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Deletion of a Cation Transporter Promotes Lysis in *Streptococcus pneumoniae*

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Table S.1. Complete list of differentially expressed genes in an *mgtA* mutant grown in GM17. Genes with a Bayes P of $< 1.0 \text{ E-}06$ were considered significantly expressed. Fold changes $0.5 <$ and > 2.0 are indicated in bold.

| TIGR Locus | TIGR Common Name | fold change | Bayes.p |
|------------|--|-------------|---------|
| SP0023 | DNA repair protein RadA, authentic point mutation | 0.62 | 9.7E-10 |
| SP0024 | conserved hypothetical protein | 0.71 | 1.7E-06 |
| SP0027 | ribose-phosphate pyrophosphokinase | 0.67 | 4.8E-09 |
| SP0032 | DNA polymerase I | 0.71 | 1.9E-10 |
| SP0034 | membrane protein | 0.71 | 4.7E-08 |
| SP0035 | aromatic amino acid aminotransferase | 0.77 | 6.1E-06 |
| SP0042 | competence factor transporting ATP-binding/permease protein ComA | 0.65 | 8.8E-09 |
| SP0043 | competence factor transport protein ComB | 0.67 | 1.6E-09 |
| SP0044 | phosphoribosylaminoimidazole-succinocarboxamide synthase | 0.64 | 3.9E-07 |
| SP0046 | Amidophosphoribosyltransferase | 0.62 | 5.8E-09 |
| SP0047 | phosphoribosylformylglycinamide cyclo-ligase | 0.70 | 4.3E-06 |
| SP0051 | phosphoribosylamine--glycine ligase | 0.69 | 9.4E-07 |
| SP0053 | phosphoribosylaminoimidazole carboxylase, catalytic subunit | 0.65 | 1.3E-06 |
| SP0081 | glycosyl transferase, family 2, authentic point mutation | 0.72 | 2.5E-06 |
| SP0097 | conserved domain protein | 1.25 | 2.6E-06 |
| SP0101 | conserved hypothetical protein | 0.58 | 1.9E-12 |
| SP0102 | glycosyl transferase | 0.63 | 1.2E-09 |
| SP0103 | capsular polysaccharide biosynthesis protein, putative | 0.65 | 2.8E-09 |
| SP0107 | LysM domain protein | 0.41 | 1.4E-07 |
| SP0108 | hypothetical protein | 0.51 | 1.2E-06 |
| SP0110 | hypothetical protein | 0.69 | 4.3E-06 |
| SP0112 | amino acid ABC transporter, periplasmic amino acid-binding protein, putative | 0.32 | 8.4E-10 |
| SP0113 | argininosuccinate synthase, truncation | 0.40 | 2.3E-11 |
| SP0137 | ABC transporter, ATP-binding protein | 0.62 | 1.0E-05 |
| SP0140 | UDP-glucose 6-dehydrogenase, authentic frameshift | 0.53 | 8.0E-07 |
| SP0142 | hypothetical protein | 1.46 | 3.3E-06 |
| SP0144 | hypothetical protein | 0.65 | 5.4E-09 |
| SP0150 | peptidase, M20/M25/M40 family | 0.67 | 1.1E-07 |

| | | | |
|--------|---|-------------|---------|
| SP0167 | hypothetical protein | 1.58 | 1.0E-06 |
| SP0175 | 6,7-dimethyl-8-ribityllumazine synthase | 0.67 | 2.1E-06 |
| SP0176 | 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II | 0.54 | 1.9E-09 |
| SP0178 | riboflavin biosynthesis protein RibD | 0.46 | 1.3E-11 |
| SP0179 | Holliday junction DNA helicase RuvA | 0.64 | 3.7E-07 |
| SP0182 | MccC family protein | 0.63 | 3.4E-06 |
| SP0204 | acetyltransferase, GNAT family | 0.66 | 8.7E-07 |
| SP0213 | ribosomal protein S19 | 0.58 | 9.3E-10 |
| SP0215 | ribosomal protein S3 | 0.79 | 3.5E-06 |
| SP0219 | ribosomal protein L14 | 0.72 | 2.9E-10 |
| SP0222 | ribosomal protein S14 | 0.79 | 1.3E-06 |
| SP0224 | ribosomal protein S8 | 0.83 | 9.4E-06 |
| SP0226 | ribosomal protein L18 | 0.84 | 8.3E-06 |
| SP0227 | ribosomal protein S5 | 0.72 | 4.0E-09 |
| SP0228 | ribosomal protein L30 | 0.70 | 6.2E-08 |
| SP0237 | ribosomal protein L17 | 0.55 | 1.0E-10 |
| SP0239 | conserved hypothetical protein | 0.80 | 7.8E-07 |
| SP0245 | pyruvate formate-lyase-activating enzyme, putative | 0.62 | 2.7E-06 |
| SP0265 | glycosyl hydrolase, family 1 | 0.69 | 1.4E-06 |
| SP0266 | glucosamine--fructose-6-phosphate aminotransferase, isomerizing | 0.63 | 1.5E-08 |
| SP0284 | PTS system, mannose-specific IIAB components | 1.22 | 2.9E-06 |
| SP0292 | bifunctional folate synthesis protein | 0.74 | 5.1E-06 |
| SP0335 | cell division protein FtsL | 1.39 | 3.9E-06 |
| SP0368 | cell wall surface anchor family protein, authentic frameshift | 0.66 | 1.8E-06 |
| SP0370 | recombination protein U | 1.23 | 1.2E-06 |
| SP0394 | PTS system, mannitol-specific IIBC components | 0.55 | 1.5E-09 |
| SP0397 | mannitol-1-phosphate 5-dehydrogenase | 0.60 | 6.4E-08 |
| SP0415 | enoyl-CoA hydratase/isomerase family protein | 1.20 | 5.4E-06 |
| SP0436 | glutamyl-tRNA(Gln) amidotransferase, B subunit | 1.28 | 1.5E-06 |
| SP0437 | glutamyl-tRNA(Gln) amidotransferase, A subunit | 1.35 | 2.2E-08 |
| SP0452 | amino acid ABC transporter, ATP-binding protein | 1.27 | 2.0E-07 |
| SP0459 | formate acetyltransferase | 1.45 | 5.1E-08 |
| SP0462 | cell wall surface anchor family protein | 2.24 | 7.4E-13 |
| SP0490 | hypothetical protein | 1.39 | 1.4E-06 |
| SP0499 | phosphoglycerate kinase | 1.51 | 7.0E-10 |
| SP0500 | conserved domain protein | 1.48 | 3.5E-08 |
| SP0501 | transcriptional regulator, MerR family | 2.85 | 3.4E-15 |
| SP0502 | glutamine synthetase, type I | 3.07 | 0.0E+00 |
| SP0503 | hypothetical protein | 2.01 | 1.0E-07 |
| SP0504 | hypothetical protein | 1.73 | 8.1E-09 |

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|--------|---|------|---------|
| SP0506 | integrase/recombinase, phage integrase family | 1.44 | 1.1E-06 |
| SP0507 | type I restriction-modification system, S subunit, putative | 1.47 | 1.0E-09 |
| SP0508 | type I restriction-modification system, S subunit | 1.38 | 1.5E-08 |
| SP0509 | type I restriction-modification system, M subunit | 1.34 | 9.4E-06 |
| SP0516 | heat shock protein GrpE | 1.41 | 3.6E-07 |
| SP0517 | dnaK protein | 1.74 | 7.2E-08 |
| SP0518 | hypothetical protein | 1.62 | 8.1E-08 |
| SP0637 | membrane protein | 0.79 | 2.1E-06 |
| SP0641 | serine protease, subtilase family | 1.39 | 1.3E-07 |
| SP0701 | orotidine 5-phosphate decarboxylase | 0.59 | 2.0E-08 |
| SP0715 | lactate oxidase | 1.24 | 8.0E-06 |
| SP0716 | transcriptional regulator, putative | 1.39 | 5.9E-09 |
| SP0718 | thiamine-phosphate pyrophosphorylase | 1.38 | 4.1E-07 |
| SP0722 | transcriptional activator TenA | 1.38 | 1.8E-06 |
| SP0724 | hydroxyethylthiazole kinase, putative | 1.28 | 8.4E-06 |
| SP0725 | thiamine-phosphate pyrophosphorylase | 1.37 | 9.8E-07 |
| SP0737 | sodium-dependent transporter | 1.36 | 8.4E-06 |
| SP0742 | conserved hypothetical protein | 1.44 | 3.6E-07 |
| SP0751 | branched-chain amino acid ABC transporter, permease protein | 0.76 | 4.3E-06 |
| SP0754 | acetoin utilization protein AcuB, putative | 0.71 | 2.2E-06 |
| SP0755 | peptide chain release factor 2, programmed frameshift | 0.63 | 6.9E-11 |
| SP0756 | cell division ABC transporter, ATP-binding protein FtsE | 0.75 | 2.3E-08 |
| SP0757 | cell division ABC transporter, permease protein FtsX | 0.64 | 1.3E-10 |
| SP0776 | KH domain protein | 0.63 | 4.2E-10 |
| SP0795 | PEP-utilizing enzymes family protein | 1.41 | 4.5E-07 |
| SP0796 | conserved hypothetical protein | 1.58 | 5.2E-10 |
| SP0800 | hypothetical protein | 0.72 | 9.9E-08 |
| SP0810 | hypothetical protein | 0.65 | 1.8E-07 |
| SP0815 | hypothetical protein | 1.41 | 8.1E-06 |
| SP0820 | ATP-dependent Clp protease, ATP-binding subunit ClpE | 1.35 | 7.7E-09 |
| SP0838 | ribosomal protein S20 | 0.59 | 3.0E-10 |
| SP0841 | conserved hypothetical protein | 1.39 | 1.6E-07 |
| SP0868 | conserved hypothetical protein | 1.34 | 2.7E-09 |
| SP0870 | NifU family protein | 1.30 | 1.5E-07 |
| SP0871 | conserved hypothetical protein | 1.27 | 5.3E-08 |
| SP0872 | D-alanyl-D-alanine carboxypeptidase | 1.22 | 5.3E-06 |
| SP0875 | lactose phosphotransferase system repressor | 1.25 | 8.3E-06 |
| SP0876 | 1-phosphofructokinase, putative | 1.40 | 3.0E-09 |
| SP0885 | hypothetical protein | 0.68 | 5.8E-06 |

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|--------|---|------|---------|
| SP0899 | conserved hypothetical protein | 1.29 | 8.8E-06 |
| SP0908 | transcriptional regulator, putative | 1.40 | 3.9E-07 |
| SP0918 | spermidine synthase | 0.81 | 9.0E-07 |
| SP0919 | conserved hypothetical protein | 0.78 | 9.3E-08 |
| SP0920 | carboxynorspermidine decarboxylase | 0.83 | 9.7E-06 |
| SP0921 | conserved hypothetical protein | 0.76 | 5.4E-08 |
| SP0922 | carbon-nitrogen hydrolase family protein | 0.75 | 1.8E-08 |
| SP0959 | translation initiation factor IF-3 | 0.81 | 3.1E-06 |
| SP0962 | lactoylglutathione lyase | 0.80 | 9.8E-07 |
| SP0963 | dihydroorotate dehydrogenase, electron transfer subunit | 0.50 | 8.4E-11 |
| SP0964 | dihydroorotate dehydrogenase B | 0.55 | 4.6E-11 |
| SP0965 | endo-beta-N-acetylglucosaminidase | 0.69 | 5.6E-08 |
| SP1000 | thioredoxin family protein | 1.61 | 2.3E-08 |
| SP1012 | conserved hypothetical protein | 0.79 | 5.4E-06 |
| SP1016 | thiophene and furan oxidation protein ThdF | 1.29 | 7.4E-07 |
| SP1021 | HemK protein | 1.33 | 8.0E-06 |
| SP1024 | serine hydroxymethyltransferase | 1.33 | 4.6E-07 |
| SP1027 | conserved hypothetical protein | 1.54 | 2.7E-07 |
| SP1032 | iron-compound ABC transporter, iron compound-binding protein | 1.27 | 2.4E-06 |
| SP1052 | phosphoesterase, putative | 1.43 | 6.0E-06 |
| SP1053 | conserved domain protein | 1.51 | 1.8E-06 |
| SP1095 | ribose-phosphate pyrophosphokinase | 1.36 | 5.3E-08 |
| SP1104 | hypothetical protein | 1.37 | 5.7E-08 |
| SP1110 | macrolide-efflux protein | 1.26 | 4.5E-07 |
| SP1171 | hydrolase, haloacid dehalogenase-like family | 1.30 | 1.4E-06 |
| SP1176 | phosphoenolpyruvate-protein phosphotransferase | 1.22 | 1.2E-06 |
| SP1190 | tagatose 1,6-diphosphate aldolase | 1.42 | 3.8E-07 |
| SP1226 | sensory box sensor histidine kinase | 1.32 | 3.8E-07 |
| SP1227 | DNA-binding response regulator | 1.24 | 4.9E-06 |
| SP1228 | A/G-specific adenine glycosylase | 1.33 | 9.7E-09 |
| SP1241 | amino acid ABC transporter, amino acid-binding protein/permease protein | 1.80 | 2.0E-13 |
| SP1242 | amino acid ABC transporter, ATP-binding protein | 1.78 | 6.4E-13 |
| SP1243 | glucose-6-phosphate 1-dehydrogenase | 1.52 | 1.1E-10 |
| SP1261 | conserved hypothetical protein | 1.40 | 6.5E-07 |
| SP1270 | alcohol dehydrogenase, zinc-containing | 1.25 | 5.8E-06 |
| SP1275 | carbamoyl-phosphate synthase, large subunit | 0.59 | 8.1E-13 |
| SP1276 | carbamoyl-phosphate synthase, small subunit | 0.58 | 9.2E-13 |
| SP1277 | aspartate carbamoyltransferase | 0.59 | 1.7E-13 |
| SP1278 | pyrimidine operon regulatory protein | 0.62 | 1.2E-08 |
| SP1286 | uracil permease | 0.70 | 8.0E-10 |

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|--------|--|-------------|---------|
| SP1296 | chorismate mutase, putative | 0.74 | 1.7E-06 |
| SP1297 | Flavodoxin | 0.75 | 3.8E-08 |
| SP1306 | NADP-specific glutamate dehydrogenase | 1.37 | 1.4E-09 |
| SP1327 | conserved hypothetical protein | 1.55 | 1.1E-06 |
| SP1328 | sodium:solute symporter family protein | 1.69 | 7.6E-06 |
| SP1329 | N-acetylneuraminase lyase | 1.56 | 2.2E-08 |
| SP1336 | type II DNA modification methyltransferase Spn5252IP | 1.82 | 1.2E-07 |
| SP1353 | hypothetical protein | 0.74 | 4.2E-06 |
| SP1396 | phosphate ABC transporter, ATP-binding protein, putative | 1.38 | 4.4E-08 |
| SP1397 | phosphate ABC transporter, ATP-binding protein, putative | 1.37 | 5.8E-08 |
| SP1410 | conserved hypothetical protein | 1.28 | 1.3E-06 |
| SP1411 | conserved hypothetical protein | 1.32 | 3.8E-07 |
| SP1431 | type II DNA modification methyltransferase, putative | 1.40 | 2.1E-07 |
| SP1467 | conserved hypothetical protein | 0.70 | 3.5E-06 |
| SP1468 | pyridoxine biosynthesis protein | 0.69 | 1.6E-09 |
| SP1479 | peptidoglycan N-acetylglucosamine deacetylase A | 1.33 | 4.2E-07 |
| SP1483 | ATP-dependent RNA helicase, DEAD/DEAH box family | 1.20 | 5.3E-06 |
| SP1499 | bacterocin transport accessory protein | 1.28 | 6.7E-06 |
| SP1507 | ATP synthase F1, epsilon subunit | 0.77 | 1.7E-07 |
| SP1517 | transcription elongation factor GreA | 0.78 | 9.5E-07 |
| SP1521 | UDP-N-acetylmuramate--alanine ligase | 0.82 | 2.4E-06 |
| SP1527 | oligopeptide ABC transporter, oligopeptide-binding protein AliB | 0.72 | 5.5E-06 |
| SP1546 | conserved domain protein | 1.31 | 3.8E-08 |
| SP1550 | glutathione S-transferase family protein | 0.37 | 2.9E-13 |
| SP1551 | cation-transporting ATPase, E1-E2 family | 0.24 | 2.1E-15 |
| SP1576 | homoserine O-succinyltransferase | 0.75 | 3.9E-08 |
| SP1606 | glycosyl transferase, family 2 | 0.68 | 2.0E-10 |
| SP1607 | UDP-glucose 4-epimerase | 0.61 | 4.8E-11 |
| SP1645 | GTP pyrophosphokinase | 0.76 | 9.1E-06 |
| SP1693 | neuraminidase A, authentic frameshift | 1.36 | 2.8E-07 |
| SP1695 | acetyl xylan esterase, putative | 0.74 | 5.4E-06 |
| SP1727 | hydroxymethylglutaryl-CoA synthase | 0.80 | 9.6E-07 |
| SP1737 | DNA-directed RNA polymerase, omega subunit, putative | 1.27 | 2.7E-08 |
| SP1753 | sodium/dicarboxylate symporter family protein | 0.76 | 3.5E-06 |
| SP1760 | conserved domain protein | 1.41 | 5.1E-06 |
| SP1765 | glycosyl transferase, family 8 | 1.47 | 5.2E-06 |
| SP1766 | glycosyl transferase, family 8 | 1.48 | 8.8E-07 |

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|--------|--|-------------|---------|
| SP1768 | conserved hypothetical protein | 1.60 | 2.2E-07 |
| SP1775 | conserved domain protein | 1.47 | 3.9E-09 |
| SP1776 | Thioredoxin | 1.37 | 1.6E-07 |
| SP1790 | ATPase, AAA family | 0.78 | 2.6E-06 |
| SP1792 | IS1167, transposase | 0.58 | 2.5E-13 |
| SP1799 | sugar-binding transcriptional regulator, LacI family | 1.52 | 9.0E-07 |
| SP1802 | hypothetical protein | 1.41 | 1.7E-08 |
| SP1804 | general stress protein 24, putative | 1.40 | 5.3E-09 |
| SP1805 | hypothetical protein | 1.41 | 1.4E-09 |
| SP1812 | tryptophan synthase, beta subunit | 0.73 | 2.1E-06 |
| SP1823 | N-(5-phosphoribosyl)-anthranilate isomerase | 0.78 | 3.6E-06 |
| SP1847 | xanthine phosphoribosyltransferase | 0.70 | 4.6E-06 |
| SP1851 | conserved hypothetical protein | 0.64 | 6.3E-07 |
| SP1852 | galactose-1-phosphate uridylyltransferase | 0.47 | 5.9E-12 |
| SP1853 | Galactokinase | 0.54 | 1.8E-12 |
| SP1854 | galactose operon repressor | 0.63 | 4.1E-07 |
| SP1855 | alcohol dehydrogenase, zinc-containing | 0.68 | 1.4E-08 |
| SP1856 | transcriptional regulator, MerR family | 0.65 | 2.4E-07 |
| SP1857 | cation efflux system protein | 0.53 | 1.8E-06 |
| SP1861 | choline transporter | 1.26 | 1.2E-06 |
| SP1869 | iron-compound ABC transporter, permease protein | 0.68 | 1.9E-07 |
| SP1875 | conserved hypothetical protein | 0.68 | 2.9E-09 |
| SP1876 | conserved hypothetical protein | 0.73 | 4.4E-09 |
| SP1878 | CBS domain protein | 0.69 | 1.0E-07 |
| SP1883 | dextran glucosidase DexS, putative | 0.70 | 5.3E-07 |
| SP1884 | PTS system, IIABC components | 0.77 | 1.3E-06 |
| SP1893 | hypothetical protein | 0.77 | 5.0E-08 |
| SP1894 | sucrose phosphorylase | 0.73 | 3.0E-06 |
| SP1895 | sugar ABC transporter, permease protein | 0.68 | 6.2E-07 |
| SP1896 | sugar ABC transporter, permease protein | 0.71 | 2.6E-07 |
| SP1897 | sugar ABC transporter, sugar-binding protein | 0.70 | 4.0E-07 |
| SP1898 | alpha-galactosidase | 0.63 | 4.7E-07 |
| SP1906 | chaperonin, 60 kDa | 1.26 | 6.0E-06 |
| SP1918 | ABC transporter, ATP-binding protein | 0.61 | 8.7E-09 |
| SP1924 | hypothetical protein | 1.32 | 4.8E-07 |
| SP1939 | MATE efflux family protein DinF | 0.80 | 3.2E-06 |
| SP1940 | recA protein | 0.75 | 9.0E-08 |
| SP1964 | DNA-entry nuclease | 0.76 | 1.7E-08 |
| SP1966 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | 0.76 | 2.5E-07 |
| SP1967 | conserved hypothetical protein | 0.81 | 6.6E-06 |
| SP1970 | aspartate--ammonia ligase | 0.54 | 4.2E-14 |
| SP1998 | L-asparaginase, putative | 0.68 | 1.3E-08 |
| SP2002 | conserved hypothetical protein | 0.74 | 2.7E-06 |

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|--------|--|-------------|---------|
| SP2006 | transcriptional regulator ComX1 | 0.63 | 5.0E-06 |
| SP2053 | competence protein CglA | 0.71 | 6.1E-07 |
| SP2058 | queuine tRNA-ribosyltransferase | 0.64 | 3.1E-11 |
| SP2060 | pyrrolidone-carboxylate peptidase | 0.69 | 2.0E-06 |
| SP2064 | hydrolase, haloacid dehalogenase-like family | 0.68 | 8.0E-06 |
| SP2065 | MATE efflux family protein | 0.63 | 4.5E-10 |
| SP2075 | ABC transporter, ATP-binding/permease protein | 0.69 | 5.2E-09 |
| SP2078 | arginyl-tRNA synthetase | 0.81 | 5.5E-06 |
| SP2091 | glycerol-3-phosphate dehydrogenase (NAD(P)+) | 0.78 | 2.3E-07 |
| SP2099 | penicillin-binding protein 1B | 0.74 | 8.9E-06 |
| SP2121 | histidyl-tRNA synthetase | 0.75 | 6.9E-08 |
| SP2123 | transcriptional regulator, authentic frameshift | 0.72 | 4.3E-06 |
| SP2126 | dihydroxy-acid dehydratase | 0.74 | 1.1E-07 |
| SP2129 | PTS system, IIC component, putative | 0.79 | 6.7E-06 |
| SP2135 | ribosomal protein L33 | 1.51 | 6.6E-06 |
| SP2142 | ROK family protein | 0.53 | 4.5E-13 |
| SP2143 | conserved hypothetical protein | 0.54 | 5.8E-10 |
| SP2144 | conserved hypothetical protein | 0.60 | 1.2E-07 |
| SP2145 | antigen, cell wall surface anchor family | 0.65 | 3.9E-08 |
| SP2146 | conserved hypothetical protein | 0.57 | 1.2E-09 |
| SP2150 | ornithine carbamoyltransferase | 0.74 | 6.1E-06 |
| SP2153 | peptidase, M20/M25/M40 family | 0.63 | 5.5E-09 |
| SP2156 | SPFH domain/Band 7 family | 0.70 | 2.0E-10 |
| SP2157 | alcohol dehydrogenase, iron-containing | 0.62 | 3.1E-08 |
| SP2159 | fucolectin-related protein | 0.80 | 9.7E-06 |
| SP2160 | conserved hypothetical protein | 0.48 | 1.1E-07 |
| SP2161 | PTS system, IID component | 0.67 | 1.0E-08 |
| SP2188 | chaperonin, 33 kDa | 0.67 | 3.8E-10 |
| SP2191 | conserved hypothetical protein | 1.64 | 1.7E-10 |
| SP2194 | ATP-dependent Clp protease, ATP-binding subunit | 0.74 | 2.6E-07 |
| SP2195 | transcriptional regulator CtsR | 0.81 | 2.9E-06 |
| SP2196 | ABC transporter, ATP-binding protein | 1.58 | 7.6E-11 |
| SP2197 | ABC transporter, substrate-binding protein, putative | 1.35 | 1.8E-08 |
| SP2198 | ABC transporter, permease protein | 1.37 | 5.7E-08 |
| SP2208 | helicase, putative | 0.55 | 3.6E-08 |
| SP2214 | translation elongation factor Ts | 0.75 | 6.0E-08 |
| SP2215 | ribosomal protein S2 | 0.68 | 1.5E-10 |
| SP2216 | secreted 45 kd protein | 0.40 | 0.0E+00 |
| SP2218 | rod shape-determining protein MreC | 0.80 | 2.1E-06 |
| SP2219 | conserved hypothetical protein | 0.74 | 6.7E-07 |
| SP2224 | peptidase, M16 family | 1.20 | 5.2E-06 |
| SP2228 | inosine-5-monophosphate dehydrogenase | 0.74 | 3.8E-08 |