | HTSR_0428 | HSR6_0413 | 99.55 |
| Magnesium and cobalt efflux protein CorC | | HTSR_0429 | HSR6_0414 | 99.1 |
| Amino acid permease (transporter substrate cationic amino acids) | | HTSR_0432 | HSR6_0417 | 98.51 |
| Permease of the drug/metabolite transporter (DMT) superfamily | | HTSR_0490 | HSR6_0474 | 97.68 |
| putative sugar transporter | | HTSR_0521 | HSR6_0505 | 97.68 |
| Mn ²⁺ and Fe ²⁺ transporters of the NRAMP family | | HTSR_0605 | HSR6_0593 | 99.77 |
| Transporter (permease) | | HTSR_0632 | HSR6_0657 | 99.74 |
| Metal transporter, ZIP family | | HTSR_0949 | HSR6_0949 | 98.94 |
| Nitrate/nitrite transporter NarK | | HTSR_0976 | HSR6_1007 | 99.51 |
| Permease of the drug/metabolite transporter (DMT) superfamily | | HTSR_1073 | HSR6_1110 | 99.41 |
| Transporter | | HTSR_1214 | HSR6_1284 | 100 |
| Phosphate transport system regulatory protein PhoU | phoU2 | HTSR_1311 | HSR6_1384 | 100 |
| Sugar transporter | | HTSR_1459 | HSR6_1531 | 99.75 |
| Permease of the drug/metabolite transporter (DMT) superfamily | | HTSR_1632 | HSR6_1701 | 100 |
| Major facilitator superfamily transporter | | HTSR_1637 | HSR6_1706 | 100 |
| Na ⁺ /solute symporter | | HTSR_1708 | HSR6_1779 | 99.6 |
| Nitrate/nitrite transporter | | HTSR_1709 | HSR6_1780 | 100 |
| Glycine betaine transporter OpuD | | HTSR_1753 | HSR6_1819 | 100 |
| metal transporter family GufA protein | zupT | HTSR_1785 | HSR6_1852 | 100 |
| Transporter | | HTSR_1948 | HSR6_2023 | 99.48 |
| Putative preQ0 transporter | | HTSR_1987 | HSR6_2063 | 100 |
| Multi antimicrobial extrusion protein (Na ⁺)/drug antiporter), MATE family of MDR efflux pumps | | HTSR_1266 | HSR6_1339 | 100 |
| Cation-transporting ATPase, E1-E2 family | | HTSR_1250 | HSR6_1322 | 96.58 |
| Amino acid permease | | HTSR_1324 | HSR6_1397 | 100 |
| hypothetical protein (sugar phosphate permease) | | HTSR_1108 | HSR6_1145 | 98.81 |
| Amino acid permease | | HTSR_0446 | HSR6_0431 | 97.54 |
| Probable Co/Zn/Cd efflux system membrane fusion protein | | HTSR_1319 | HSR6_1392 | 100 |
| oxalate/formate antiporter (oxIT-2) | | HTSR_1713 | HSR6_1784 | 98.37 |
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| Carbohydrate metabolism | | | | |
| Glycolysis | | | | |
| Glucose-6-phosphatase(EC:3.1.3.9) | | HTSR_0832 | HSR6_0859 | 97.24 |
| Glucose-6-phosphate isomerase (EC 5.3.1.9) | pgi | HTSR_0138 | HSR6_0139 | 100 |
| Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11) | fbp | HTSR_1162 | HSR6_1197 | 100 |
| Fructose-bisphosphate aldolase, archaeal class I (EC 4.1.2.13) | fba | HTSR_1163 | HSR6_1198 | 100 |
| Triosephosphate isomerase (EC 5.3.1.1) | tpiA | HTSR_0915 | HSR6_0929 | 99.06 |
| NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase archaeal (EC 1.2.1.59) | gapB | HTSR_0246 | HSR6_0233 | 100 |
| Phosphoglycerate kinase (EC 2.7.2.3) | pgk | HTSR_0715 | HSR6_0741 | 99.75 |
| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) | gpmI | HTSR_1830 | HSR6_1899 | 100 |
| Enolase (EC 4.2.1.11) | eno | HTSR_0767 | HSR6_0793 | 100 |
| Pyruvate kinase (EC 2.7.1.40) | pykF | HTSR_1429 | HSR6_1501 | 100 |
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| Gluconeogenesis | | | | |
| Phosphoenolpyruvate synthase (EC 2.7.9.2) | ppsA | HTSR_1423 | HSR6_1495 | 98 |
| Enolase (EC 4.2.1.11) | eno | HTSR_0767 | HSR6_0793 | 100 |
| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) | gpmI | HTSR_1830 | HSR6_1899 | 100 |
| Phosphoglycerate kinase (EC 2.7.2.3) | pgk | HTSR_0715 | HSR6_0741 | 99.75 |
| NAD(P)-dependent glyceraldehyde 3-phosphate dehydrogenase archaeal (EC 1.2.1.59) | gapB | HTSR_0246 | HSR6_0233 | 100 |
| Triosephosphate isomerase (EC 5.3.1.1) | tpiA | HTSR_0915 | HSR6_0929 | 99.06 |
| Fructose-bisphosphate aldolase, archaeal class I (EC 4.1.2.13) | fba | HTSR_1163 | HSR6_1198 | 100 |
| Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11) | fbp | HTSR_1162 | HSR6_1197 | 100 |
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| Glycerol metabolism | | | | |
| Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3) | glpA | HTSR_0841 | HSR6_0869 | 98.11 |
| Anaerobic glycerol-3-phosphate dehydrogenase subunit C (EC 1.1.5.3) | glpC | HTSR_0842 | HSR6_0870 | 98.56 |
| Glycerol dehydrogenase (EC 1.1.1.6) | | HTSR_0114 | HSR6_0113 | 100 |
| Glycerol dehydrogenase (EC 1.1.1.6) | glpA | HTSR_0740 | HSR6_0766 | 77.32 |
| Glycerol-1-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261) | egsA | HTSR_1341 | HSR6_1413 | 100 |
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| Citric acid Cycle (oxidative) | | | | |
| Acetyl-coenzyme A synthetase (EC 6.2.1.1) | acs1 | HTSR_1608 | HSR6_1676 | 99.07 |
| Citrate synthase (si) (EC 2.3.3.1) | glfA | HTSR_1879 | HSR6_1949 | 99.74 |
| Aconitate hydratase (EC 4.2.1.3) | acnA | HTSR_1672 | HSR6_1740 | 99.78 |
| Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) | icd | HTSR_1855 | HSR6_1924 | 100 |
| 2-oxoglutarate oxidoreductase, alpha subunit (EC 1.2.7.3) | korA | HTSR_0781 | HSR6_0808 | 100 |
| 2-oxoglutarate oxidoreductase, beta subunit (EC 1.2.7.3) | korB | HTSR_0782 | HSR6_0809 | 100 |
| Dihydropyrimidine dehydrogenase of acetoin dehydrogenase (EC 1.8.1.4) / Dihydropyrimidine dehydrogenase (EC 1.8.1.4) | lpdA | HTSR_0182 | HSR6_0180 | 87.47 |
| Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) | sucD | HTSR_0528 | HSR6_0512 | 99.66 |
| Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) | sucC | HTSR_0529 | HSR6_0513 | 98.71 |
| Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | sdhA | HTSR_0612 | HSR6_0600 | 98.68 |
| Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | sdhB | HTSR_0613 | HSR6_0601 | 100 |
| Succinate dehydrogenase hydrophobic membrane anchor protein | sdhD | HTSR_0614 | HSR6_0602 | 98.36 |
| Succinate dehydrogenase cytochrome b subunit | sdhC | HTSR_0615 | HSR6_0603 | 97.2 |
| succinate dehydrogenase subunit | | HTSR_0616 | HSR6_0604 | 94.12 |
| Fumarate hydratase class II (EC 4.2.1.2) | fumC | HTSR_1079 | HSR6_1116 | 99.79 |
| Phosphoenolpyruvate carboxylase (EC 4.1.1.31) | ppc | HTSR_1261 | HSR6_1334 | 99.89 |
| NADP-dependent malic enzyme (EC 1.1.1.40) | maeB | HTSR_0493 | HSR6_0477 | 99.74 |
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| Respiration | | | | |
| V-type ATP synthase subunit D (EC 3.6.3.14) | atpD | HTSR_1802 | HSR6_1871 | 100 |
| 5-methyltetrahydropteroyltryglutamate-homocysteine methyltransferase (EC 2.1.1.14) | metE | HTSR_1803 | HSR6_1872 | 99.43 |
| V-type ATP synthase subunit B (EC 3.6.3.14) | atpB | HTSR_1804 | HSR6_1873 | 99.79 |
| V-type ATP synthase subunit A (EC 3.6.3.14) | atpA | HTSR_1805 | HSR6_1874 | 100 |
| V-type ATP synthase subunit F (EC 3.6.3.14) | atpF | HTSR_1806 | HSR6_1875 | 100 |
| V-type ATP synthase subunit C (EC 3.6.3.14) | atpC | HTSR_1807 | HSR6_1876 | 100 |

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|--|--------|-----------|-----------|-------|
| V-type ATP synthase subunit E (EC 3.6.3.14) | atpE | HTSR_1808 | HSR6_1877 | 100 |
| V-type ATP synthase subunit K (EC 3.6.3.14) | atpK | HTSR_1809 | HSR6_1878 | 100 |
| V-type ATP synthase subunit I (EC 3.6.3.14) | atpI | HTSR_1810 | HSR6_1879 | 99.04 |
| V-type ATP synthase subunit G (EC 3.6.3.14) | | HTSR_1811 | HSR6_1880 | 100 |
| Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-) | cydA | HTSR_0807 | HSR6_0834 | 100 |
| Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-) | cydB | HTSR_0808 | HSR6_0835 | 96.68 |
| Transport ATP-binding protein CydC | | HTSR_1769 | HSR6_1835 | 99.84 |
| Polysulfide reductase, subunit C, putative | | HTSR_1345 | HSR6_1417 | 100 |
| Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) | | HTSR_1346 | HSR6_1418 | 100 |
| Polysulfide reductase, subunit C, putative | | HTSR_1697 | HSR6_1766 | 97.78 |
| Polysulfide reductase, subunit C, putative | | HTSR_1523 | HSR6_1594 | 100 |
| Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) | dmsB2 | HTSR_1698 | HSR6_1767 | 100 |
| 4Fe-4S ferredoxin iron-sulfur binding domain protein | | HTSR_1700 | HSR6_1769 | 100 |
| Uncharacterized protein DmsE associated with anaerobic dimethyl sulfoxide respiration and trimethylamine-N-oxide respiration | | HTSR_0422 | HSR6_0407 | 97.3 |
| Anaerobic dehydrogenases, typically selenocysteine-containing (dimethylsulfoxide reductase) | | HTSR_0423 | HSR6_0408 | 99.76 |
| Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) @ Respiratory trimethylamine-N-oxide reductase, iron-sulfur subunit | | HTSR_0424 | HSR6_0409 | 100 |
| Anaerobic dimethyl sulfoxide reductase, membrane subunit @ Respiratory trimethylamine-N-oxide reductase, membrane subunit | | HTSR_0425 | HSR6_0410 | 100 |
| Anaerobic dimethyl sulfoxide reductase chaperone DmsD @ Chaperone protein TorD | | HTSR_0426 | HSR6_0411 | 100 |
| Anaerobic dimethyl sulfoxide reductase chaperone DmsD @ Chaperone protein TorD | | HTSR_0514 | HSR6_0498 | 99.45 |
| Anaerobic dimethyl sulfoxide reductase chaperone DmsD @ Chaperone protein TorD | | HTSR_1344 | HSR6_1416 | 99.09 |
| Anaerobic dimethyl sulfoxide reductase chaperone DmsD @ Chaperone protein TorD | | HTSR_1521 | HSR6_1592 | 99.55 |
| Anaerobic dimethyl sulfoxide reductase chaperone DmsD @ Chaperone protein TorD | | HTSR_1572 | HSR6_1641 | 100 |
| Polysulfide reductase, NrfD | | HTSR_0515 | HSR6_0499 | 100 |
| Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.99.-) @ Respiratory trimethylamine-N-oxide reductase, iron-sulfur subunit | | HTSR_0516 | HSR6_0500 | 100 |
| Anaerobic dehydrogenases, typically selenocysteine-containing (dimethylsulfoxide reductase) | | HTSR_0517 | HSR6_0501 | 99.88 |
| Uncharacterized protein DmsE associated with anaerobic dimethyl sulfoxide respiration and trimethylamine-N-oxide respiration | | HTSR_0518 | HSR6_0502 | 100 |
| Formate dehydrogenase -O, gamma subunit (EC 1.2.1.2) | | HTSR_0751 | HSR6_0777 | 59.49 |
| hypothetical protein (cytochrome b subunit of formate dehydrogenase) | | HTSR_1573 | HSR6_1642 | 99.67 |
| Formate dehydrogenase-O, iron-sulfur subunit (EC 1.2.1.2); Putative formate dehydrogenase iron-sulfur subunit (EC 1.2.1.2) | fdoH | HTSR_1575 | HSR6_1644 | 98.91 |
| Formate dehydrogenase-O, major subunit (EC 1.2.1.2) | fdoG | HTSR_1576 | HSR6_1645 | 98.78 |
| Formate dehydrogenase H (EC 1.2.1.2) | fdhA | HTSR_1736 | HSR6_1802 | 98.97 |
| Formate dehydrogenase (EC 1.2.1.2) (molybdopterin oxidoreductase) | | HTSR_0627 | - | - |
| Tetrathionate reductase subunit B | | HTSR_0628 | - | - |
| Sulfite reduction-associated complex DsrMKJOP protein DsrP (= HmeB) | | HTSR_0629 | - | - |
| Anaerobic dimethyl sulfoxide reductase chaperone DmsD @ Chaperone protein TorD | | HTSR_0630 | - | - |
| O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) | | HTSR_0631 | HSR6_0656 | 100 |
| Trimethylamine methyltransferase family protein | mttB | HTSR_1738 | HSR6_1804 | 100 |
| Formate-tetrahydrofolate ligase (EC 6.3.4.3) | fhs | HTSR_1739 | HSR6_1805 | 99.65 |
| Formate dehydrogenase-O, major subunit (EC 1.2.1.2) | fdhA2 | HTSR_1740 | HSR6_1806 | 100 |
| Arsenate reductase (EC 1.20.4.1) | arsC | HTSR_0173 | HSR6_0169 | 94.08 |
| Fe-S-cluster-containing hydrogenase components 1 | | HTSR_1524 | HSR6_1595 | 100 |
| Anaerobic dimethyl sulfoxide reductase chain B (EC 1.8.5.3) | dmsB | HTSR_1660 | HSR6_1728 | 77.5 |
| Anaerobic dehydrogenases, typically selenocysteine-containing (molybdopterin oxidoreductase) | | HTSR_1347 | HSR6_1419 | 100 |
| Anaerobic dehydrogenases, typically selenocysteine-containing (molybdopterin oxidoreductase) | | HTSR_1522 | HSR6_1593 | |
| Anaerobic dehydrogenases, typically selenocysteine-containing (molybdopterin oxidoreductase) | | HTSR_1661 | HSR6_1729 | 54.23 |
| Anaerobic dehydrogenases, typically selenocysteine-containing (molybdopterin oxidoreductase) | | HTSR_1699 | HSR6_1768 | 100 |
| 4Fe-4S ferredoxin iron-sulfur binding domain protein | | HTSR_1662 | HSR6_1730 | 98.15 |
| NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3) | nuoN | HTSR_1171 | HSR6_1206 | 100 |
| NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3) | nuoM | HTSR_1172 | HSR6_1207 | 100 |
| NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3) | nuoL | HTSR_1173 | HSR6_1208 | 100 |
| NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3) | nuoK | HTSR_1174 | HSR6_1209 | 100 |
| NADH dehydrogenase-like complex, subunit J2 | nuoJ2 | HTSR_1175 | HSR6_1210 | 100 |
| NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3) | nuoJ | HTSR_1176 | HSR6_1211 | 100 |
| NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3) | nuoI | HTSR_1177 | HSR6_1212 | 100 |
| NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3) | nuoH | HTSR_1178 | HSR6_1213 | 100 |
| NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3) / NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3) | nuoC | HTSR_1179 | HSR6_1214 | 99.46 |
| NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3) | nuoB | HTSR_1180 | HSR6_1215 | 99.57 |
| NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3) | nuoA | HTSR_1181 | HSR6_1216 | 100 |
| Glycerol dehydrogenase (EC 1.1.1.6) | | HTSR_0114 | HSR6_0113 | 100 |
| Glycerol dehydrogenase (EC 1.1.1.6) | gldA | HTSR_0740 | HSR6_0766 | 77.32 |
| NADH dehydrogenase (EC 1.6.99.3) | | HTSR_0023 | HSR6_0023 | 100 |
| NADH dehydrogenase (EC 1.6.99.3) | ndh | HTSR_1044 | HSR6_1077 | 99.74 |
| NADH dehydrogenase (EC 1.6.99.3) | fadH2 | HTSR_2023 | HSR6_2099 | 100 |
| Pyridine nucleotide-disulfide oxidoreductase; NADH dehydrogenase (EC 1.6.99.3) | | HTSR_1094 | HSR6_1131 | 100 |
| Glycerol-1-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261) | egsA | HTSR_1341 | HSR6_1413 | 100 |
| Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3) | glpA | HTSR_0841 | HSR6_0869 | 98.11 |
| Anaerobic glycerol-3-phosphate dehydrogenase subunit C (EC 1.1.5.3) | glpC | HTSR_0842 | HSR6_0870 | 98.56 |
| [NiFe] hydrogenase metallocenter assembly protein HypF | hypF | HTSR_0649 | HSR6_0674 | 99.87 |
| [NiFe] hydrogenase nickel incorporation-associated protein HypB | hypB | HTSR_0650 | HSR6_0675 | 98.53 |
| [NiFe] hydrogenase nickel incorporation protein HypA | hypA | HTSR_0651 | HSR6_0676 | 98.57 |
| [NiFe] hydrogenase metallocenter assembly protein HypE | hypE | HTSR_0652 | HSR6_0677 | 100 |
| [NiFe] hydrogenase metallocenter assembly protein HypD | hypD | HTSR_0653 | HSR6_0678 | 99.73 |
| [NiFe] hydrogenase metallocenter assembly protein HypC | hypC | HTSR_0654 | HSR6_0679 | 100 |
| Hydrogenase maturation protease (EC 3.4.24.-) | | HTSR_0655 | HSR6_0681 | 100 |
| NiFe-hydrogenase large subunit (EC 1.12.99.6) | | HTSR_0657 | HSR6_0683 | 99.81 |
| NiFe-hydrogenase small subunit (EC 1.12.5.1) | | HTSR_0658 | HSR6_0684 | 100 |
| hypothetical protein | | HTSR_0659 | HSR6_0685 | 100 |
| Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1) | sdhA | HTSR_0612 | HSR6_0600 | 98.68 |
| Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1) | sdhB | HTSR_0613 | HSR6_0601 | 100 |
| Succinate dehydrogenase hydrophobic membrane anchor protein | sdhD | HTSR_0614 | HSR6_0602 | 98.36 |
| Succinate dehydrogenase cytochrome b subunit | sdhC | HTSR_0615 | HSR6_0603 | 97.2 |
| succinate dehydrogenase subunit | | HTSR_0616 | HSR6_0604 | 94.12 |
| Putative oxidoreductase YncB | | HTSR_1104 | HSR6_1141 | 99.69 |
| soluble [2Fe-2S] ferredoxin | fdx | HTSR_1312 | HSR6_1385 | 100 |
| soluble [2Fe-2S] ferredoxin | fdx | HTSR_1558 | HSR6_1628 | 99.62 |
| Ferredoxin | | HTSR_0081 | HSR6_0080 | 100 |
| Ferredoxin-like protein | | HTSR_0167 | HSR6_0163 | 100 |
| Ferredoxin-like protein | | HTSR_1571 | HSR6_1640 | 99.85 |
| Ferredoxin | uspA12 | HTSR_1233 | HSR6_1304 | 100 |
| soluble [2Fe-2S] ferredoxin | fdx | HTSR_1312 | HSR6_1385 | 100 |
| Aldehyde ferredoxin oxidoreductase | aor | HTSR_1751 | HSR6_1817 | 99.85 |
| Tungsten-containing aldehyde:ferredoxin oxidoreductase (EC 1.2.7.5) | aor2 | HTSR_1962 | HSR6_2037 | 100 |
| Ribulose-1,5-bisphosphate carboxylase, Type III (EC 4.1.1.39) | rbcl | HTSR_1161 | HSR6_1196 | 100 |
| Fatty acid biosynthesis | | | | |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG | HTSR_0229 | HSR6_0216 | 100 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG2 | HTSR_0447 | HSR6_0432 | 99.6 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG1 | HTSR_1202 | HSR6_0432 | 52 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG2 | HTSR_1404 | HSR6_1476 | 100 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG3 | HTSR_1684 | HSR6_1752 | 100 |
| Amino acid biosynthesis | | | | |
| Aspartate aminotransferase (EC 2.6.1.1) (Asp) | aspC | HTSR_0414 | HSR6_0399 | 100 |
| Aspartate aminotransferase (EC 2.6.1.1) (Asp) | aspC3 | HTSR_0975 | HSR6_1006 | 99.73 |
| Aspartate aminotransferase (EC 2.6.1.1) (Asp) | aspC4 | HTSR_1169 | HSR6_1204 | 100 |
| Aspartate aminotransferase (EC 2.6.1.1) (Asp) | aspC5 | HTSR_1188 | HSR6_1223 | 98.48 |
| Aspartate aminotransferase (EC 2.6.1.1) (Asp) | aspC2 | HTSR_0784 | HSR6_0811 | 99.7 |
| NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (Glu) | gdhA | HTSR_1189 | HSR6_1224 | 99.28 |
| Glutamine synthetase type I (EC 6.3.1.2) (Gln) | glnA | HTSR_1888 | HSR6_1958 | 99.34 |
| N-acetylglutamate synthase (EC 2.3.1.1); Lysine biosynthesis protein LysX (Arg) | lysX | HTSR_2057 | HSR6_2133 | 100 |
| N-acetyl-gamma-aminoadipyl-phosphate reductase (EC 1.2.1.-); N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (Arg) | argC | HTSR_0665 | HSR6_0691 | 98.27 |
| Acetylglutamate kinase (EC 2.7.2.8) @ Acetylaminoadipate kinase (EC 2.7.2.-) (Arg) | argB | HTSR_0666 | HSR6_0692 | 99.27 |
| Acetylornithine aminotransferase (EC 2.6.1.11); N-acetyl-lysine aminotransferase (EC 2.6.1.-) (Arg) | argD | HTSR_0667 | HSR6_0693 | 99.73 |
| Acetylornithine deacetylase (EC 3.5.1.16); N-acetyl-lysine deacetylase (EC 3.5.1.-) (Arg) | argE | HTSR_0668 | HSR6_0694 | 99.7 |
| Ornithine carbamoyltransferase (EC 2.1.3.3) (Arg) | argF | HTSR_1006 | HSR6_1039 | 100 |
| Argininosuccinate synthase (EC 6.3.4.5) (Arg) | argG | HTSR_2054 | HSR6_2130 | 100 |

| | | | | |
|---|-------|-----------|-----------|--------|
| Argininosuccinate lyase (EC 4.3.2.1) (Arg) | argH | HTSR_2055 | HSR6_2131 | 98.59 |
| Pyroline-5-carboxylate reductase (EC 1.5.1.2) (Pro) | proC | HTSR_1054 | HSR6_1087 | 100 |
| Glutamate 5-kinase (EC 2.7.2.11) (Pro) | proB | HTSR_1055 | HSR6_1088 | 99.3 |
| Gamma-glutamyl phosphate reductase (EC 1.2.1.41) (Pro) | proA | HTSR_1056 | HSR6_1089 | 99.55 |
| | | | | |
| Ornithine cyclodeaminase (EC 4.3.1.12) (Pro) | | HTSR_0178 | HSR6_0176 | 99.36 |
| | | | | |
| Aspartokinase (EC 2.7.2.4) (Asn - Lsn) | lysC | HTSR_0006 | HSR6_0006 | 100 |
| Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (Thr Lys) | asd | HTSR_0538 | HSR6_0522 | 99.71 |
| 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) (Lys) | dapA | HTSR_1329 | HSR6_1401 | 100 |
| Homoserine dehydrogenase (EC 1.1.1.3) (Thr) | lysC | HTSR_1561 | HSR6_1631 | 100 |
| Homoserine kinase (EC 2.7.1.39) (Thr) | thrB | HTSR_0379 | HSR6_0364 | 99.66 |
| Threonine synthase (EC 4.2.3.1) (Thr) | thrC | HTSR_1004 | HSR6_1037 | 99.23 |
| Threonine synthase (EC 4.2.3.1) (Thr) | thrC2 | HTSR_1058 | HSR6_1091 | 98.78 |
| Threonine synthase (EC 4.2.3.1) (Thr) | thrC3 | HTSR_1876 | HSR6_1946 | 98.68 |
| Threonine synthase (EC 4.2.3.1) (Thr) | thrC3 | HTSR_2058 | HSR6_2134 | 99.52 |
| Homoserine O-acetyltransferase (EC 2.3.1.31) (Met) | metX | HTSR_2059 | HSR6_2135 | 99.74 |
| Lysine Biosynthetic Amino Acid Carrier Protein LysW (Met) | lysW | HTSR_2056 | HSR6_2132 | 100 |
| O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) (Met) | | HTSR_0631 | HSR6_0656 | 100 |
| O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) (Met) | metY | HTSR_1687 | HSR6_1755 | 99.3 |
| 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase (EC 2.1.1.14) (Met) | | HTSR_1803 | HSR6_1872 | 99.43 |
| Diaminopimelate decarboxylase (EC 4.1.1.20) (Lys) | lysA | HTSR_1332 | HSR6_1404 | 99.75 |
| Diaminopimelate epimerase (EC 5.1.1.7) (Lys) | dapF | HTSR_1333 | HSR6_1405 | 99.26 |
| Probable succinyl-diaminopimelate desuccinylase,DapE (EC 3.5.1.18) (Lys) | dapE | HTSR_1334 | HSR6_1406 | 100 |
| 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) (Lys) | dapA | HTSR_1329 | HSR6_1401 | 100 |
| 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.1.7.8) (Lys) | dapB | HTSR_1330 | HSR6_1402 | 100 |
| 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) (Lys) | dapD | HTSR_1331 | HSR6_1403 | 100 |
| | | | | |
| Fructose-bisphosphate aldolase, archaeal class I (EC 4.1.2.13) (Trp) | faa | HTSR_1163 | HSR6_1198 | 100 |
| 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) (Trp) | aroA | HTSR_0725 | HSR6_0751 | 94.38 |
| 3-dehydroquinate dehydratase I (EC 4.2.1.10) (Trp) | aroD | HTSR_1436 | HSR6_1508 | 100 |
| Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) (Trp) | aroE | HTSR_1392 | HSR6_1464 | 100 |
| Shikimate kinase II (EC 2.7.1.71) (Trp) | aroK | HTSR_0733 | HSR6_0759 | 98.84 |
| 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) (Trp) | aroA | HTSR_0725 | HSR6_0751 | 98.95 |
| Chorismate synthase (EC 4.2.3.5) (Trp) | aroC | HTSR_0724 | HSR6_0750 | 94.38 |
| Anthranilate synthase, aminase component (EC 4.1.3.27) (Trp) | trpE1 | HTSR_0479 | HSR6_0463 | 100 |
| Anthranilate synthase, amidotransferase component (EC 4.1.3.27) (Trp) | trpE2 | HTSR_0480 | HSR6_0464 | 98.99 |
| Anthranilate phosphoribosyltransferase (EC 2.4.2.18) (Trp) | trpD | HTSR_0477 | HSR6_0461 | 99.7 |
| Phosphoribosylanthranilate isomerase (EC 5.3.1.24) (Trp) | trpF | HTSR_0478 | HSR6_0462 | 99.52 |
| Indole-3-glycerol phosphate synthase (EC 4.1.1.48) (Trp) | trpC | HTSR_1442 | HSR6_1514 | 89.76 |
| Tryptophan synthase beta chain (EC 4.2.1.20) (Trp) | trpB | HTSR_0028 | HSR6_0028 | 100 |
| Tryptophan synthase alpha chain (EC 4.2.1.20) (Trp) | trpA | HTSR_1440 | HSR6_1512 | 98.08 |
| Tryptophan synthase beta chain (EC 4.2.1.20) (Trp) | trpB | HTSR_1441 | HSR6_1513 | 100 |
| | | | | |
| 3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) | kdsB | HTSR_0858 | HSR6_0875 | 74.56 |
| 2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase (EC 2.5.1.55) | kdsA | HTSR_0859 | HSR6_0876 | 92.22 |
| Chorismate mutase I (EC 5.4.9.5) (Tyr Phe) | aroQ | HTSR_0732 | HSR6_0758 | 100 |
| Prephenate and/or argenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43) (Tyr) | tyrA | HTSR_0727 | HSR6_0753 | 100 |
| Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) @ Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Tyr) | hisC | HTSR_0911 | HSR6_0925 | 96.91 |
| Prephenate dehydratase (EC 4.2.1.51) (Phe) | pheA | HTSR_0181 | HSR6_0179 | 98.88 |
| | | | | |
| Branched-chain amino acid aminotransferase (EC 2.6.1.42) (Ile) | ilvE | HTSR_0277 | HSR6_0263 | 100 |
| Dihydroxy-acid dehydratase (EC 4.2.1.9) (Ile) | ilvD | HTSR_1107 | HSR6_1144 | 100 |
| Dihydroxy-acid dehydratase (EC 4.2.1.9) (Ile) | ilvD2 | HTSR_1218 | HSR6_1288 | 100 |
| Keto-acid reductoisomerase (EC 1.1.1.86) (Ile) | ilvC | HTSR_0363 | HSR6_0368 | 99.7 |
| Acetolactate synthase small subunit (EC 2.2.1.6) (Ile) | ilvH | HTSR_0384 | HSR6_0369 | 100 |
| Acetolactate synthase large subunit (EC 2.2.1.6) (Ile) | ilvH2 | HTSR_0385 | HSR6_0370 | 99.83 |
| Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1) (Ala) | sseA | HTSR_1348 | HSR6_1420 | 99.76 |
| Keto-acid reductoisomerase (EC 1.1.1.86) (Val) | | HTSR_0383 | HSR6_0368 | 99.7 |
| Dihydroxy-acid dehydratase (EC 4.2.1.9) (Val) | ilvD | HTSR_1107 | HSR6_1144 | 100 |
| Dihydroxy-acid dehydratase (EC 4.2.1.9) (Val) | ilvD2 | HTSR_1218 | HSR6_1288 | 100 |
| Branched-chain amino acid aminotransferase (EC 2.6.1.42) (Val) | | HTSR_0277 | HSR6_0263 | 100 |
| | | | | |
| 2-isopropylmalate synthase (EC 2.3.3.13) (Leu) | leuA | HTSR_0386 | HSR6_0371 | 100 |
| 2-isopropylmalate synthase (EC 2.3.3.13) (Leu) | leuA2 | HTSR_1495 | HSR6_1566 | 99.4 |
| 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Leu) | leuB | HTSR_0380 | HSR6_0365 | 99.69 |
| 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) (Leu) | leuD | HTSR_0381 | HSR6_0366 | 100 |
| 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Leu) | leuC | HTSR_0382 | HSR6_0367 | 99.15 |
| Branched-chain amino acid aminotransferase (EC 2.6.1.42) (Leu) | | HTSR_0277 | HSR6_0263 | 100 |
| | | | | |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) | serA | HTSR_0539 | HSR6_0523 | 99.37 |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (His) | gyaR | HTSR_1168 | HSR6_1203 | 100 |
| Threonine dehydratase (EC 4.3.1.19) (Ser) | ilvA | HTSR_1880 | HSR6_1950 | 100 |
| Phosphoserine phosphatase (EC 3.1.3.3) (Ser) | pspH | HTSR_1388 | HSR6_1460 | 100 |
| Serine hydroxymethyltransferase (EC 2.1.2.1) (Gly) | glyA | HTSR_0671 | HSR6_0697 | 100 |
| Serine acetyltransferase (EC 2.3.1.30) (Cys) | cysE | HTSR_0237 | HSR6_0224 | 99.65 |
| Cysteine synthase (EC 2.5.1.47) (Cys) | cysK | HTSR_1258 | HSR6_1331 | 97.07 |
| Cysteine synthase (EC 2.5.1.47) (Cys) | cysK2 | HTSR_1625 | HSR6_1693 | 99.68 |
| O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) (Cys) | | HTSR_0631 | HSR6_0656 | 100 |
| O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) / O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) (Cys) | metY | HTSR_1687 | | |
| | | | | |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (His) | serA | HTSR_0539 | HSR6_0523 | 99.37 |
| D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (His) | gyaR | HTSR_1168 | HSR6_1203 | 100 |
| ATP phosphoribosyltransferase (EC 2.4.2.17) (His) | hisG | HTSR_0162 | HSR6_0158 | 100 |
| Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (His) | hisE | HTSR_1616 | HSR6_1684 | 100 |
| Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) (His) | hisL | HTSR_0083 | HSR6_0082 | 97.52 |
| Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) (His) | hisA | HTSR_0080 | HSR6_0079 | 99.59 |
| Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-) (His) | hisH | HTSR_1894 | HSR6_1964 | 100 |
| Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) (His) | hisB | HTSR_0079 | HSR6_0078 | 98.97 |
| Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) @ Histidinol-phosphate aminotransferase (EC 2.6.1.9) (His) | hisC | HTSR_0911 | HSR6_0925 | 96.91 |
| Histidinol dehydrogenase (EC 1.1.1.23) (His) | hisD | HTSR_0555 | HSR6_0542 | 98.12 |
| Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-) (His) | hisF | HTSR_1303 | HSR6_1376 | 100 |
| | | | | |
| Amino acid catabolism | | | | |
| Pyruvoyl-dependent arginine decarboxylase (EC 4.1.1.19) (Arg) | pdaD | HTSR_0131 | HSR6_0130 | 100 |
| Agmatinase (EC 3.5.3.11) (Arg) | speB | HTSR_0416 | HSR6_0401 | 100 |
| Tryptophanase (EC 4.1.99.1) (Trp) | tnaA | HTSR_0012 | HSR6_0012 | 99.545 |
| Branched-chain amino acid aminotransferase (EC 2.6.1.42) (Ile, Leu,Val) | | HTSR_0277 | HSR6_0263 | 100 |
| Dihydroliipoamide dehydrogenase of acetoin dehydrogenase (EC 1.8.1.4) / Dihydroliipoamide dehydrogenase (EC 1.8.1.4) | | HTSR_0182 | HSR6_0180 | 87.47 |
| L-tyrosine decarboxylase (EC 4.1.1.25) (Tyr) | gadD | HTSR_1425 | HSR6_1497 | 99.72 |
| Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) (Gly) | gcvT | HTSR_0503 | HSR6_0487 | 100 |
| Glycine cleavage system H protein (Gly) | | HTSR_0504 | HSR6_0488 | 100 |
| Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) (Gly) | gcvP1 | HTSR_0505 | HSR6_0489 | 99.77 |
| Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) (Gly) | gcvP2 | HTSR_0506 | HSR6_0490 | 99.79 |
| Archaeal S-adenosylmethionine synthetase (EC 2.5.1.6) (Met) | metK | HTSR_0607 | HSR6_0595 | 99 |
| Adenosylhomocysteinase (EC 3.3.1.1) (Met) | ahcY | HTSR_0160 | HSR6_0156 | 99.77 |
| Cysteine desulfurase (EC 2.8.1.7) (Cys) | sufS | HTSR_1091 | HSR6_1128 | 100 |
| Putative iron-sulfur cluster assembly scaffold protein for SUF system, SufE2 (Cys) | nifU | HTSR_2025 | HSR6_2101 | 96.35 |
| | | | | |
| Urea degradation | | | | |
| Urea channel UreI | | HTSR_0637 | HSR6_0662 | 100 |
| 3.5.1.5 (UreB/UreC/UreA) | | | | |
| UreG,UreH, UreE/UreD, UreF | | | | |
| | | | | |
| Fatty acid biosynthesis | | | | |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG | HTSR_0229 | HSR6_0216 | 100 |

| | | | | |
|---|-------|-----------|-----------|-------|
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG2 | HTSR_0447 | HSR6_0432 | 99.6 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG1 | HTSR_1202 | HSR6_0432 | 52 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG2 | HTSR_1404 | HSR6_1476 | 100 |
| 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) | fabG3 | HTSR_1684 | HSR6_1752 | 100 |
| Nitrogen metabolism | | | | |
| Nitrate/nitrite transporter NarK | | HTSR_0976 | HSR6_1007 | 99.51 |
| Nitrite reductase probable [NAD(P)H] subunit (EC 1.7.1.4) | | HTSR_0303 | HSR6_0289 | 100 |
| NrfC protein | | HTSR_0754 | SR6_0780 | 99.59 |
| NrfD protein | | HTSR_1557 | HSR6_1627 | 100 |
| Nitrate/nitrite transporter | | HTSR_1709 | HSR6_1780 | 100 |
| ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | | HTSR_0918 | HSR6_0932 | 92.94 |
| hypothetical protein | | HTSR_0919 | HSR6_0933 | 88.1 |
| ABC-type nitrate/sulfonate/bicarbonate transport system, permease component | | HTSR_0920 | HSR6_0934 | 95.42 |
| ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component | | HTSR_0921 | HSR6_0935 | 99.62 |
| ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components | | HTSR_1851 | HSR6_1920 | 100 |
| ABC-type nitrate/sulfonate/bicarbonate transport system, permease component | | HTSR_1852 | HSR6_1921 | 100 |
| ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component; sulfonate ABC transporter ATP binding protein (EC:3.6.3.25) | | HTSR_1853 | HSR6_1922 | 98.83 |
| Molybdopterin-guanine dinucleotide biosynthesis protein MobB | mobB | HTSR_1147 | HSR6_1182 | 100 |
| Molybdopterin-guanine dinucleotide biosynthesis protein MobA | mobA | HTSR_1664 | HSR6_1732 | 99.43 |
| Molybdopterin-guanine dinucleotide biosynthesis protein MobB / Molybdenum cofactor biosynthesis protein MoaE | moaE | HTSR_1951 | HSR6_2026 | 98.07 |
| Nitric oxide reductase activation protein NorQ | | HTSR_0389 | HSR6_0374 | 100 |
| Nitric oxide reductase activation protein NorQ | | HTSR_1679 | HSR6_1747 | 99.1 |
| Glutamine synthetase type I (EC 6.3.1.2) | glnA | HTSR_1888 | HSR6_1958 | 99.34 |
| N-acetylglutamate synthase (EC 2.3.1.1); Lysine biosynthesis protein LysX | lysX | HTSR_2057 | HSR6_2133 | 100 |
| NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | gdhA | HTSR_1189 | HSR6_1224 | 99.28 |
| niU protein C-terminal domain homolog | | HTSR_1597 | HSR6_1666 | 100 |
| Capsular polysaccharide biosynthesis / N-glycosylation | | | | |
| Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) | glmS | HTSR_0882 | HSR6_0897 | 99.67 |
| N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) | glmU | HTSR_0890 | HSR6_0906 | 99.24 |
| UDP-glucose dehydrogenase (EC 1.1.1.22) | ugd | HTSR_0878 | HSR6_0893 | 95.83 |
| transmembrane oligosaccharyl transferase | aglB | HTSR_0845 | HSR6_0872 | 87.82 |
| Osmotic balance - homeostasis | | | | |
| Trk system potassium uptake protein TrkA (NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporter) | | HTSR_0255 | HSR6_0242 | 99.51 |
| Potassium uptake protein TrkH | | HTSR_0357 | HSR6_0342 | 98.28 |
| Trk system potassium uptake protein TrkA | | HTSR_0358 | HSR6_0343 | 94.27 |
| Potassium uptake protein TrkH | trkH | HTSR_0461 | HSR6_0446 | 99.81 |
| Trk system potassium uptake protein TrkA | trkA | HTSR_0462 | HSR6_0447 | 97.75 |
| Trk system potassium uptake protein TrkA | | HTSR_0925 | HSR6_0939 | 100 |
| Sulfate permease, Trk-type | | HTSR_0957 | HSR6_0988 | 99.84 |
| Trk system potassium uptake protein TrkA (NhaP-type Na ⁺ /H ⁺ and K ⁺ /H ⁺ antiporter) | | HTSR_0255 | HSR6_0242 | 99.51 |
| Na ⁺ /H ⁺ antiporter NhaC | | HTSR_0998 | HSR6_1031 | 99.11 |
| Na ⁺ /H ⁺ antiporter | nhaC | HTSR_1314 | HSR6_1387 | 80.08 |
| Sodium/calcium exchanger | | HTSR_0573 | HSR6_0561 | 96.79 |
| PH adaptation potassium efflux system protein E; sodium- potassium/hydrogen antiporter subunit E (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1024 | HSR6_1057 | 99.73 |
| Multiple resistance and pH regulation protein F precursor (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1025 | HSR6_1058 | 100 |
| PH adaptation potassium efflux system protein G; sodium- potassium/hydrogen antiporter subunit G (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1026 | HSR6_1059 | 100 |
| PH adaptation potassium efflux system protein B1; sodium- potassium/hydrogen antiporter subunit B1 (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1027 | HSR6_1060 | 100 |
| PH adaptation potassium efflux system protein B2; sodium- potassium/hydrogen antiporter subunit B2 (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1028 | HSR6_1061 | 100 |
| PH adaptation potassium efflux system protein C; sodium- potassium/hydrogen antiporter subunit C (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1029 | HSR6_1062 | 100 |
| PH adaptation potassium efflux system protein D 1 (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1030 | HSR6_1063 | 100 |
| pH adaptation potassium efflux system protein D 2 (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1031 | HSR6_1064 | 99.82 |
| pH adaptation potassium efflux system protein D 3 (multisubunit Na ⁺ /H ⁺ antiporter, Mnh) | | HTSR_1032 | HSR6_1065 | 100 |
| High-affinity choline uptake protein BetT | | HTSR_0054 | HSR6_0054 | 100 |
| Glycine betaine transporter OpuD | | HTSR_0234 | HSR6_0221 | 100 |
| Choline-sulfatase (EC 3.1.6.6) | | HTSR_0994 | HSR6_1027 | 96.10 |
| Glycine betaine transporter OpuD | | HTSR_1753 | HSR6_1819 | 100 |
| Carbonic anhydrase (EC 4.2.1.1) | cynT | HTSR_0257 | HSR6_0244 | 90.79 |
| Rhodopsins | | | | |
| Phytoene synthase (EC 2.5.1.32) | crtB | HTSR_0319 | HSR6_0305 | 98.74 |
| putative carotenoid biosynthesis protein | | HTSR_0320 | HSR6_0306 | 100 |
| Lycopene elongase (EC 2.5.1.-) | ubiA | HTSR_0321 | HSR6_0307 | 100 |
| Phytoene dehydrogenase (EC 1.14.99.-) | crtI | HTSR_0322 | HSR6_0308 | 100 |
| Bacterio-opsin activator domain-containing protein | | HTSR_0056 | HSR6_0056 | 100 |
| Bacterio-opsin activator domain-containing protein | | HTSR_0057 | HSR6_0057 | 98.57 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_0421 | HSR6_0406 | 100 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_0520 | HSR6_0504 | 99.02 |
| Bacterio-opsin activator domain-containing protein | | HTSR_0542 | HSR6_0526 | 100 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_0625 | - | - |
| Bacterio-opsin activator domain-containing protein | | HTSR_0755 | HSR6_0781 | 99.51 |
| Bacterio-opsin activator domain-containing protein | | HTSR_0789 | HSR6_0816 | 95.39 |
| Bacterio-opsin activator domain-containing protein | | HTSR_0790 | HSR6_0817 | 92.59 |
| Octaprenyl diphosphate synthase (EC 2.5.1.90) / Dimethylallyltransferase (EC 2.5.1.1) / (2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) / Geranylgeranyl diphosphate synthase (EC 2.5.1.11) | idsA | HTSR_1035 | HSR6_1068 | 99.72 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1343 | HSR6_1415 | 99.01 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1349 | HSR6_1421 | 99.51 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1350 | HSR6_1422 | 99.53 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1545 | HSR6_1615 | 99.1 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1546 | HSR6_1616 | 99.12 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1547 | HSR6_1617 | 100 |
| bacterio-opsin activator HTH domain-containing protein | | HTSR_1663 | HSR6_1731 | 100 |
| Bacterio-opsin activator domain-containing protein | | HTSR_1789 | HSR6_1858 | 97.02 |
| Octaprenyl diphosphate synthase (EC 2.5.1.90) / Dimethylallyltransferase (EC 2.5.1.1) / (2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) / Geranylgeranyl diphosphate synthase (EC 2.5.1.11) | idsA2 | HTSR_1817 | HSR6_1886 | 100 |
| HTR-like protein | | HTSR_0443 | HSR6_0428 | 97.48 |
| HTR-like protein | | HTSR_0470 | HSR6_0454 | 100 |
| Htr-like protein | htlA | HTSR_0674 | HSR6_0700 | 94.3 |
| Ubiquinone and other terpenoid-quinone biosynthesis | | | | |
| Ubiquinone/menaquinone biosynthesis methyltransferase UbiE/COQ5 (EC 2.1.1.-) | ubiE | HTSR_1450 | HSR6_1522 | 97.45 |
| 2-heptaprenyl-1,4-naphthoquinone methyltransferase (EC 2.1.1.163) | | HTSR_1106 | HSR6_1143 | 99.46 |
| 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase (EC 2.2.1.9) | menD | HTSR_1291 | HSR6_1364 | 99.49 |
| Lycopene elongase (EC 2.5.1.-) | ubiA | HTSR_0321 | HSR6_0307 | 100 |
| 1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) | menA | HTSR_1105 | HSR6_1142 | 97.25 |
| 1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74) | menA | HTSR_1293 | HSR6_1366 | 100 |
| Isochorismate synthase (EC 5.4.4.2) @ Menaquinone-specific isochorismate synthase (EC 5.4.4.2) | menF | HTSR_1290 | HSR6_1363 | 99.78 |
| Naphthoate synthase (EC 4.1.3.36) | menB | HTSR_1292 | HSR6_1365 | 100 |
| O-succinylbenzoate synthase (EC 4.2.1.113) | menC | HTSR_1294 | HSR6_1367 | 100 |
| O-succinylbenzoic acid-CoA ligase (EC 6.2.1.26) | menE | HTSR_1295 | HSR6_1368 | 96.57 |
| Excision repair | | | | |
| Excinuclease ABC subunit A | uvrA | HTSR_1594 | HSR6_1663 | 99.62 |
| DNA ligase (EC 6.5.1.2) | ligA | HTSR_2061 | HSR6_2137 | 98.59 |
| unknown | | HTSR_2062 | HSR6_2138 | 98.02 |
| Excinuclease ABC subunit C | uvrC | HTSR_2063 | HSR6_2139 | 100 |
| Heme-degrading monooxygenase IsdG (EC 1.14.99.3) | | HTSR_2064 | HSR6_2140 | 95.33 |

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|---|-------|-----------|-----------|-------|
| Excinuclease ABC subunit B | uvrB | HTSR_2065 | HSR6_2141 | 100 |
| ATP-dependent DNA helicase pcrA (EC 3.6.1.-) | uvrD | HTSR_1601 | HSR6_1670 | 98.52 |
| ATP-dependent DNA helicase pcrA (EC 3.6.1.-) | | HTSR_1724 | HSR6_1794 | 96.23 |
| Oxidative stress | | | | |
| Superoxide dismutase [Mn] (EC 1.15.1.1) | sod | HTSR_1099 | HSR6_1136 | 100 |
| Catalase (EC 1.11.1.6) / Peroxidase (EC 1.11.1.7) | katG | HTSR_1111 | HSR6_1146 | 100 |
| Flagella | | | | |
| Flagella-related protein FlaI | | HTSR_0799 | HSR6_0826 | 99.82 |
| Flagella-related protein FlaI | | HTSR_1215 | HSR6_1285 | 99.88 |
| Flagella accessory protein FlaCE | flaE | HTSR_1353 | HSR6_1425 | 100 |
| Flagella-related protein FlaF | flaF | HTSR_1354 | HSR6_1426 | 99.35 |
| Flagella-related protein FlaG | flaG | HTSR_1355 | HSR6_1427 | 99.33 |
| Flagella-related protein FlaH | flaH | HTSR_1356 | HSR6_1428 | 100 |
| Flagella-related protein FlaI | flaI | HTSR_1357 | HSR6_1429 | 100 |
| Flagella-related protein FlaJ | flaJ | HTSR_1358 | HSR6_1430 | 99.65 |
| Flagellin FlaB2 | FlaB2 | HTSR_1378 | HSR6_1450 | 98.52 |
| hypothetical protein | | HTSR_1379 | HSR6_1451 | 99.45 |
| Flagellin FlaB2 | FlaB2 | HTSR_1380 | HSR6_1452 | 97.02 |
| Flagellin FlaB2 | FlaB2 | HTSR_1381 | HSR6_1453 | 90.86 |
| hypothetical protein | | HTSR_1382 | HSR6_1454 | 99.29 |
| Flagella-related protein FlaE | FlaE | HTSR_1383 | HSR6_1455 | 100 |
| Gas vesicle | | | | |
| GvpA_L_F_G_H_K_O | | | | |
| Sec system | | | | |
| Protein-export membrane protein SecF (TC 3.A.5.1.1) | SecF | HTSR_0141 | HSR6_0142 | 100 |
| Protein-export membrane protein SecD (TC 3.A.5.1.1) | SecD | HTSR_0142 | HSR6_0143 | 100 |
| Preprotein translocase secY subunit (TC 3.A.5.1.1) | secY | HTSR_0354 | HSR6_0339 | 100 |
| Preprotein translocase subunit secE (Protein transport protein SEC61 gamma subunit homolog) | secE | HTSR_1397 | HSR6_1469 | 100 |
| Preprotein translocase secG subunit (Protein transport protein SEC61 subunit beta homolog) | | HTSR_1614 | HSR6_1682 | 100 |
| Tat complex | | | | |
| TatA-C | | | | |