|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Genomic Feature** | **Length (bp)** | **Length (bp)** | **Length (bp)** | **(Observed+1)/(Expected+1)** | **Log2((Observed+1)/(Expected+1))** | **Feature Product** |
| LargeSubunitRibosomalRNAlsuRNALSUrRNA | 2903 | 0 | 33.75 | 0.03 | -5.12 | Putative Membrane Protein Putative |
| spxB | 1776 | 0 | 20.65 | 0.05 | -4.44 | 50S Ribosomal Protein L650S |
| alsS | 1701 | 0 | 19.78 | 0.05 | -4.38 | Acetolactate Synthase Large Subunit Acetolactate |
| 1728377\_1730066 | 1689 | 0 | 19.64 | 0.05 | -4.37 |  |
| INV10403820 | 1635 | 0 | 19.01 | 0.05 | -4.32 | Heparinase II/III-Like Proteinheparinase |
| INV10404050 | 1428 | 0 | 16.6 | 0.06 | -4.14 |  |
| FIG01118148-hypotheticalprotein | 1410 | 0 | 16.39 | 0.06 | -4.12 | FIG01116089: Hypothetical Protein Fig01116089: |
| SPn1Transposase | 1354 | 0 | 15.74 | 0.06 | -4.07 | 50S Ribosomal Protein L450S |
| vicK | 1350 | 0 | 15.7 | 0.06 | -4.06 | Tn916, Transcriptional Regulator, Putative Tn916, |
| 1433608\_1434955 | 1347 | 0 | 15.66 | 0.06 | -4.06 |  |
| INV10407400 | 1347 | 0 | 15.66 | 0.06 | -4.06 | Conserved Hypothetical Proteinconserved |
| xseA | 1341 | 0 | 15.59 | 0.06 | -4.05 | Transcriptional Regulator, XRE Family Transcriptional |
| INV10404700 | 1335 | 0 | 15.52 | 0.06 | -4.05 | Putative Uncharacterized Protein Putative |
| wzy | 1305 | 0 | 15.17 | 0.06 | -4.02 | Transcriptional Regulator, Arsr Family Transcriptional |
| malC | 1293 | 0 | 15.03 | 0.06 | -4 | IS1381, Transposase Orfais1381, |
| hom | 1287 | 0 | 14.96 | 0.06 | -4 | Grpe Protein (HSP-70 Cofactor) Grpe |
| 2083564\_2084815 | 1251 | 0 | 14.54 | 0.06 | -3.96 |  |
| INV10419260 | 1251 | 0 | 14.54 | 0.06 | -3.96 | Putative Exported Glycosyl Hydrolase Putative |
| INV10400800 | 1167 | 0 | 13.57 | 0.07 | -3.86 | Putative Membrane Protein Putative |
| INV10411620 | 1158 | 0 | 13.46 | 0.07 | -3.85 | Putative Uncharacterized Protein Putative |
| wchB | 1137 | 0 | 13.22 | 0.07 | -3.83 | Putative IS1167 Transposase Putative |
| mutS2 | 2324 | 1 | 27.02 | 0.07 | -3.81 | Putative Maltodextrose Utilization Protein Mala Putative |
| INV10412980 | 1095 | 0 | 12.73 | 0.07 | -3.78 | Putative Membrane Protein Putative |
| INV10407260 | 2226 | 1 | 25.88 | 0.07 | -3.75 | Putative Oxidoreductase Putative |
| aroB | 1068 | 0 | 12.42 | 0.07 | -3.75 | 3-Phosphoshikimate 1-Carboxyvinyltransferase3-Phosphoshikimate |
| INV10401540 | 1062 | 0 | 12.35 | 0.07 | -3.74 | Conserved Hypothetical Proteinconserved |
| INV10417710 | 1059 | 0 | 12.31 | 0.08 | -3.73 | Tatd Related Dnasetatd |
| INV10400680 | 1053 | 0 | 12.24 | 0.08 | -3.73 | Putative ATP-Binding PP-Loop Family Protein Putative |
| INV10416320 | 1044 | 0 | 12.14 | 0.08 | -3.72 | ABC Transporter, ATP-Binding/Permease Protein ABC |
| tsf | 1041 | 0 | 12.1 | 0.08 | -3.71 | Tetracycline Resistance Protein Tetm Tetracycline |
| UDP-glucose4-epimerase(EC5 | 1029 | 0 | 11.96 | 0.08 | -3.7 | Putative Thiamin Pyrophosphokinase Putative |
| gpsA | 1017 | 0 | 11.82 | 0.08 | -3.68 | Glutamate Racemaseglutamate |
| fni | 1011 | 0 | 11.75 | 0.08 | -3.67 | FIG01117752: Hypothetical Protein Fig01117752: |
| 1419440\_1420449 | 1009 | 0 | 11.73 | 0.08 | -3.67 |  |
| INV10412880 | 1009 | 0 | 11.73 | 0.08 | -3.67 | Putative Membrane Protein Putative |
| IS1380-Spn1\_transposase | 1008 | 0 | 11.72 | 0.08 | -3.67 | Putative Membrane Protein Putative |
| penA | 2043 | 1 | 23.75 | 0.08 | -3.63 | DNA Mismatch Repair Protein Muts Dna |
| HollidayjunctionDNAhelicaseRuvB | 972 | 0 | 11.3 | 0.08 | -3.62 | 10 Kda Chaperonin10 |
| prsA1 | 969 | 0 | 11.27 | 0.08 | -3.62 | Peptidase Tpeptidase |
| glkA | 960 | 0 | 11.16 | 0.08 | -3.6 | Glutamyl-Trna Amidotransferase Subunit Aglutamyl-Trna |
| INV10417690 | 942 | 0 | 10.95 | 0.08 | -3.58 | Putative DNA-Binding Protein Putative |
| pyrB | 924 | 0 | 10.74 | 0.09 | -3.55 | Putative Alkaline Phosphatase Synthesis Sensor Protein Putative |
| INV10411930 | 918 | 0 | 10.67 | 0.09 | -3.54 | Conserved Hypothetical Protein Conserved |
| rpmA | 918 | 0 | 10.67 | 0.09 | -3.54 | Phosphoribosylaminoimidazole-Succinocarboxamide Synthasephosphoribosylaminoimidazole-Succinocarboxamide |
| INV10400770 | 912 | 0 | 10.6 | 0.09 | -3.54 | Putative Membrane Protein (Pseudogene) Putative |
| INV10409640 | 1902 | 1 | 22.11 | 0.09 | -3.53 | Putative Uncharacterized Protein Putative |
| uvrA | 2832 | 2 | 32.92 | 0.09 | -3.5 | Tn5252, Orf 10 Proteintn5252, |
| fba | 882 | 0 | 10.25 | 0.09 | -3.49 | Enolaseenolase |
| mvaK1 | 879 | 0 | 10.22 | 0.09 | -3.49 | Putative Mannose-Specific Phosphotransferase System (PTS), IIAB Component Putative |
| metF | 867 | 0 | 10.08 | 0.09 | -3.47 | Galactose-6-Phosphate Isomerase Lacb Subunit 1galactose-6-Phosphate |
| INV10417730 | 1818 | 1 | 21.14 | 0.09 | -3.47 | Putative Aminotransferase Putative |
| INV10400140 | 865 | 0 | 10.06 | 0.09 | -3.47 | Hypothetical Proteinhypothetical |
| INV10417520 | 864 | 0 | 10.04 | 0.09 | -3.46 | Putative Membrane Protein Putative |
| INV10417750 | 858 | 0 | 9.98 | 0.09 | -3.46 | Putative Membrane Protein Putative |
| INV10404070 | 849 | 0 | 9.87 | 0.09 | -3.44 | Putative Membrane Protein Putative |
| INV10409610 | 849 | 0 | 9.87 | 0.09 | -3.44 | Conserved Hypothetical Proteinconserved |
| INV10418140 | 849 | 0 | 9.87 | 0.09 | -3.44 | Conserved Hypothetical Proteinconserved |
| malD | 843 | 0 | 9.8 | 0.09 | -3.43 | IS1381, Transposase Orfbis1381, |
| INV10419210 | 840 | 0 | 9.77 | 0.09 | -3.43 | Putative Petidase Putative |
| CysteineABCtransporter\_substrate-bindingprotein | 831 | 0 | 9.66 | 0.09 | -3.41 | Transcriptional Regulatortranscriptional |
| INV10415870 | 828 | 0 | 9.63 | 0.09 | -3.41 | ABC Transporterabc |
| INV10419240 | 822 | 0 | 9.56 | 0.09 | -3.4 | Putative Membrane Protein Putative |
| INV10411130 | 807 | 0 | 9.38 | 0.1 | -3.38 | Ion Channel Transport Proteinion |
| INV10415980 | 807 | 0 | 9.38 | 0.1 | -3.38 | Conserved Hypothetical Proteinconserved |
| Integraserecombinase(XerCCodVfamily) | 798 | 0 | 9.28 | 0.1 | -3.36 | Hypothetical Phage Proteinhypothetical |
| INV10417500 | 1674 | 1 | 19.46 | 0.1 | -3.35 | Putative Uncharacterized Protein Putative |
| fhs1 | 1671 | 1 | 19.43 | 0.1 | -3.35 | Putative Putative Malonyl Coa-Acyl Carrier Protein Transacylase Putative |
| rplB | 789 | 0 | 9.17 | 0.1 | -3.35 | Protein Of Unknown Function DUF208Protein |
| mutS | 2535 | 2 | 29.47 | 0.1 | -3.34 | Macrolide-Efflux Protein Macrolide-Efflux |
| INV10405330 | 786 | 0 | 9.14 | 0.1 | -3.34 | Beta-Glucoside-Specific Phosphotransferase System (PTS), IIABC Componentbeta-Glucoside-Specific |
| rpsB | 780 | 0 | 9.07 | 0.1 | -3.33 | Putative Dihydroorotase Putative |
| 20393\_22039 | 1646 | 1 | 19.14 | 0.1 | -3.33 |  |
| trpA | 777 | 0 | 9.03 | 0.1 | -3.33 | Pyruvate Oxidasepyruvate |
| INV10417060 | 774 | 0 | 9 | 0.1 | -3.32 | Putative PAP2 Superfamily Membrane Protein Putative |
| gyrA | 2469 | 2 | 28.7 | 0.1 | -3.31 | Guanylate Kinaseguanylate |
| INV10419000 | 759 | 0 | 8.82 | 0.1 | -3.3 | Putative Sugar-Specific Permease, Sgat/Ulaa Family Putative |
| glnQ1 | 741 | 0 | 8.61 | 0.1 | -3.26 | Glutamyl-Trna Amidotransferase Subunit Cglutamyl-Trna |
| INV10403450 | 2367 | 2 | 27.52 | 0.11 | -3.25 | Putative Membrane Protein Putative |
| purH | 1548 | 1 | 18 | 0.11 | -3.25 | Phage Proteinphage |
| INV10418980 | 729 | 0 | 8.48 | 0.11 | -3.24 | Putative Transketolase Subunit Putative |
| INV10401630 | 1533 | 1 | 17.82 | 0.11 | -3.23 | Putative Transposase Putative |
| malQ | 1518 | 1 | 17.65 | 0.11 | -3.22 | IS1381, Transposase Orfbis1381, |
| TrsE-likeprotein | 2316 | 2 | 26.93 | 0.11 | -3.22 | DNA-3-Methyladenine Glycosylase IDNA-3-Methyladenine |
| ccdA | 711 | 0 | 8.27 | 0.11 | -3.21 | Choline Binding Protein Jcholine |
| phoP | 708 | 0 | 8.23 | 0.11 | -3.21 | Sialidase B Precursor (Neuraminidase B)Sialidase |
| INV10417510 | 705 | 0 | 8.2 | 0.11 | -3.2 | Putative Transport Protein Putative |
| INV10400670 | 699 | 0 | 8.13 | 0.11 | -3.19 | Putative Exported Protein Putative |
| guaB | 1479 | 1 | 17.19 | 0.11 | -3.19 | Glycyl-Trna Synthetase Beta Chainglycyl-Trna |
| ftsE | 693 | 0 | 8.06 | 0.11 | -3.18 | Peptide Deformylasepeptide |
| gpmA | 693 | 0 | 8.06 | 0.11 | -3.18 | Alpha-Glycerophosphate Oxidasealpha-Glycerophosphate |
| wzd | 693 | 0 | 8.06 | 0.11 | -3.18 | Triosephosphate Isomerasetriosephosphate |
| gatA | 1467 | 1 | 17.06 | 0.11 | -3.17 | Putative Cell Division Protein Putative |
| pncO | 690 | 0 | 8.02 | 0.11 | -3.17 | Oligopeptide Transport System Permease Protein Oppb (TC 3.A.1.5.1)Oligopeptide |
| gatB | 1443 | 1 | 16.78 | 0.11 | -3.15 | Putative Signal Recognition Particle 54 Ftsy Putative |
| sdhB | 672 | 0 | 7.81 | 0.11 | -3.14 | Ribosomal Large Subunit Pseudouridine Synthase Bribosomal |
| INV10417530 | 663 | 0 | 7.71 | 0.11 | -3.12 | Putative Exported Protein Putative |
| INV10418950 | 654 | 0 | 7.6 | 0.12 | -3.1 | Putative Membrane Protein Putative |
| INV10417760 | 645 | 0 | 7.5 | 0.12 | -3.09 | Putative Universal Stress Protein Putative |
| INV10412760 | 642 | 0 | 7.46 | 0.12 | -3.08 | Putative ABC Transporter Putative |
| tmk | 639 | 0 | 7.43 | 0.12 | -3.08 | 50S Ribosomal Protein L3550S |
| ribE | 636 | 0 | 7.39 | 0.12 | -3.07 | Spermidine/Putrescine Extracellular Binding Protein Spermidine/Putrescine |
| 1134692\_1136046 | 1354 | 1 | 15.74 | 0.12 | -3.07 |  |
| INV10412750 | 630 | 0 | 7.32 | 0.12 | -3.06 | Putative Membrane Protein Putative |
| INV10406330 | 1344 | 1 | 15.63 | 0.12 | -3.06 | Putative Uncharacterized Protein Putative |
| INV10418940 | 1341 | 1 | 15.59 | 0.12 | -3.05 | Putative Ribosomal RNA Large Subunit Methyltransferase A Putative |
| rplC | 627 | 0 | 7.29 | 0.12 | -3.05 | Ribose-Phosphate Pyrophosphokinase 1ribose-Phosphate |
| rpsC | 627 | 0 | 7.29 | 0.12 | -3.05 | Putative Dihydroorotate Dehydrogenase Putative |
| murC | 1335 | 1 | 15.52 | 0.12 | -3.05 | Lipoprotein, NLP/P60 Familylipoprotein, |
| INV10400250 | 624 | 0 | 7.25 | 0.12 | -3.04 | Hypothetical Proteinhypothetical |
| USGprotein | 2748 | 3 | 31.95 | 0.12 | -3.04 | Tn5252, Orf 10 Proteintn5252, |
| INV10405030 | 1329 | 1 | 15.45 | 0.12 | -3.04 | Putative HIT-Family Nucleotide-Binding Protein Putative |
| INV10417800 | 621 | 0 | 7.22 | 0.12 | -3.04 | Puttaive Ftsx-Family Transport Proteinputtaive |
| INV10419380 | 1326 | 1 | 15.42 | 0.12 | -3.04 | Marr-Family Regulatory Protein Marr-Family |
| INV10405100 | 2025 | 2 | 23.54 | 0.12 | -3.03 | Conserved Hypothetical Proteinconserved |
| INV10415360 | 1314 | 1 | 15.28 | 0.12 | -3.03 | ABC Transporter, ATP-Binding Protein ABC |
| speA | 1311 | 1 | 15.24 | 0.12 | -3.02 | 50S Ribosomal Protein L150S |
| cbpG | 611 | 0 | 7.1 | 0.12 | -3.02 | Choline Binding Protein Dcholine |
| eno | 1305 | 1 | 15.17 | 0.12 | -3.02 | DNA Polymerase III Alpha Subunit (EC 2.7.7.7); DNA Polymerase III Epsilon Chain (EC 2.7.7.7)DNA |
| INV10411950 | 1305 | 1 | 15.17 | 0.12 | -3.02 | Putative Polysaccharide Biosynthesis Flippase Putative |
| INV10410100 | 603 | 0 | 7.01 | 0.12 | -3 | Conserved Hypothetical Proteinconserved |
| stk1 | 1980 | 2 | 23.02 | 0.12 | -3 | 50S Ribosomal Protein L1350S |
| tdk | 600 | 0 | 6.98 | 0.13 | -3 | 50S Ribosomal Protein L1950S |
| INV10419250 | 1286 | 1 | 14.95 | 0.13 | -3 | Probable Alcohol Dehydrogenaseprobable |
| pyrP | 1284 | 1 | 14.93 | 0.13 | -2.99 | Plasmid Addiction System Poison Protein Plasmid |
| tig | 1284 | 1 | 14.93 | 0.13 | -2.99 | 50S Ribosomal Protein L33 150S |
| recR | 597 | 0 | 6.94 | 0.13 | -2.99 | Polyribonucleotide Nucleotidyltransferasepolyribonucleotide |
| INV10404990 | 1278 | 1 | 14.86 | 0.13 | -2.99 | Type I Restriction-Modification System Protein Type |
| INV10411640 | 1275 | 1 | 14.82 | 0.13 | -2.98 | Putative Conserved Hypothetical Protein (Pseudogene) Putative |
| serS | 1275 | 1 | 14.82 | 0.13 | -2.98 | Dtdp-4-Keto-L-Rhamnose Reductase Rmlddtdp-4-Keto-L-Rhamnose |
| INV10400780 | 594 | 0 | 6.91 | 0.13 | -2.98 | Putative Uncharacterized Protein (Pseudogene) Putative |
| thrS | 1944 | 2 | 22.6 | 0.13 | -2.98 | 50S Ribosomal Protein L3150S |
| IntramembraneproteaseRasPYluC\_implicatedincelldivisionbasedonFtsLcleavage | 1260 | 1 | 14.65 | 0.13 | -2.97 | Hypothetical Phage Protein Hypothetical |
| cinA | 1257 | 1 | 14.61 | 0.13 | -2.96 | Sensor Histidine Kinase Sensor |
| Phagemajortailprotein | 579 | 0 | 6.73 | 0.13 | -2.95 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10409050 | 567 | 0 | 6.59 | 0.13 | -2.92 | Conserved Hypothetical Protein Conserved |
| INV10410590 | 564 | 0 | 6.56 | 0.13 | -2.92 | Transposase, Orf 1Transposase, |
| INV10411060 | 561 | 0 | 6.52 | 0.13 | -2.91 | Hemolysin-Like Protein Hemolysin-Like |
| Phageportalprotein | 1203 | 1 | 13.99 | 0.13 | -2.91 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| pgk | 1197 | 1 | 13.92 | 0.13 | -2.9 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| tufA | 1197 | 1 | 13.92 | 0.13 | -2.9 | Queuine Trna-Ribosyltransferasequeuine |
| sms | 1194 | 1 | 13.88 | 0.13 | -2.9 | Ribonuclease P Protein Componentribonuclease |
| coaC | 552 | 0 | 6.42 | 0.13 | -2.89 | Cytidylate Kinasecytidylate |
| INV10419170 | 1179 | 1 | 13.71 | 0.14 | -2.88 | Putative Alpha-1,2-Mannosidase Putative |
| purN | 546 | 0 | 6.35 | 0.14 | -2.88 | Phage Terminase, Small Subunit Phage |
| clpC | 2433 | 3 | 28.29 | 0.14 | -2.87 | Response Regulator Protein Response |
| INV10411740 | 1173 | 1 | 13.64 | 0.14 | -2.87 | Putative Membrane Protein Putative |
| prophageLambdaSa2\_site-specificrecombinase\_phageintegrasefamily | 543 | 0 | 6.31 | 0.14 | -2.87 | Putative Endopeptidase O Putative |
| rplE | 543 | 0 | 6.31 | 0.14 | -2.87 | Pneumococcal Surface Protein Apneumococcal |
| INV10412780 | 1167 | 1 | 13.57 | 0.14 | -2.86 | Putative Transposase (Pseudogene) Putative |
| recA | 1167 | 1 | 13.57 | 0.14 | -2.86 | Mannose-6-Phosphate Isomerasemannose-6-Phosphate |
| atpH | 537 | 0 | 6.24 | 0.14 | -2.86 | ATP Synthase B Chainatp |
| rplF | 537 | 0 | 6.24 | 0.14 | -2.86 | Phosphate Import ATP-Binding Protein 1phosphate |
| wchD | 1155 | 1 | 13.43 | 0.14 | -2.85 | DNA Topoisomerase IDNA |
| INV10416420 | 534 | 0 | 6.21 | 0.14 | -2.85 | Type II Restriction Enzymetype |
| INV10406020 | 525 | 0 | 6.1 | 0.14 | -2.83 | Putative Rrna Methylase Putative |
| pyrR | 522 | 0 | 6.07 | 0.14 | -2.82 | Pleiotropic Regulator Of Exopolysaccharide Synthesis, Competence And Biofilm Formation Ftr, XRE Familypleiotropic |
| infB | 1731 | 2 | 20.12 | 0.14 | -2.82 | Heat-Inducible Transcription Repressor Hrcaheat-Inducible |
| INV10400200 | 516 | 0 | 6 | 0.14 | -2.81 | Hypothetical Protein Hypothetical |
| INV10400040 | 1116 | 1 | 12.97 | 0.14 | -2.8 | Hypothetical Protein Hypothetical |
| INV10405050 | 1114 | 1 | 12.95 | 0.14 | -2.8 | ABC Transporter ATP-Binding Protein ABC |
| INV10400970 | 1680 | 2 | 19.53 | 0.15 | -2.77 | Sugar Phosphotransferase System (PTS), Mannose/Fructose/Sorbose Family, IID Component Sugar |
| LSUribosomalproteinL10p(P0) | 501 | 0 | 5.82 | 0.15 | -2.77 | Putative Response Regulator Protein Putative |
| carA | 1080 | 1 | 12.56 | 0.15 | -2.76 | Cadmium Resistance Protein Cadmium |
| INV10405110 | 1662 | 2 | 19.32 | 0.15 | -2.76 | Conserved Hypothetical Protein Conserved |
| INV10402030 | 1079 | 1 | 12.54 | 0.15 | -2.76 | Putative Azlc-Family Transport Protein Putative |
| atpF | 495 | 0 | 5.75 | 0.15 | -2.75 | ATP Synthase Beta Chain Atp |
| rpsE | 495 | 0 | 5.75 | 0.15 | -2.75 | Orotate Phosphoribosyltransferaseorotate |
| INV10417540 | 486 | 0 | 5.65 | 0.15 | -2.73 | Putative Methylase Putative |
| Competence-specificsigmafactorComX | 481 | 0 | 5.59 | 0.15 | -2.72 | Putative Late Competence Protein Putative |
| INV10419400 | 480 | 0 | 5.58 | 0.15 | -2.72 | Putative Membrane Protein Putative |
| ddlA | 1044 | 1 | 12.14 | 0.15 | -2.72 | Cytidine Deaminase (EC 3.5.4.5) Cytidine |
| wzx | 1041 | 1 | 12.1 | 0.15 | -2.71 | Transcriptional Regulator Transcriptional |
| ilvH | 477 | 0 | 5.55 | 0.15 | -2.71 | Putative DNA Polymerase III, Delta' Subunit Putative |
| INV10410670 | 2166 | 3 | 25.18 | 0.15 | -2.71 | Putative DNA-Binding Protein Putative |
| INV10415940 | 1038 | 1 | 12.07 | 0.15 | -2.71 | Putative Mga-Like Regulatory Protein Putative |
| INV10407220 | 1032 | 1 | 12 | 0.15 | -2.7 | Padr-Like Family Regulator Proteinpadr-Like |
| INV10403260 | 472 | 0 | 5.49 | 0.15 | -2.7 | Sugar Phosphotransferase System (PTS), Lactose/Cellobiose-Specific Family, IIB Component Sugar |
| rpsG | 471 | 0 | 5.48 | 0.15 | -2.7 | Putative CTP Synthase Putative |
| INV10400180 | 468 | 0 | 5.44 | 0.16 | -2.69 | Hypothetical Protein Hypothetical |
| mutX | 465 | 0 | 5.41 | 0.16 | -2.68 | Putative Maltose/Maltodextrin ABC Transport System Permease Protein Putative |
| INV10412790 | 1014 | 1 | 11.79 | 0.16 | -2.68 | Gntr Family Regulatory Protein Gntr |
| ABCtransportermembrane-spanningpermease-aminoacidtransport | 2111 | 3 | 24.54 | 0.16 | -2.67 | ABC Transporter Membrane-Spanning Permease - Amino Acid Transportabc |
| INV10417640 | 462 | 0 | 5.37 | 0.16 | -2.67 | Cell Wall Surface Anchored Protein Cell |
| INV10418990 | 1008 | 1 | 11.72 | 0.16 | -2.67 | Putative Transketolase Subunit Putative |
| INV10400950 | 456 | 0 | 5.3 | 0.16 | -2.66 | Sugar Phosphotransferase System (PTS), Sorbose-Specific Family, IIC Component Sugar |
| INV10407010 | 1536 | 2 | 17.86 | 0.16 | -2.65 | ABC Transporter ATP-Binding Protein ABC |
| pdhB | 993 | 1 | 11.54 | 0.16 | -2.65 | DNA Mismatch Repair Protein Mutl Dna |
| INV10417190 | 453 | 0 | 5.27 | 0.16 | -2.65 | Putative Uncharacterized Protein Putative |
| INV10411610 | 987 | 1 | 11.47 | 0.16 | -2.64 | GMP Reductase Gmp |
| INV10417580 | 987 | 1 | 11.47 | 0.16 | -2.64 | Membrane Protein Oxaa 2 Precursor Membrane |
| ldh | 987 | 1 | 11.47 | 0.16 | -2.64 | ABC Transporter ATP-Binding Protein ABC |
| PTSsystem\_IIAcomponent | 450 | 0 | 5.23 | 0.16 | -2.64 | Phage Capsid Protein Phage |
| argR | 447 | 0 | 5.2 | 0.16 | -2.63 | Arginine Repressor Arginine |
| INV10409750 | 447 | 0 | 5.2 | 0.16 | -2.63 | Tn5252 Relaxase Tn5252 |
| rplO | 441 | 0 | 5.13 | 0.16 | -2.62 | Putative Phosphate Acetyltransferase Putative |
| INV10416060 | 960 | 1 | 11.16 | 0.16 | -2.6 | Sugar Phosphotransferase System (PTS), IIC Component Sugar |
| INV10407030 | 957 | 1 | 11.13 | 0.16 | -2.6 | Putative Uncharacterized Protein Putative |
| INV10403580 | 435 | 0 | 5.06 | 0.17 | -2.6 | Putative Hyaluronate Lyase Putative |
| INV10417620 | 954 | 1 | 11.09 | 0.17 | -2.6 | Putative 3'-5' Exoribonuclease Putative |
| INV10410350 | 432 | 0 | 5.02 | 0.17 | -2.59 | Putative IS1381 Transposase (Pseudogene) Putative |
| INV10414100 | 431 | 0 | 5.01 | 0.17 | -2.59 | Isochorismatase Family Protein Isochorismatase |
| INV10401520 | 945 | 1 | 10.99 | 0.17 | -2.58 | Metallo-Beta-Lactamase Superfamily Protein Metallo-Beta-Lactamase |
| PTSsystem\_nitrogenregulatorycomponentIIA\_ putative | 429 | 0 | 4.99 | 0.17 | -2.58 | Phage Endolysin Phage |
| INV10417560 | 1458 | 2 | 16.95 | 0.17 | -2.58 | Spou Rrna Methylase Family Protein Spou |
| Integralmembraneprotein | 942 | 1 | 10.95 | 0.17 | -2.58 | Serine Protease Serine |
| mutL | 1950 | 3 | 22.67 | 0.17 | -2.56 | Putative Endo-Beta-N-Acetylglucosaminidase Putative |
| INV10406600 | 927 | 1 | 10.78 | 0.17 | -2.56 | Putative Hydroxyethylthiazole Kinase Putative |
| atpC | 420 | 0 | 4.88 | 0.17 | -2.56 | ATP Synthase Alpha Chain Atp |
| conservedhypotheticalprotein | 420 | 0 | 4.88 | 0.17 | -2.56 | Conjugative Transposon Membrane Protein Conjugative |
| topA | 1932 | 3 | 22.46 | 0.17 | -2.55 | 30S Ribosomal Protein S430S |
| cysM | 921 | 1 | 10.71 | 0.17 | -2.55 | Putative Cysteine Desulfurase Putative |
| INV10402170 | 417 | 0 | 4.85 | 0.17 | -2.55 | Putative Nrdi-Like Protein Putative |
| N-acetylneuraminatelyase(EC4 | 918 | 1 | 10.67 | 0.17 | -2.54 | Membrane Protein, Putative Membrane |
| INV10406310 | 3426 | 6 | 39.83 | 0.17 | -2.54 | Putative Membrane Protein Putative |
| INV10407350 | 414 | 0 | 4.81 | 0.17 | -2.54 | Putative Exonuclease Putative |
| gidA | 1914 | 3 | 22.25 | 0.17 | -2.54 | Putative Fuculokinase Putative |
| INV10412400 | 912 | 1 | 10.6 | 0.17 | -2.54 | Putative Extracellular Amino Acid-Binding Protein Putative |
| INV10418090 | 912 | 1 | 10.6 | 0.17 | -2.54 | Conserved Hypothetical Protein Conserved |
| INV10405080 | 897 | 1 | 10.43 | 0.18 | -2.51 | Phosphotransferase Enzyme Family Protein Phosphotransferase |
| INV10403210 | 1388 | 2 | 16.14 | 0.18 | -2.51 | Putative Sugar-Binding Regulatory Protein Putative |
| INV10415900 | 405 | 0 | 4.71 | 0.18 | -2.51 | Sugar Binding Transcriptional Regulator Sugar |
| spxA | 402 | 0 | 4.67 | 0.18 | -2.5 | 50S Ribosomal Protein L550S |
| INV10411920 | 885 | 1 | 10.29 | 0.18 | -2.5 | Putative Zinc-Binding Dehydrogenase Putative |
| rpsH | 399 | 0 | 4.64 | 0.18 | -2.5 | Uridylate Kinaseuridylate |
| INV10413620 | 883 | 1 | 10.27 | 0.18 | -2.49 | Putative Polysaccharide Biosynthesis Protein Putative |
| INV10419310 | 1365 | 2 | 15.87 | 0.18 | -2.49 | PTS System, Iid Component Pts |
| uvrC | 1846 | 3 | 21.46 | 0.18 | -2.49 | Tn5252, Orf 9 Protein Tn5252, |
| INV10410060 | 1362 | 2 | 15.83 | 0.18 | -2.49 | ABC Transporter ATP-Binding Protein ABC |
| pstS | 879 | 1 | 10.22 | 0.18 | -2.49 | Putative Formate Acetyltransferase Putative |
| INV10416450 | 396 | 0 | 4.6 | 0.18 | -2.49 | DNA Methylase Dna |
| INV10417960 | 876 | 1 | 10.18 | 0.18 | -2.48 | Putative Phosphotyrosine Protein Phosphatase Putative |
| addB | 3276 | 6 | 38.09 | 0.18 | -2.48 | Putative ATP-Dependent Exonuclease Subunit B Putative |
| sdhA | 873 | 1 | 10.15 | 0.18 | -2.48 | 16S Rrna Processing Protein 16s |
| Phageterminase\_smallsubunit | 393 | 0 | 4.57 | 0.18 | -2.48 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| CholinebindingproteinA | 390 | 0 | 4.53 | 0.18 | -2.47 | Cell Wall-Associated Murein Hydrolase Lytacell |
| INV10403730 | 390 | 0 | 4.53 | 0.18 | -2.47 | Putative Sugar-Phosphate Isomerase Putative |
| INV10403470 | 866 | 1 | 10.07 | 0.18 | -2.47 | Putative Ribosomal Small Subunit Pseudouridine Synthase B Putative |
| INV10416410 | 864 | 1 | 10.04 | 0.18 | -2.46 | Hypothetical Protein Hypothetical |
| Phagetaillengthtape-measureprotein | 2760 | 5 | 32.09 | 0.18 | -2.46 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| ciaH | 1335 | 2 | 15.52 | 0.18 | -2.46 | Chlorohydrolase Chlorohydrolase |
| INV10415340 | 856 | 1 | 9.95 | 0.18 | -2.45 | Putative Membrane Protein Putative |
| INV10415890 | 855 | 1 | 9.94 | 0.18 | -2.45 | ABC Transporter, Substrate Binding Protein ABC |
| FIG00627694-hypotheticalprotein | 384 | 0 | 4.46 | 0.18 | -2.45 | 3-Oxoacyl-[Acyl-Carrier Protein] Reductase3-Oxoacyl-[Acyl-Carrier |
| gapN | 1320 | 2 | 15.35 | 0.18 | -2.45 | Putative Cell Division Protein Putative |
| INV10405690 | 381 | 0 | 4.43 | 0.18 | -2.44 | Putative Extracellular Solute-Binding Protein Putative |
| 1403638\_1404484 | 846 | 1 | 9.84 | 0.18 | -2.44 |  |
| INV10411630 | 846 | 1 | 9.84 | 0.18 | -2.44 | Putative Endonuclease Putative |
| INV10412710 | 846 | 1 | 9.84 | 0.18 | -2.44 | Putative ABC Transporter Putative |
| INV10409620 | 840 | 1 | 9.77 | 0.19 | -2.43 | Putative Site-Specific Recombinase (Pseudogene) Putative |
| relA | 2223 | 4 | 25.84 | 0.19 | -2.42 | Positive Transcriptional Regulator, Mutr Family Positive |
| dnaA | 1299 | 2 | 15.1 | 0.19 | -2.42 | Dephospho-Coa Kinase (EC 2.7.1.24) Dephospho-Coa |
| INV10412740 | 837 | 1 | 9.73 | 0.19 | -2.42 | Putative Membrane Protein Putative |
| ftsY | 1290 | 2 | 15 | 0.19 | -2.42 | GTP Cyclohydrolase IGTP |
| INV10417590 | 831 | 1 | 9.66 | 0.19 | -2.41 | Pyridoxal-Dependent Decarboxylasepyridoxal-Dependent |
| INV10403550 | 372 | 0 | 4.32 | 0.19 | -2.41 | Hypothetical Proteinhypothetical |
| purA | 1287 | 2 | 14.96 | 0.19 | -2.41 | Phage Hyaluronidasephage |
| INV10419270 | 369 | 0 | 4.29 | 0.19 | -2.4 | Conserved Hypothetical Protein Conserved |
| Phagetranscriptionalregulator\_CroCIfamily | 369 | 0 | 4.29 | 0.19 | -2.4 | Putative Nicotinate-Nucleotide Pyrophosphorylase Putative |
| rplN | 369 | 0 | 4.29 | 0.19 | -2.4 | Putative Phosphate ABC Transporter, Extracellular Phosphate-Binding Lipoprotein Putative |
| Phageterminaselargesubunit | 1731 | 3 | 20.12 | 0.19 | -2.4 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10403810 | 366 | 0 | 4.26 | 0.19 | -2.4 | Putative Membrane Protein Putative |
| INV10417700 | 366 | 0 | 4.26 | 0.19 | -2.4 | Conserved Hypothetical Proteinconserved |
| rpsM | 366 | 0 | 4.26 | 0.19 | -2.4 | DNA Repair Protein Radcdna |
| pabB | 1722 | 3 | 20.02 | 0.19 | -2.39 | Multidrug Resistance Efflux Pump Pmra Multidrug |
| INV10400530 | 816 | 1 | 9.49 | 0.19 | -2.39 | Translation Initiation Factor IF-3translation |
| INV10406590 | 816 | 1 | 9.49 | 0.19 | -2.39 | Putative Membrane Protein Putative |
| INV10417980 | 816 | 1 | 9.49 | 0.19 | -2.39 | Conserved Hypothetical Protein Conserved |
| INV10404730 | 364 | 0 | 4.23 | 0.19 | -2.39 | PTS Transporterpts |
| INV10417000 | 1251 | 2 | 14.54 | 0.19 | -2.37 | Putative Cell Wall-Binding Protein Putative |
| INV10406030 | 804 | 1 | 9.35 | 0.19 | -2.37 | Putative Uncharacterized Protein Putative |
| Phosphatidatecytidylyltransferase(EC2 | 804 | 1 | 9.35 | 0.19 | -2.37 | Nucleoside Diphosphate Kinase Nucleoside |
| INV10405530 | 1693 | 3 | 19.68 | 0.19 | -2.37 | Putative Flavocytochrome Putative |
| argS | 1692 | 3 | 19.67 | 0.19 | -2.37 | Putative Arginine Repressor Putative |
| INV10418650 | 801 | 1 | 9.31 | 0.19 | -2.37 | ABC Transporter ATP-Binding Membrane Protein ABC |
| malA | 801 | 1 | 9.31 | 0.19 | -2.37 | IS1381, Transposase Orfais1381, |
| rplR | 357 | 0 | 4.15 | 0.19 | -2.36 | Hpr Kinase/Phosphorylase Hpr |
| INV10404570 | 795 | 1 | 9.24 | 0.2 | -2.36 | Conserved Hypothetical Protein Conserved |
| INV10408980 | 795 | 1 | 9.24 | 0.2 | -2.36 | Tetrapyrrole (Corrin/Porphyrin) Methylase Family Protein Tetrapyrrole |
| murN | 1233 | 2 | 14.33 | 0.2 | -2.35 | LSU Ribosomal Protein L7/L12 (P1/P2) LSU |
| ugd | 1233 | 2 | 14.33 | 0.2 | -2.35 | Homoserine Kinasehomoserine |
| recN | 1668 | 3 | 19.39 | 0.2 | -2.35 | Putative Bacteeriocin ABC Transporter Transmembrane Domain Blpy (CAAX Protease) Putative |
| INV10406730 | 1224 | 2 | 14.23 | 0.2 | -2.34 | Tetr Family Regulatory Protein Tetr |
| murM | 1221 | 2 | 14.2 | 0.2 | -2.34 | LSU Ribosomal Protein L27plsu |
| dnaH | 1656 | 3 | 19.25 | 0.2 | -2.34 | D-Alanine--Poly(Phosphoribitol) Ligase Subunit 1D-Alanine--Poly(Phosphoribitol) |
| putativetransposonintegraseTn916ORF3-like | 1218 | 2 | 14.16 | 0.2 | -2.34 | Phenylalanyl-Trna Synthetase Beta Chainphenylalanyl-Trna |
| INV10412730 | 348 | 0 | 4.05 | 0.2 | -2.34 | Putative ABC Transporter Putative |
| prophagepi2protein37 | 348 | 0 | 4.05 | 0.2 | -2.34 | Putative Xaa-Pro Dipeptidase Putative |
| rplS | 348 | 0 | 4.05 | 0.2 | -2.34 | PTS System, Fructose-Specific IIA Component (EC 2.7.1.69) / PTS System, Fructose-Specific IIB Component (EC 2.7.1.69) / PTS System, Fructose-Specific IIC Component (EC 2.7.1.69) PTS |
| thiI | 1215 | 2 | 14.13 | 0.2 | -2.33 | 50S Ribosomal Protein L2750S |
| INV10400150 | 781 | 1 | 9.08 | 0.2 | -2.33 | Hypothetical Protein Hypothetical |
| INV10405120 | 781 | 1 | 9.08 | 0.2 | -2.33 | Ribosomal Protein L7Ae/L30e/S12e/Gadd45 Family Protein Ribosomal |
| INV10412770 | 1212 | 2 | 14.09 | 0.2 | -2.33 | Putative Transposase Remnant (Pseudogene) Putative |
| ribA | 1206 | 2 | 14.02 | 0.2 | -2.32 | Putative Spermidine/Putrescine ABC Transporter ATP-Binding Protein Putative |
| INV10418120 | 2064 | 4 | 24 | 0.2 | -2.32 | Putative Ssdna-Binding Protein Putative |
| Zetatoxin | 772 | 1 | 8.98 | 0.2 | -2.32 | Transcriptional Regulator Spxa2transcriptional |
| OligopeptideABCtransporter\_periplasmicoligopeptide-bindingproteinOppA(TC3 | 1629 | 3 | 18.94 | 0.2 | -2.32 | Multiple Sugar-Binding Transport System Permease Protein Multiple |
| INV10415880 | 771 | 1 | 8.96 | 0.2 | -2.32 | ABC Transporter Abc |
| ugl | 1191 | 2 | 13.85 | 0.2 | -2.31 | Threonyl-Trna Synthetasethreonyl-Trna |
| pbp1B | 2466 | 5 | 28.67 | 0.2 | -2.31 | UDP-N-Acetylmuramoylalanyl-D-Glutamate--2,6-Dia Minopimelate Ligaseudp-N-Acetylmuramoylalanyl-D-Glutamate--2,6-Dia |
| INV10416460 | 762 | 1 | 8.86 | 0.2 | -2.3 | DNA Methylasedna |
| htrA | 1182 | 2 | 13.74 | 0.2 | -2.3 | DNA Gyrase Subunit ADNA |
| rmlD | 754 | 1 | 8.77 | 0.2 | -2.29 | Putative Gamma-Glutamyl Phosphate Reductase Putative |
| Phagecapsidprotein | 1173 | 2 | 13.64 | 0.2 | -2.29 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| pstB3 | 753 | 1 | 8.75 | 0.21 | -2.29 | Formate Acetyltransferaseformate |
| INV10411100 | 333 | 0 | 3.87 | 0.21 | -2.28 | Putative Bacteriocin Immunity Protein Putative |
| INV10400290 | 1170 | 2 | 13.6 | 0.21 | -2.28 | Putative Gluconate 5-Dehydrogenase Putative |
| CelldivisionproteinGpsB\_coordinatestheswitchbetweencylindricalandseptalcellwallsynthesisbyre-localizationofPBP1 | 330 | 0 | 3.84 | 0.21 | -2.28 | Cytidine Deaminasecytidine |
| OligopeptidetransportATP-bindingproteinOppD(TC3 | 1983 | 4 | 23.05 | 0.21 | -2.27 | Multiple Sugar-Binding Transport System Permease Protein (Pseudogene) Multiple |
| Transcriptionalregulator\_MerRfamily | 741 | 1 | 8.61 | 0.21 | -2.26 | 30S Ribosomal Protein S1130S |
| tkt | 1977 | 4 | 22.98 | 0.21 | -2.26 | 50S Ribosomal Protein L3450S |
| INV10405520 | 738 | 1 | 8.58 | 0.21 | -2.26 | Two-Component System, Sensor Histidine Kinase Two-Component |
| xerD | 735 | 1 | 8.55 | 0.21 | -2.26 | Transcriptional Regulator, Cro/CI Family Transcriptional |
| fabG | 732 | 1 | 8.51 | 0.21 | -2.25 | Putative Competence Associated Endonuclease Putative |
| INV10413000 | 1959 | 4 | 22.78 | 0.21 | -2.25 | ABC Transporter Permease Protein ABC |
| lig | 1959 | 4 | 22.78 | 0.21 | -2.25 | Putative Membrane Protein Putative |
| INV10410330 | 729 | 1 | 8.48 | 0.21 | -2.24 | Putative Metallopeptidase Putative |
| INV10411600 | 1134 | 2 | 13.18 | 0.21 | -2.24 | Putative Haloacid Dehalogenase-Like Hydrolase Putative |
| FIG01115816-hypotheticalprotein | 723 | 1 | 8.41 | 0.21 | -2.23 | FIG01114767: Hypothetical Proteinfig01114767: |
| INV10411030 | 318 | 0 | 3.7 | 0.21 | -2.23 | Calcineurin-Like Phosphoesterase Calcineurin-Like |
| INV10416480 | 318 | 0 | 3.7 | 0.21 | -2.23 | Zinc-Binding Dehydrogenasezinc-Binding |
| ribC | 318 | 0 | 3.7 | 0.21 | -2.23 | Putative Spermidine/Putrescine ABC Transporter Permease Protein Putative |
| atpB | 717 | 1 | 8.34 | 0.21 | -2.22 | Aspartate Aminotransferaseaspartate |
| LSUribosomalproteinL21p | 315 | 0 | 3.66 | 0.21 | -2.22 | Putative Sensor Histidine Kinase (Pseudogene) Putative |
| proB | 1110 | 2 | 12.9 | 0.22 | -2.21 | Penicillin-Binding Protein 2bpenicillin-Binding |
| PTSsystem\_fructose-specificIIAcomponent(EC2 | 312 | 0 | 3.63 | 0.22 | -2.21 | Phage Antirepressor Proteinphage |
| 1940076\_1940387 | 311 | 0 | 3.62 | 0.22 | -2.21 |  |
| INV10417880 | 311 | 0 | 3.62 | 0.22 | -2.21 | Putative Exported PTS System Protein Putative |
| INV10411960 | 708 | 1 | 8.23 | 0.22 | -2.21 | Putative Phosphotransferase Licd1 Putative |
| INV10402100 | 309 | 0 | 3.59 | 0.22 | -2.2 | Putative Histidine Sensor Kinase Putative |
| INV10407320 | 1494 | 3 | 17.37 | 0.22 | -2.2 | Conserved Hypothetical Protein Conserved |
| recF | 1098 | 2 | 12.77 | 0.22 | -2.2 | Putative Immunity Protein Putative |
| INV10417490 | 1092 | 2 | 12.7 | 0.22 | -2.19 | Putative ABC Transporter ATP-Binding Protein Putative |
| INV10418080 | 699 | 1 | 8.13 | 0.22 | -2.19 | Putative Sugar-Specific Permease, Sgat/Ulaa Family Putative |
| N-acetylmannosamine-6-phosphate2-epimerase(EC5 | 699 | 1 | 8.13 | 0.22 | -2.19 | Adapter Protein Mecaadapter |
| INV10401600 | 306 | 0 | 3.56 | 0.22 | -2.19 | Putative Glycoprotease Putative |
| INV10402160 | 696 | 1 | 8.09 | 0.22 | -2.18 | Putative Membrane Protein Putative |
| INV10407870 | 1086 | 2 | 12.63 | 0.22 | -2.18 | Conserved Hypothetical Protein Conserved |
| INV10409460 | 1083 | 2 | 12.59 | 0.22 | -2.18 | Conserved Hypothetical Protein Conserved |
| INV10401260 | 693 | 1 | 8.06 | 0.22 | -2.18 | Putative Membrane Protein Putative |
| dpfB | 690 | 1 | 8.02 | 0.22 | -2.17 | DNA Polymerase III Alpha Subunit Dna |
| INV10401560 | 690 | 1 | 8.02 | 0.22 | -2.17 | Putative Membrane Protein Putative |
| 1013649\_1014727 | 1078 | 2 | 12.53 | 0.22 | -2.17 |  |
| zmpA | 6481 | 16 | 75.35 | 0.22 | -2.17 | Transcription Regulator, Probable Transcription |
| INV10404620 | 300 | 0 | 3.49 | 0.22 | -2.17 | Conserved Hypothetical Protein Conserved |
| INV10409540 | 300 | 0 | 3.49 | 0.22 | -2.17 | Putative Transposase (Fragment) Putative |
| INV10417470 | 300 | 0 | 3.49 | 0.22 | -2.17 | Transporter |
| FIG01114045-hypotheticalprotein | 297 | 0 | 3.45 | 0.22 | -2.15 | Ferrous Iron Transport Peroxidase Efeb Ferrous |
| rplW | 297 | 0 | 3.45 | 0.22 | -2.15 | Adenylosuccinate Synthetase Adenylosuccinate |
| INV10405070 | 678 | 1 | 7.88 | 0.23 | -2.15 | Conserved Hypothetical Protein Conserved |
| 74892\_75187 | 295 | 0 | 3.43 | 0.23 | -2.15 |  |
| INV10400330 | 295 | 0 | 3.43 | 0.23 | -2.15 | Threonine Dehydratase Biosynthetic Threonine |
| ciaR | 675 | 1 | 7.85 | 0.23 | -2.15 | Choline Binding Protein Acholine |
| LSUribosomalproteinL27p | 294 | 0 | 3.42 | 0.23 | -2.14 | Conserved Hypothetical Protein Conserved |
| rpsK | 294 | 0 | 3.42 | 0.23 | -2.14 | Pyrr Bifunctional Protein [Includes: Pyrimidine Operon Regulatory Protein; Uracil Phosphoribosyltransferase]Pyrr |
| 846743\_847794 | 1051 | 2 | 12.22 | 0.23 | -2.14 |  |
| INV10407810 | 1051 | 2 | 12.22 | 0.23 | -2.14 | Putative Membrane Protein Putative |
| INV10402260 | 1050 | 2 | 12.21 | 0.23 | -2.14 | Putative Integral Membrane Protein Putative |
| INV10416490 | 291 | 0 | 3.38 | 0.23 | -2.13 | Merr Family Regulatory Protein Merr |
| INV10419010 | 291 | 0 | 3.38 | 0.23 | -2.13 | Sugar Phosphotransferase System (PTS), Lactose/Cellobiose-Specific Family, IIB Subunit Protein Sugar |
| rpsF | 291 | 0 | 3.38 | 0.23 | -2.13 | Orotidine 5'-Phosphate Decarboxylase Orotidine |
| Degeneratetransposase | 290 | 0 | 3.37 | 0.23 | -2.13 | D-Alanyl-D-Alanine Carboxypeptidase (EC 3.4.16.4)D-Alanyl-D-Alanine |
| INV10400630 | 666 | 1 | 7.74 | 0.23 | -2.13 | Putative Putative GTP-Binding Protein Putative |
| comFC | 663 | 1 | 7.71 | 0.23 | -2.12 | Putative Competence Protein Putative |
| INV10406700 | 288 | 0 | 3.35 | 0.23 | -2.12 | Sodium:Neurotransmitter Symporter Family Protein (Pseudogene) Sodium:Neurotransmitter |
| INV10411590 | 1035 | 2 | 12.03 | 0.23 | -2.12 | Haloacid Dehalogenase-Like Hydrolase Haloacid |
| INV10400350 | 2154 | 5 | 25.04 | 0.23 | -2.12 | Ketol-Acid Reductoisomeraseketol-Acid |
| INV10413100 | 1401 | 3 | 16.29 | 0.23 | -2.11 | Putative NADPH-Dependent FMN Reductase Putative |
| IroncompoundABCuptaketransportersubstrate-bindingproteinPiaA | 1026 | 2 | 11.93 | 0.23 | -2.11 | Major Facilitator Family Transport Protein Major |
| phoU | 654 | 1 | 7.6 | 0.23 | -2.1 | Anaerobic Ribonucleoside-Triphosphate Reductaseanaerobic |
| INV10406000 | 651 | 1 | 7.57 | 0.23 | -2.1 | Putative Membrane Protein Putative |
| INV10418000 | 651 | 1 | 7.57 | 0.23 | -2.1 | Putative Transcriptional Antiterminator Putative |
| INV10417550 | 282 | 0 | 3.28 | 0.23 | -2.1 | Putative Membrane Protein Putative |
| Orf46 | 282 | 0 | 3.28 | 0.23 | -2.1 | Metal ABC Transporter Substrate-Binding Lipoprotein Precursormetal |
| rpsS | 282 | 0 | 3.28 | 0.23 | -2.1 | Putative DNA Repair Protein Putative |
| INV10412480 | 648 | 1 | 7.53 | 0.23 | -2.09 | Haloacid Dehalogenase-Like Hydrolasehaloacid |
| Beta-glucosidase(EC3 | 1380 | 3 | 16.04 | 0.23 | -2.09 | Bacteriocin Immunity Protein Blplbacteriocin |
| INV10400620 | 1380 | 3 | 16.04 | 0.23 | -2.09 | Conserved Hypothetical Proteinconserved |
| INV10400280 | 1011 | 2 | 11.75 | 0.24 | -2.09 | Hypothetical Proteinhypothetical |
| INV10411970 | 279 | 0 | 3.24 | 0.24 | -2.08 | Putative Phosphotransferase Licd2 Putative |
| INV10418130 | 279 | 0 | 3.24 | 0.24 | -2.08 | Membrane Protein Oxaa 1 Precursormembrane |
| murF | 1374 | 3 | 15.97 | 0.24 | -2.08 | LSU Ribosomal Protein L10p (P0)LSU |
| trmE | 1374 | 3 | 15.97 | 0.24 | -2.08 | S-Adenosylhomocysteine Deaminase (EC 3.5.4.28); Methylthioadenosine Deaminases-Adenosylhomocysteine |
| Membrane-boundprotease\_CAAXfamily | 642 | 1 | 7.46 | 0.24 | -2.08 | IS861, Transposase (Orf1), IS3 Family, Truncatedis861, |
| INV10403560 | 1365 | 3 | 15.87 | 0.24 | -2.08 | Putative Glycosylhydrolase Putative |
| adk | 639 | 1 | 7.43 | 0.24 | -2.08 | Adenylate Kinaseadenylate |
| udk | 639 | 1 | 7.43 | 0.24 | -2.08 | Hydroxyethylthiazole Kinasehydroxyethylthiazole |
| INV10411140 | 1000 | 2 | 11.63 | 0.24 | -2.07 | Putative Plasmid Addiction System, Toxin Protein Putative |
| pgmA | 1719 | 4 | 19.99 | 0.24 | -2.07 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10415370 | 996 | 2 | 11.58 | 0.24 | -2.07 | Putative Membrane Protein Putative |
| dnaC | 1353 | 3 | 15.73 | 0.24 | -2.06 | Diacylglycerol Kinase (EC 2.7.1.107)Diacylglycerol |
| INV10402010 | 993 | 2 | 11.54 | 0.24 | -2.06 | Putative Membrane Protease Putative |
| INV10412220 | 993 | 2 | 11.54 | 0.24 | -2.06 | Putative Membrane Protein Putative |
| rpsP | 273 | 0 | 3.17 | 0.24 | -2.06 | Reca Recombinase (Recombinase A) Reca |
| INV10400360 | 1350 | 3 | 15.7 | 0.24 | -2.06 | Dihydroxy-Acid Dehydratasedihydroxy-Acid |
| INV10404060 | 1350 | 3 | 15.7 | 0.24 | -2.06 | Choline Binding Protein (Fragment) Choline |
| nth | 630 | 1 | 7.32 | 0.24 | -2.06 | Mobile Element Proteinmobile |
| INV10419120 | 271 | 0 | 3.15 | 0.24 | -2.05 | ROK Family Proteinrok |
| INV10401840 | 270 | 0 | 3.14 | 0.24 | -2.05 | Hypothetical Protein (Fragment) Hypothetical |
| INV10401990 | 1338 | 3 | 15.56 | 0.24 | -2.05 | Hypothetical Proteinhypothetical |
| INV10412680 | 625 | 1 | 7.27 | 0.24 | -2.05 | Putative Restriction Endonuclease (Pseudogene) Putative |
| INV10400890 | 978 | 2 | 11.37 | 0.24 | -2.04 | Gntr Family Regulatory Proteingntr |
| prfB | 978 | 2 | 11.37 | 0.24 | -2.04 | Pyrrolidone-Carboxylate Peptidasepyrrolidone-Carboxylate |
| glyS | 2037 | 5 | 23.68 | 0.24 | -2.04 | Putative Glutamine Transporter, ATP-Binding Protein 3 Putative |
| INV10400070 | 267 | 0 | 3.1 | 0.24 | -2.04 | Hypothetical Proteinhypothetical |
| INV10401580 | 267 | 0 | 3.1 | 0.24 | -2.04 | Glycoprotease Family Proteinglycoprotease |
| INV10401980 | 267 | 0 | 3.1 | 0.24 | -2.04 | Putative Acetyltransferase Putative |
| INV10403510 | 1323 | 3 | 15.38 | 0.24 | -2.03 | Putative CAAX Amino Terminal Protease Family Membrane Protein Putative |
| INV10405570 | 618 | 1 | 7.18 | 0.24 | -2.03 | Putative Amino Acid ABC Transporter, Permease Protein Putative |
| INV10411990 | 618 | 1 | 7.18 | 0.24 | -2.03 | Conserved Hypothetical Proteinconserved |
| 600828\_601795 | 967 | 2 | 11.24 | 0.25 | -2.03 |  |
| INV10401190 | 615 | 1 | 7.15 | 0.25 | -2.03 | Conserved Hypothetical Proteinconserved |
| secY | 1311 | 3 | 15.24 | 0.25 | -2.02 | Dtdp-D-Glucose 4,6-Dehydratase Rmlbdtdp-D-Glucose |
| pncP | 612 | 1 | 7.12 | 0.25 | -2.02 | Oligopeptide Transport System Permease Protein Oppc (TC 3.A.1.5.1)Oligopeptide |
| rpsQ | 261 | 0 | 3.03 | 0.25 | -2.01 | DNA Replication And Repair Protein Recfdna |
| INV10410660 | 954 | 2 | 11.09 | 0.25 | -2.01 | ABC Transporter ATP-Binding Protein ABC |
| OligopeptidetransportsystempermeaseproteinOppB(TC3 | 951 | 2 | 11.06 | 0.25 | -2.01 | Multiple Sugar-Binding Transport ATP-Binding Proteinmultiple |
| 476902\_485073 | 8171 | 23 | 95 | 0.25 | -2 |  |
| Histidyl-tRNAsynthetase(EC6 | 1290 | 3 | 15 | 0.25 | -2 | 2,3-Bisphosphoglycerate-Dependent Phosphoglycerate Mutase2,3-Bisphosphoglycerate-Dependent |
| treA | 1626 | 4 | 18.9 | 0.25 | -1.99 | 30S Ribosomal Protein S2130S |
| rmlC | 597 | 1 | 6.94 | 0.25 | -1.99 | Putative Primosomal Protein N' Putative |
| INV10404710 | 255 | 0 | 2.96 | 0.25 | -1.99 | Putative Uncharacterized Protein Putative |
| birA | 936 | 2 | 10.88 | 0.25 | -1.99 | Beta-Glucosidase (EC 3.2.1.21)Beta-Glucosidase |
| INV10411200 | 936 | 2 | 10.88 | 0.25 | -1.99 | Mutt/NUDIX Hydrolase Family Proteinmutt/NUDIX |
| rpoA | 936 | 2 | 10.88 | 0.25 | -1.99 | Putative Methyltransferase Putative |
| FIG01117121-hypotheticalprotein | 933 | 2 | 10.85 | 0.25 | -1.98 | FIG01115786: Hypothetical Proteinfig01115786: |
| INV10411870 | 1272 | 3 | 14.79 | 0.25 | -1.98 | Putative Licb-Family Membrane Protein Putative |
| gyrB | 1947 | 5 | 22.64 | 0.25 | -1.98 | 6-Phosphogluconate Dehydrogenase, Decarboxylating6-Phosphogluconate |
| rnz | 930 | 2 | 10.81 | 0.25 | -1.98 | Prolyl-Trna Synthetase (EC 6.1.1.15), Bacterial Typeprolyl-Trna |
| nrdG | 591 | 1 | 6.87 | 0.25 | -1.98 | Mobile Element Proteinmobile |
| INV10409680 | 2280 | 6 | 26.51 | 0.25 | -1.97 | Putative Hydrolase Putative |
| ftsX | 927 | 2 | 10.78 | 0.25 | -1.97 | Fold Bifunctional Protein [Includes: Methylenetetrahydrofolate Dehydrogenase/Methenyltetrahydrofolate Cyclohydrolase]Fold |
| INV10416290 | 927 | 2 | 10.78 | 0.25 | -1.97 | Putative Degt/Dnrj/Eryc1/Strs Family Amino Sugar Synthetase Putative |
| INV10409550 | 1939 | 5 | 22.54 | 0.25 | -1.97 | Putative Uncharacterized Protein Putative |
| sufD | 1263 | 3 | 14.68 | 0.26 | -1.97 | 50S Ribosomal Protein L1750S |
| INV10409580 | 250 | 0 | 2.91 | 0.26 | -1.97 | Putative Uncharacterized Protein Putative |
| tyrS | 1257 | 3 | 14.61 | 0.26 | -1.96 | Putative Thiamine Biosynthesis Protein Putative |
| INV10406200 | 249 | 0 | 2.89 | 0.26 | -1.96 | Conserved Hypothetical Proteinconserved |
| INV10416190 | 249 | 0 | 2.89 | 0.26 | -1.96 | Putative Cation Transporter Putative |
| glgP | 2259 | 6 | 26.26 | 0.26 | -1.96 | Putative NADP-Dependent Glyceraldehyde-3-Phosphate Dehydrogenase Putative |
| INV10410770 | 1914 | 5 | 22.25 | 0.26 | -1.95 | Conserved Hypothetical Proteinconserved |
| INV10409140 | 1909 | 5 | 22.19 | 0.26 | -1.95 | ABC Transporter ATP-Binding Protein ABC |
| INV10405300 | 246 | 0 | 2.86 | 0.26 | -1.95 | Cell Filamentation Protein Fic-Related Proteincell |
| INV10407210 | 1242 | 3 | 14.44 | 0.26 | -1.95 | Putative Permease Putative |
| ffh | 1572 | 4 | 18.28 | 0.26 | -1.95 | Septation Ring Formation Regulatorseptation |
| INV10405630 | 1239 | 3 | 14.4 | 0.26 | -1.94 | Putative Phosphoesterase Putative |
| INV10419320 | 2553 | 7 | 29.68 | 0.26 | -1.94 | PTS System, Iic Componentpts |
| INV10418150 | 573 | 1 | 6.66 | 0.26 | -1.94 | Putative Exported Protein Putative |
| INV10410510 | 243 | 0 | 2.83 | 0.26 | -1.94 | Putative RNA Pseudouridylate Synthase Putative |
| INV10403530 | 900 | 2 | 10.46 | 0.26 | -1.93 | Conserved Hypothetical Proteinconserved |
| pth | 570 | 1 | 6.63 | 0.26 | -1.93 | Phosphoglycerate Kinasephosphoglycerate |
| FIG01114589-hypotheticalprotein | 567 | 1 | 6.59 | 0.26 | -1.92 | FIG00628965: Hypothetical Proteinfig00628965: |
| INV10405500 | 567 | 1 | 6.59 | 0.26 | -1.92 | Two-Component System, Response Regulatortwo-Component |
| INV10415400 | 567 | 1 | 6.59 | 0.26 | -1.92 | Putative Membrane Protein Putative |
| prfC | 1545 | 4 | 17.96 | 0.26 | -1.92 | Putative ATP-Dependent DNA Helicase Putative |
| INV10403360 | 240 | 0 | 2.79 | 0.26 | -1.92 | Putative Plasmid Stabilization System Antitoxin Protein Putative |
| INV10415960 | 891 | 2 | 10.36 | 0.26 | -1.92 | Putative Membrane Protein Putative |
| INV10405540 | 564 | 1 | 6.56 | 0.26 | -1.92 | Putative Amino Acid ABC Transporter, Permease Protein Putative |
| INV10410640 | 564 | 1 | 6.56 | 0.26 | -1.92 | Conserved Hypothetical Proteinconserved |
| INV10405980 | 562 | 1 | 6.53 | 0.27 | -1.91 | Putative Uncharacterized Protein Putative |
| INV10404950 | 885 | 2 | 10.29 | 0.27 | -1.91 | Putative Na+/Pi-Cotransporter Protein Putative |
| INV10404740 | 561 | 1 | 6.52 | 0.27 | -1.91 |  |
| FIG01120216-hypotheticalprotein | 237 | 0 | 2.76 | 0.27 | -1.91 | FIG01116413: Hypothetical Proteinfig01116413: |
| INV10400160 | 237 | 0 | 2.76 | 0.27 | -1.91 | Hypothetical Proteinhypothetical |
| INV10407340 | 237 | 0 | 2.76 | 0.27 | -1.91 | Putative Peptidase Putative |
| INV10400820 | 1851 | 5 | 21.52 | 0.27 | -1.91 | Putative Acyl Carrier Protein Putative |
| INV10411040 | 1527 | 4 | 17.75 | 0.27 | -1.91 | Putative Repressor Protein Putative |
| INV10407880 | 876 | 2 | 10.18 | 0.27 | -1.9 | Putative D-Alanyl-D-Alanine Carboxypeptidase Putative |
| INV10412500 | 876 | 2 | 10.18 | 0.27 | -1.9 | Putative Exported Hydrophilic Protein Putative |
| INV10406740 | 555 | 1 | 6.45 | 0.27 | -1.9 | Putative Cytidine And Deoxycytidylate Deaminase Putative |
| INV10400320 | 234 | 0 | 2.72 | 0.27 | -1.9 | Isoleucyl-Trna Synthetaseisoleucyl-Trna |
| INV10404690 | 234 | 0 | 2.72 | 0.27 | -1.9 | Putative Transposase (Pseudogene) Putative |
| PreproteintranslocasesubunitSecG(TC3 | 234 | 0 | 2.72 | 0.27 | -1.9 | Penicillin Binding Protein 2xpenicillin |
| ackA | 1191 | 3 | 13.85 | 0.27 | -1.89 | Acetate Kinaseacetate |
| metK | 1191 | 3 | 13.85 | 0.27 | -1.89 | Putative Lactose-Specific Phosphotransferase System (PTS), IIBC Component 2 Putative |
| INV10409360 | 552 | 1 | 6.42 | 0.27 | -1.89 | Putative Methyltransferase Putative |
| wchC | 552 | 1 | 6.42 | 0.27 | -1.89 | Putative IS1670 Transposase (Pseudogene) Putative |
| dnaK | 1824 | 5 | 21.21 | 0.27 | -1.89 | DNA-Cytosine Methyltransferase (EC 2.1.1.37)DNA-Cytosine |
| INV10403520 | 549 | 1 | 6.38 | 0.27 | -1.88 | Putative 2-Amino-4-Hydroxy-6-Hydroxymethyldihydropteridine Pyrophosphokinase Putative |
| INV10419070 | 549 | 1 | 6.38 | 0.27 | -1.88 | Putative Membrane Protein Putative |
| INV10405680 | 231 | 0 | 2.69 | 0.27 | -1.88 | Putative Uncharacterized Protein Putative |
| INV10406810 | 231 | 0 | 2.69 | 0.27 | -1.88 | Branched-Chain Amino Acid Transport System Permease Proteinbranched-Chain |
| INV10407120 | 231 | 0 | 2.69 | 0.27 | -1.88 | Bioy Family Membrane Proteinbioy |
| INV10412700 | 231 | 0 | 2.69 | 0.27 | -1.88 | Putative Arac-Family Transcriptional Regulator Putative |
| INV10413630 | 548 | 1 | 6.37 | 0.27 | -1.88 | Csbd-Like Proteincsbd-Like |
| INV10416300 | 1497 | 4 | 17.4 | 0.27 | -1.88 | Probable Sugar Transferaseprobable |
| galK | 1179 | 3 | 13.71 | 0.27 | -1.88 | Putative Cell Division ATP-Binding Protein Putative |
| msmR | 862 | 2 | 10.02 | 0.27 | -1.88 | 3-Isopropylmalate Dehydrogenase3-Isopropylmalate |
| mutY | 1176 | 3 | 13.67 | 0.27 | -1.87 | Putative 4-Alpha-Glucanotransferase Putative |
| INV10419360 | 543 | 1 | 6.31 | 0.27 | -1.87 | ABC Transporter Permease Protein ABC |
| INV10417820 | 1485 | 4 | 17.26 | 0.27 | -1.87 | Dicarboxylate Carrier Proteindicarboxylate |
| aroE | 855 | 2 | 9.94 | 0.27 | -1.87 | 3-Dehydroquinate Dehydratase3-Dehydroquinate |
| INV10412970 | 1167 | 3 | 13.57 | 0.27 | -1.86 | Putative Thioredoxin Reductase Putative |
| INV10400500 | 1788 | 5 | 20.79 | 0.28 | -1.86 | Induced During Competenceinduced |
| INV10417680 | 849 | 2 | 9.87 | 0.28 | -1.86 | Putative Membrane Protein Putative |
| INV10415970 | 537 | 1 | 6.24 | 0.28 | -1.86 | Putative Membrane Protein Putative |
| nusG | 537 | 1 | 6.24 | 0.28 | -1.86 | Rod Shape-Determining Protein Mrecrod |
| acpP | 225 | 0 | 2.62 | 0.28 | -1.86 | Acyl Carrier Protein (ACP)Acyl |
| INV10413670 | 1152 | 3 | 13.39 | 0.28 | -1.85 | Putative Uncharacterized Protein Putative |
| INV10417720 | 1152 | 3 | 13.39 | 0.28 | -1.85 | Putative Surface Anchored Protein (Pseudogene) Putative |
| Phageintegrase-site-specificrecombinase | 1149 | 3 | 13.36 | 0.28 | -1.84 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10411250 | 531 | 1 | 6.17 | 0.28 | -1.84 | Conserved Hypothetical Proteinconserved |
| Aspartyl-tRNAsynthetase(EC6 | 1764 | 5 | 20.51 | 0.28 | -1.84 | Putative L-Asparaginase Putative |
| INV10409190 | 222 | 0 | 2.58 | 0.28 | -1.84 | Putative Membrane Protein Putative |
| INV10417450 | 222 | 0 | 2.58 | 0.28 | -1.84 | Putative Transcriptional Regulator (Pseudogene) Putative |
| Phagereplicationinitiationprotein | 837 | 2 | 9.73 | 0.28 | -1.84 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| glgC | 1143 | 3 | 13.29 | 0.28 | -1.84 | Galactose-1-Phosphate Uridylyltransferasegalactose-1-Phosphate |
| INV10418930 | 528 | 1 | 6.14 | 0.28 | -1.84 | Putative Exported Protein Putative |
| msmG | 835 | 2 | 9.71 | 0.28 | -1.84 | GTP-Binding Protein Lepagtp-Binding |
| INV10409720 | 1140 | 3 | 13.25 | 0.28 | -1.83 | Conserved Hypothetical Proteinconserved |
| ABCtransporter\_ATP-bindingpermeaseprotein | 1749 | 5 | 20.33 | 0.28 | -1.83 | ABC Transporter, ATP-Binding/Permease Protein ABC |
| INV10416330 | 1443 | 4 | 16.78 | 0.28 | -1.83 | Hypothetical Protein (Pseudogene)Hypothetical |
| dnaN | 1137 | 3 | 13.22 | 0.28 | -1.83 | DNA-Cytosine Methyltransferase (EC 2.1.1.37)DNA-Cytosine |
| INV10400810 | 1137 | 3 | 13.22 | 0.28 | -1.83 | Putative Aminotransferase Putative |
| grpE | 525 | 1 | 6.1 | 0.28 | -1.83 | Glycerate Kinase (EC 2.7.1.31)Glycerate |
| INV10408930 | 219 | 0 | 2.55 | 0.28 | -1.83 | Lysr-Family Regulatory Proteinlysr-Family |
| nrdH | 219 | 0 | 2.55 | 0.28 | -1.83 | Mobile Element Proteinmobile |
| INV10419220 | 828 | 2 | 9.63 | 0.28 | -1.83 | Putative Surface Protein (Fragment) Putative |
| hemN | 1131 | 3 | 13.15 | 0.28 | -1.82 | Gp9gp9 |
| glgA | 1434 | 4 | 16.67 | 0.28 | -1.82 | Galactokinasegalactokinase |
| INV10409530 | 520 | 1 | 6.05 | 0.28 | -1.82 | Ferric Siderophore ABC Transporter, ATP-Binding Proteinferric |
| INV10408020 | 519 | 1 | 6.03 | 0.28 | -1.81 | Conserved Hypothetical Proteinconserved |
| galT | 1425 | 4 | 16.57 | 0.28 | -1.81 | Putative Cell Division Protein Putative |
| gnd | 1425 | 4 | 16.57 | 0.28 | -1.81 | Putative Lactoylglutathione Lyase Putative |
| INV10400940 | 1122 | 3 | 13.04 | 0.28 | -1.81 | Sugar Phosphotransferase System (PTS), Sorbose Subfamily, IIB Componentsugar |
| INV10408950 | 2027 | 6 | 23.57 | 0.28 | -1.81 | Putative RNA Pseudouridylate Synthase Putative |
| INV10405320 | 819 | 2 | 9.52 | 0.29 | -1.81 | Transcription Antiterminatortranscription |
| INV10410610 | 516 | 1 | 6 | 0.29 | -1.81 | Putative Membrane Protein (Pseudogene) Putative |
| INV10410360 | 816 | 2 | 9.49 | 0.29 | -1.81 | Putative Peptidase Putative |
| INV10417970 | 816 | 2 | 9.49 | 0.29 | -1.81 | Putative Exported Protein Putative |
| msrAB | 1113 | 3 | 12.94 | 0.29 | -1.8 | Leucyl-Trna Synthetaseleucyl-Trna |
| INV10408770 | 510 | 1 | 5.93 | 0.29 | -1.79 | ABC Transporter, Permease Protein ABC |
| AminoacidABCtransporter\_aminoacid-bindingpermeaseprotein | 808 | 2 | 9.39 | 0.29 | -1.79 | Amino Acid ABC Transporter, Amino Acid-Binding/Permease Proteinamino |
| ribD | 1101 | 3 | 12.8 | 0.29 | -1.79 | Spermidine/Putrescine ABC Transporter Permease Proteinspermidine/Putrescine |
| INV10409000 | 210 | 0 | 2.44 | 0.29 | -1.78 | Putative Replication Initiation Protein (Pseudogene) Putative |
| INV10400230 | 801 | 2 | 9.31 | 0.29 | -1.78 | Hypothetical Proteinhypothetical |
| FIG01115429-hypotheticalprotein | 1095 | 3 | 12.73 | 0.29 | -1.78 | FIG01114468: Hypothetical Proteinfig01114468: |
| INV10410450 | 798 | 2 | 9.28 | 0.29 | -1.78 | Putative Cysteine Desulfurase Putative |
| INV10413770 | 798 | 2 | 9.28 | 0.29 | -1.78 | Putative NADPH-Dependent FMN Reductase Putative |
| FIG00628088-hypotheticalprotein | 1386 | 4 | 16.11 | 0.29 | -1.77 | 3-Oxoacyl-[Acyl-Carrier-Protein] Synthase III3-Oxoacyl-[Acyl-Carrier-Protein] |
| FIG01115415-hypotheticalprotein | 207 | 0 | 2.41 | 0.29 | -1.77 | FIG01114344: Hypothetical Proteinfig01114344: |
| rpmC | 207 | 0 | 2.41 | 0.29 | -1.77 | Putative Phosphoribosylaminoimidazole Carboxylase Catalytic Subunit Putative |
| INV10407140 | 498 | 1 | 5.79 | 0.29 | -1.76 | ABC Transporter ATP-Binding Protein ABC |
| INV10401220 | 1082 | 3 | 12.58 | 0.29 | -1.76 | Putative Uncharacterized Protein Putative |
| INV10403570 | 786 | 2 | 9.14 | 0.3 | -1.76 | Putative Glutathione Peroxidase Putative |
| INV10412920 | 495 | 1 | 5.75 | 0.3 | -1.75 | GDSL-Like Lipase/Acylhydrolase Family Proteingdsl-Like |
| Bacteriocin-likepeptideNBlpN | 204 | 0 | 2.37 | 0.3 | -1.75 | Bacteriocin, Putativebacteriocin, |
| N-acetylmannosaminekinase(EC2 | 204 | 0 | 2.37 | 0.3 | -1.75 | Membrane-Bound Protease, CAAX Familymembrane-Bound |
| putativetransposonexcisionaseTn916ORF1-like | 204 | 0 | 2.37 | 0.3 | -1.75 | Phenylalanyl-Trna Synthetase Alpha Chainphenylalanyl-Trna |
| INV10416400 | 1354 | 4 | 15.74 | 0.3 | -1.74 | Putative Membrane Protein (Pseudo) Putative |
| glgB | 1929 | 6 | 22.43 | 0.3 | -1.74 | Galactose Operon Repressorgalactose |
| INV10402060 | 777 | 2 | 9.03 | 0.3 | -1.74 | Putative ABC Transporter ATP-Binding Protein Putative |
| pnpA | 2214 | 7 | 25.74 | 0.3 | -1.74 | Orf17orf17 |
| atpE | 201 | 0 | 2.34 | 0.3 | -1.74 | ATP Synthase Epsilon Chainatp |
| rpmI | 201 | 0 | 2.34 | 0.3 | -1.74 | Putative Pur Operon Repressor Putative |
| thiD | 774 | 2 | 9 | 0.3 | -1.74 | 50S Ribosomal Protein L2350S |
| INV10400880 | 1059 | 3 | 12.31 | 0.3 | -1.73 | Putative Phosphoribosylformylglycinamidine Synthase Protein Putative |
| ABC\_transporter\_ATP-bindingprotein | 771 | 2 | 8.96 | 0.3 | -1.73 | ABC, Transporter, ATP-Binding Protein ABC, |
| INV10413010 | 1623 | 5 | 18.87 | 0.3 | -1.73 | Arsc Family Proteinarsc |
| greA | 483 | 1 | 5.62 | 0.3 | -1.73 | Glutamyl-Trna Synthetaseglutamyl-Trna |
| luxS | 483 | 1 | 5.62 | 0.3 | -1.73 | IS1167, Transposaseis1167, |
| phoR | 1332 | 4 | 15.49 | 0.3 | -1.72 | Putative N-Acetylneuraminate Lyase Putative |
| transcriptionregulator\_probable | 479 | 1 | 5.57 | 0.3 | -1.72 | 30S Ribosomal Protein S1630S |
| INV10409290 | 1044 | 3 | 12.14 | 0.3 | -1.72 | Pneumococcal Histidine Triad Proteinpneumococcal |
| brnQ | 1326 | 4 | 15.42 | 0.3 | -1.72 | Putative Immunity Protein Blpx Putative |
| pyrG | 1608 | 5 | 18.69 | 0.3 | -1.71 | Putative Streptococcal Histidine Triad Protein Phpa Putative |
| INV10405090 | 759 | 2 | 8.82 | 0.31 | -1.71 | Trna (Guanine-N(7)-)-Methyltransferasetrna |
| parB | 759 | 2 | 8.82 | 0.31 | -1.71 | UDP-N-Acetylglucosamine 1-Carboxyvinyltransferase 1UDP-N-Acetylglucosamine |
| Undecaprenylpyrophosphatesynthetase(EC2 | 759 | 2 | 8.82 | 0.31 | -1.71 | Trigger Factor (Prolyl Isomerase)Trigger |
| INV10400510 | 477 | 1 | 5.55 | 0.31 | -1.71 | Translation Initiation Factor IF-1translation |
| FIG01114205-hypotheticalprotein | 195 | 0 | 2.27 | 0.31 | -1.71 | Formate--Tetrahydrofolate Ligase 1formate--Tetrahydrofolate |
| INV10400030 | 195 | 0 | 2.27 | 0.31 | -1.71 | Hypothetical Proteinhypothetical |
| INV10404760 | 756 | 2 | 8.79 | 0.31 | -1.71 | 6 Phospho Beta Galactosidase6 |
| 1947729\_1948204 | 475 | 1 | 5.52 | 0.31 | -1.7 |  |
| IS1381\_transposaseOrfB | 475 | 1 | 5.52 | 0.31 | -1.7 | Putative DNA-Binding Protein Putative |
| INV10400560 | 1036 | 3 | 12.04 | 0.31 | -1.7 | Integral Membrane Proteinintegral |
| ABCtransportermembrane-spanningpermease-macrolideefflux | 753 | 2 | 8.75 | 0.31 | -1.7 | ABC Transporter Membrane-Spanning Permease - Macrolide Effluxabc |
| INV10419370 | 753 | 2 | 8.75 | 0.31 | -1.7 | ABC Transporter ATP-Binding Protein ABC |
| INV10401500 | 1032 | 3 | 12 | 0.31 | -1.7 | Putative Trna (5-Methylaminomethyl-2-Thiouridylate)-Methyltransferase Putative |
| INV10411760 | 750 | 2 | 8.72 | 0.31 | -1.7 | Cutc Family Proteincutc |
| ribH | 468 | 1 | 5.44 | 0.31 | -1.69 | Manganese-Dependent Inorganic Pyrophosphatasemanganese-Dependent |
| comFA | 1299 | 4 | 15.1 | 0.31 | -1.69 | Putative Competence Protein Putative |
| cbpJ | 1020 | 3 | 11.86 | 0.31 | -1.68 | Choline Binding Protein Echoline |
| INV10414090 | 190 | 0 | 2.21 | 0.31 | -1.68 | Putative Uncharacterized Protein Putative |
| INV10416740 | 1017 | 3 | 11.82 | 0.31 | -1.68 | Transport System Permease Protein (Pseudogene)Transport |
| INV10418050 | 189 | 0 | 2.2 | 0.31 | -1.68 | Putative Hexulose-6-Phosphate Synthase Putative |
| rpmB | 189 | 0 | 2.2 | 0.31 | -1.68 | Phosphoribosylamine-Glycine Ligasephosphoribosylamine-Glycine |
| mecA | 738 | 2 | 8.58 | 0.31 | -1.68 | IS861, Transposase (Orf1), IS3 Family, Truncatedis861, |
| INV10401040 | 1011 | 3 | 11.75 | 0.31 | -1.67 | Putative Gene Fragment Putative |
| FIG01114344-hypotheticalprotein | 735 | 2 | 8.55 | 0.31 | -1.67 | FIG00627241: Hypothetical Proteinfig00627241: |
| galR | 1008 | 3 | 11.72 | 0.31 | -1.67 | Putative Putative Cell Division Protease Ftsh Putative |
| INV10408960 | 1008 | 3 | 11.72 | 0.31 | -1.67 | Initiation-Control Protein Yabainitiation-Control |
| mvaK2 | 1008 | 3 | 11.72 | 0.31 | -1.67 | Putative Mannose-Specific Phosphotransferase System (PTS), IIC Component Putative |
| INV10417830 | 1278 | 4 | 14.86 | 0.32 | -1.67 | Putative Transposase (Fragment) Putative |
| ctsR | 459 | 1 | 5.34 | 0.32 | -1.66 | Conserved Domain Proteinconserved |
| INV10416620 | 459 | 1 | 5.34 | 0.32 | -1.66 | Siderophore Uptake ATP-Binding Proteinsiderophore |
| INV10410430 | 1275 | 4 | 14.82 | 0.32 | -1.66 | Conserved Hypothetical Proteinconserved |
| carB | 3177 | 11 | 36.94 | 0.32 | -1.66 | Calcium-Binding Protein, Putativecalcium-Binding |
| malX | 1272 | 4 | 14.79 | 0.32 | -1.66 | IS1381, Transposase Orfbis1381, |
| INV10403330 | 996 | 3 | 11.58 | 0.32 | -1.65 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| pbuX | 1263 | 4 | 14.68 | 0.32 | -1.65 | Putative Peptidoglycan Pentaglycine Interpeptide Biosynthesis Protein Putative |
| plsX | 993 | 3 | 11.54 | 0.32 | -1.65 | Transcription Antitermination Factortranscription |
| INV10407850 | 1260 | 4 | 14.65 | 0.32 | -1.65 | Conserved Hypothetical Proteinconserved |
| rpmD | 183 | 0 | 2.13 | 0.32 | -1.65 | Putative Amidophosphoribosyltransferase Precursor Putative |
| rpmF | 183 | 0 | 2.13 | 0.32 | -1.65 | Putative Phosphoribosylaminoimidazole Carboxylase Atpase Subunit Putative |
| S-adenosylmethionine-dependentmethyltransferase | 183 | 0 | 2.13 | 0.32 | -1.65 | Putative Redox-Sensing Transcriptional Repressor Putative |
| malR | 987 | 3 | 11.47 | 0.32 | -1.64 | IS1381, Transposase Orfbis1381, |
| INV10402080 | 981 | 3 | 11.41 | 0.32 | -1.63 | Putative Membrane Protein Putative |
| Phageantirepressorprotein | 714 | 2 | 8.3 | 0.32 | -1.63 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| rplM | 447 | 1 | 5.2 | 0.32 | -1.63 | Phosphoenolpyruvate-Protein Phosphotransferasephosphoenolpyruvate-Protein |
| FIG01116413-hypotheticalprotein | 180 | 0 | 2.09 | 0.32 | -1.63 | FIG01115429: Hypothetical Proteinfig01115429: |
| pncM | 180 | 0 | 2.09 | 0.32 | -1.63 | Oligopeptide Transport ATP-Binding Protein Oppd (TC 3.A.1.5.1)Oligopeptide |
| deoD | 711 | 2 | 8.27 | 0.32 | -1.63 | Degenerate Transposasedegenerate |
| INV10412910 | 1506 | 5 | 17.51 | 0.32 | -1.63 | Conserved Hypothetical Proteinconserved |
| pyk | 1506 | 5 | 17.51 | 0.32 | -1.63 | Alkaline Phosphatase Synthesis Transcriptional Regulatory Proteinalkaline |
| INV10400190 | 444 | 1 | 5.16 | 0.32 | -1.62 | Hypothetical Proteinhypothetical |
| INV10411190 | 444 | 1 | 5.16 | 0.32 | -1.62 | Putative Small-Molecule-Binding Protein Putative |
| INV10417810 | 1236 | 4 | 14.37 | 0.33 | -1.62 | Putative IS630-Spn1 Transposase (Pseudogene) Putative |
| Glycerophosphoryldiesterphosphodiesterase(EC3 | 1764 | 6 | 20.51 | 0.33 | -1.62 | Putative Glutamine ABC Transporter, ATP-Binding Protein 1 Putative |
| pcrA | 2292 | 8 | 26.65 | 0.33 | -1.62 | UDP-N-Acetylglucosamine 1-Carboxyvinyltransferase 2UDP-N-Acetylglucosamine |
| INV10403250 | 1233 | 4 | 14.33 | 0.33 | -1.62 | Sugar Phosphotransferase System (PTS), Lactose/Cellobiose-Specific Family, IIA Componentsugar |
| pdhA | 969 | 3 | 11.27 | 0.33 | -1.62 | Mutator Mutt Protein (7,8-Dihydro-8-Oxoguanine-Triphosphatase) (EC 3.6.1.-)Mutator |
| INV10406660 | 441 | 1 | 5.13 | 0.33 | -1.62 | Putative Glycosyl Hydrolase Putative |
| pepN | 2547 | 9 | 29.61 | 0.33 | -1.61 | Mutt/Nudix Family Proteinmutt/Nudix |
| INV10409310 | 177 | 0 | 2.06 | 0.33 | -1.61 | Putative Uncharacterized Protein (Pseudogene) Putative |
| INV10417290 | 177 | 0 | 2.06 | 0.33 | -1.61 | Putative Uncharacterized Protein Putative |
| rpsU | 177 | 0 | 2.06 | 0.33 | -1.61 | Recombination Protein Recrrecombination |
| INV10403790 | 439 | 1 | 5.1 | 0.33 | -1.61 | Putative N-Acetylgalactosamine-Specific Phosphotransferase System (PTS), IIA Component Putative |
| INV10400270 | 438 | 1 | 5.09 | 0.33 | -1.61 | Hypothetical Proteinhypothetical |
| INV10404000 | 1224 | 4 | 14.23 | 0.33 | -1.61 | Cell Wall Surface Anchored Proteincell |
| INV10403320 | 699 | 2 | 8.13 | 0.33 | -1.61 | Putative GNAT-Family Acetyltransferase Putative |
| INV10406620 | 699 | 2 | 8.13 | 0.33 | -1.61 | Putative Exported Protein Putative |
| INV10417170 | 1215 | 4 | 14.13 | 0.33 | -1.6 | Putative Membrane Protein Putative |
| FIG01115489-hypotheticalprotein | 174 | 0 | 2.02 | 0.33 | -1.59 | FIG01114476: Hypothetical Proteinfig01114476: |
| INV10415780 | 693 | 2 | 8.06 | 0.33 | -1.59 | Ribosomal Protein L11 Methyltransferaseribosomal |
| Transcriptionalantiterminatoroflichenanoperon\_BglGfamily | 1464 | 5 | 17.02 | 0.33 | -1.59 | 30S Ribosomal Protein S730S |
| INV10412890 | 429 | 1 | 4.99 | 0.33 | -1.58 | Putative Beta-Lactamase Putative |
| INV10417460 | 429 | 1 | 4.99 | 0.33 | -1.58 | Putative Secreted Protein Putative |
| INV10405610 | 171 | 0 | 1.99 | 0.33 | -1.58 | Putative Glutamine Transporter, ATP-Binding Protein (Pseudogene) Putative |
| INV10416690 | 171 | 0 | 1.99 | 0.33 | -1.58 | Sugar Phosphotransferase System (PTS), IIABC Componentsugar |
| INV10401510 | 684 | 2 | 7.95 | 0.34 | -1.58 | Mutt/NUDIX Hydrolase Family Proteinmutt/NUDIX |
| INV10416950 | 684 | 2 | 7.95 | 0.34 | -1.58 | Putative NADP-Dependent L-Serine/L-Allo-Threonine Dehydrogenase Putative |
| PeptidemethioninesulfoxidereductaseMsrA(EC1 | 939 | 3 | 10.92 | 0.34 | -1.58 | Mevalonate Kinasemevalonate |
| ptsK | 936 | 3 | 10.88 | 0.34 | -1.57 | Putative CDP-Diacylglycerol--Glycerol-3-Phosphate 3-Phosphatidyltransferase Putative |
| fruA | 1953 | 7 | 22.71 | 0.34 | -1.57 | FIG01120216: Hypothetical Proteinfig01120216: |
| FIG01116379-hypotheticalprotein | 168 | 0 | 1.95 | 0.34 | -1.56 | FIG01115377: Hypothetical Proteinfig01115377: |
| pbp2A | 2196 | 8 | 25.53 | 0.34 | -1.56 | Putative UDP-N-Acetylmuramoyl-Tripeptide--D-Alanyl-D-Alanine Ligase Putative |
| INV10409950 | 1179 | 4 | 13.71 | 0.34 | -1.56 | Putative DNA\_Binding Protein Putative |
| INV10413250 | 2697 | 10 | 31.36 | 0.34 | -1.56 | Putative RNA Helicase Putative |
| Sialicacid-inducedtransmembraneproteinYjhT(NanM)\_possiblemutarotase | 924 | 3 | 10.74 | 0.34 | -1.55 | Ribonuclease Iiiribonuclease |
| fsaA | 669 | 2 | 7.78 | 0.34 | -1.55 | FIG086557: Conjugation Related Proteinfig086557: |
| Phageendolysin | 417 | 1 | 4.85 | 0.34 | -1.55 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| glyQ | 918 | 3 | 10.67 | 0.34 | -1.54 | Putative Putative Glutamine ABC Transporter, ATP-Binding Protein 2 Putative |
| TetracyclineresistanceproteinTetM | 1920 | 7 | 22.32 | 0.34 | -1.54 | 50S Ribosomal Protein L2150S |
| ply | 1416 | 5 | 16.46 | 0.34 | -1.54 | Putative Methylated-DNA--Protein-Cysteine Methyltransferase Putative |
| rplP | 414 | 1 | 4.81 | 0.34 | -1.54 | Peptidyl-Trna Hydrolasepeptidyl-Trna |
| rpsL | 414 | 1 | 4.81 | 0.34 | -1.54 | S-Adenosylmethionine:Trna Ribosyltransferase-Isomerases-Adenosylmethionine:Trna |
| rpoC | 3651 | 14 | 42.45 | 0.35 | -1.53 | Putative Transposon Excisionase; Tn916 ORF1-Like Putative |
| atpD | 1407 | 5 | 16.36 | 0.35 | -1.53 | ATP Synthase A Chainatp |
| INV10403200 | 1158 | 4 | 13.46 | 0.35 | -1.53 | Deor Family Regulatory Proteindeor |
| INV10401590 | 411 | 1 | 4.78 | 0.35 | -1.53 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10404380 | 411 | 1 | 4.78 | 0.35 | -1.53 | Hypothetical Proteinhypothetical |
| INV10409030 | 162 | 0 | 1.88 | 0.35 | -1.53 | Putative Uncharacterized Protein (Pseudogene) Putative |
| INV10405020 | 657 | 2 | 7.64 | 0.35 | -1.53 | Conserved Hypothetical Proteinconserved |
| INV10400900 | 904 | 3 | 10.51 | 0.35 | -1.52 | Putative Beta-Galactosidase Putative |
| Cytidinedeaminase(EC3 | 408 | 1 | 4.74 | 0.35 | -1.52 | O-Acetylhomoserine (Thiol)-Lyase (Pseudogene)O-Acetylhomoserine |
| INV10417110 | 900 | 3 | 10.46 | 0.35 | -1.52 | Marr Family Regulatory Protein (Pseudogene)Marr |
| INV10411750 | 1635 | 6 | 19.01 | 0.35 | -1.52 | Putative Conserved Hypothetical Protein Putative |
| FIG01115840-hypotheticalprotein | 159 | 0 | 1.85 | 0.35 | -1.51 | FIG01114768: Hypothetical Proteinfig01114768: |
| FIG01117752-hypotheticalprotein | 159 | 0 | 1.85 | 0.35 | -1.51 | FIG01115816: Hypothetical Proteinfig01115816: |
| INV10412520 | 894 | 3 | 10.39 | 0.35 | -1.51 | Putative Exported Protein Putative |
| INV10412960 | 3099 | 12 | 36.03 | 0.35 | -1.51 | Spou Rrna Methylase Family Proteinspou |
| INV10405000 | 648 | 2 | 7.53 | 0.35 | -1.51 | Putative Membrane Protein Putative |
| INV10408030 | 648 | 2 | 7.53 | 0.35 | -1.51 | Putative Type I RM Modification Enzyme Putative |
| INV10405010 | 1380 | 5 | 16.04 | 0.35 | -1.51 | Putative Membrane Protein Putative |
| INV10404290 | 1130 | 4 | 13.14 | 0.35 | -1.5 | Putative C4-Dicarboxylate Transporter Putative |
| INV10407860 | 1128 | 4 | 13.11 | 0.35 | -1.5 | Putative 30S Ribosomal Protein S1 Putative |
| ABCtransporter\_ATP-bindingprotein | 885 | 3 | 10.29 | 0.35 | -1.5 | ABC Transporter, ATP-Binding Protein ABC |
| miaA | 885 | 3 | 10.29 | 0.35 | -1.5 | PTS System, Lactose-Specific IIA Componentpts |
| TranscriptionalregulatorSpxA2 | 399 | 1 | 4.64 | 0.35 | -1.5 | 30S Ribosomal Protein S1530S |
| INV10409010 | 156 | 0 | 1.81 | 0.36 | -1.49 | Putative IS1381 Transposase (Pseudogene) Putative |
| pncG | 156 | 0 | 1.81 | 0.36 | -1.49 | Oligopeptide ABC Transporter, Periplasmic Oligopeptide-Binding Protein Oppa (TC 3.A.1.5.1)Oligopeptide |
| INV10410780 | 398 | 1 | 4.63 | 0.36 | -1.49 | Putative Phage Integrase (Pseudogene) Putative |
| INV10402040 | 1123 | 4 | 13.06 | 0.36 | -1.49 | ABC Transporter, Substrate Binding Protein ABC |
| INV10404720 | 396 | 1 | 4.6 | 0.36 | -1.49 | ROK Family Regulatorrok |
| INV10406060 | 396 | 1 | 4.6 | 0.36 | -1.49 | Putative Sodium Hydrogen Exchange Transporter Putative |
| INV10403340 | 636 | 2 | 7.39 | 0.36 | -1.48 | Luciferase-Like Monooxygenaseluciferase-Like |
| INV10419100 | 636 | 2 | 7.39 | 0.36 | -1.48 | Putative Uncharacterized Protein Putative |
| INV10400830 | 633 | 2 | 7.36 | 0.36 | -1.48 | Putative IS1381 Transposase (Pseudogene) Putative |
| pgi | 1350 | 5 | 15.7 | 0.36 | -1.48 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10401000 | 153 | 0 | 1.78 | 0.36 | -1.48 | Putative Aldose 1-Epimerase Putative |
| 2-hydroxy-3-oxopropionatereductase(EC1 | 870 | 3 | 10.11 | 0.36 | -1.47 | 2-Hydroxy-3-Oxopropionate Reductase (EC 1.1.1.60)2-Hydroxy-3-Oxopropionate |
| INV10406220 | 870 | 3 | 10.11 | 0.36 | -1.47 | Lysr Family Regulatory Proteinlysr |
| gdh | 1347 | 5 | 15.66 | 0.36 | -1.47 | Putative L-Fucose Isomerase Putative |
| lepA | 1824 | 7 | 21.21 | 0.36 | -1.47 | ABC Transporter ATP-Binding Protein ABC |
| INV10413680 | 630 | 2 | 7.32 | 0.36 | -1.47 | Conserved Hypothetical Proteinconserved |
| INV10413980 | 630 | 2 | 7.32 | 0.36 | -1.47 | Putative Exported Protein Putative |
| INV10412690 | 1107 | 4 | 12.87 | 0.36 | -1.47 | Putative DNA Modification Methylase Putative |
| INV10406790 | 868 | 3 | 10.09 | 0.36 | -1.47 | Branched-Chain Amino Acid Transport System Permease Proteinbranched-Chain |
| accD | 867 | 3 | 10.08 | 0.36 | -1.47 | Acetyl-Coenzyme A Carboxylase Carboxyl Transferase Subunit Betaacetyl-Coenzyme |
| INV10414320 | 867 | 3 | 10.08 | 0.36 | -1.47 | Hypothetical Proteinhypothetical |
| Bacteriocin-likepeptideOBlpO | 152 | 0 | 1.77 | 0.36 | -1.47 | Bacteriocin-Like Peptide M Blpmbacteriocin-Like |
| INV10402020 | 627 | 2 | 7.29 | 0.36 | -1.47 | Putative Transport Protein Putative |
| INV10416470 | 627 | 2 | 7.29 | 0.36 | -1.47 | Thioesterase Superfamily Proteinthioesterase |
| INV10409650 | 864 | 3 | 10.04 | 0.36 | -1.46 | Putative Uncharacterized Protein Putative |
| INV10405480 | 861 | 3 | 10.01 | 0.36 | -1.46 | ABC Transporter, Permease Protein ABC |
| INV10405640 | 624 | 2 | 7.25 | 0.36 | -1.46 | Metallo-Beta-Lactamase Superfamily Proteinmetallo-Beta-Lactamase |
| rplD | 624 | 2 | 7.25 | 0.36 | -1.46 | Putative Ribose-Phosphate Pyrophosphokinase 2 Putative |
| rplQ | 387 | 1 | 4.5 | 0.36 | -1.46 | Histidine-Containing Phosphocarrier Protein (Hpr)Histidine-Containing |
| blpX | 385 | 1 | 4.48 | 0.37 | -1.45 | Response Regulator Protein Blprresponse |
| OligopeptidetransportsystempermeaseproteinOppC(TC3 | 852 | 3 | 9.91 | 0.37 | -1.45 | Arac Family Regulatory Proteinarac |
| addA | 3651 | 15 | 42.45 | 0.37 | -1.44 | Putative ATP-Dependent Exonuclease Subunit A Putative |
| FIG01115961-hypotheticalprotein | 381 | 1 | 4.43 | 0.37 | -1.44 | FIG01114872: Hypothetical Proteinfig01114872: |
| INV10409920 | 381 | 1 | 4.43 | 0.37 | -1.44 | Putative Lantibiotic Export Protein (Pseudogene) Putative |
| INV10413390 | 381 | 1 | 4.43 | 0.37 | -1.44 | Putative Membrane Protein Putative |
| INV10415580 | 381 | 1 | 4.43 | 0.37 | -1.44 | Cora-Like Mg2+ Transporter Proteincora-Like |
| gp5 | 147 | 0 | 1.71 | 0.37 | -1.44 | Glpg Protein (Membrane Protein Of Glp Regulon)Glpg |
| Phosphoenolpyruvate-dihydroxyacetonephosphotransferase(EC2 | 147 | 0 | 1.71 | 0.37 | -1.44 | Oxygen-Insensitive NADPH Nitroreductaseoxygen-Insensitive |
| INV10406080 | 2244 | 9 | 26.09 | 0.37 | -1.44 | Putative Redoxin Putative |
| def | 612 | 2 | 7.12 | 0.37 | -1.44 | Cytidine/Deoxycytidylate Deaminase Family Proteincytidine/Deoxycytidylate |
| INV10401640 | 1539 | 6 | 17.89 | 0.37 | -1.43 | Putative Transposase (Pseudogene) Putative |
| INV10416610 | 609 | 2 | 7.08 | 0.37 | -1.43 | Putative Iron Compound ABC Transporter, Permease Protein Putative |
| INV10411170 | 375 | 1 | 4.36 | 0.37 | -1.42 | Putative Membrane Protein Putative |
| Inducedduringcompetence | 144 | 0 | 1.67 | 0.37 | -1.42 | Homoserine Dehydrogenasehomoserine |
| IS1167\_transposase | 144 | 0 | 1.67 | 0.37 | -1.42 | Putative Reverse Transcriptase - Group II Intron (Pseudogene) Putative |
| rpoE | 603 | 2 | 7.01 | 0.37 | -1.42 | Putative Pyruvate Kinase Putative |
| pflD | 2439 | 10 | 28.36 | 0.37 | -1.42 | N-Acetylneuraminate Lyase (EC 4.1.3.3)N-Acetylneuraminate |
| nrdD | 2208 | 9 | 25.67 | 0.37 | -1.42 | Mobile Element Proteinmobile |
| INV10406070 | 372 | 1 | 4.32 | 0.38 | -1.41 | Ribonuclease BN-Like Family Proteinribonuclease |
| rnpA | 372 | 1 | 4.32 | 0.38 | -1.41 | Putative Pyrroline-5-Carboxylate Reductase Putative |
| INV10418630 | 3117 | 13 | 36.24 | 0.38 | -1.41 | Putative Uncharacterized Protein Putative |
| INV10407000 | 1053 | 4 | 12.24 | 0.38 | -1.4 | Vanz Like Family Proteinvanz |
| rmlB | 1050 | 4 | 12.21 | 0.38 | -1.4 | Peptide Chain Release Factor 3peptide |
| INV10414070 | 2412 | 10 | 28.04 | 0.38 | -1.4 | Putative Methyltransferase Putative |
| INV10401660 | 141 | 0 | 1.64 | 0.38 | -1.4 | Putative Glycosyl Transferase (Pseudogene) Putative |
| ruvA | 594 | 2 | 6.91 | 0.38 | -1.4 | Regulatory Protein Recxregulatory |
| INV10410710 | 819 | 3 | 9.52 | 0.38 | -1.4 | Putative Membrane Transport Protein Putative |
| mreC | 819 | 3 | 9.52 | 0.38 | -1.4 | Large Subunit Ribosomal RNA; Lsurna; LSU Rrnalarge |
| INV10411110 | 366 | 1 | 4.26 | 0.38 | -1.4 | Conserved Hypothetical Proteinconserved |
| INV10414610 | 366 | 1 | 4.26 | 0.38 | -1.4 | Putative Membrane Protein Putative |
| acoC | 1044 | 4 | 12.14 | 0.38 | -1.39 | E2 Component Of Acetoin Dehydrogenase Enzyme System (Dihydrolipoamide Acetyltransferase)E2 |
| INV10402430 | 814 | 3 | 9.46 | 0.38 | -1.39 | Putative Membrane Protein Putative |
| INV10417630 | 363 | 1 | 4.22 | 0.38 | -1.38 | Rmuc Family Proteinrmuc |
| INV10410960 | 812 | 3 | 9.44 | 0.38 | -1.38 | Putative Transposase (Pseudogene) Putative |
| ftsZ | 1260 | 5 | 14.65 | 0.38 | -1.38 | Dihydropteroate Synthasedihydropteroate |
| murZ | 1260 | 5 | 14.65 | 0.38 | -1.38 | S-Ribosylhomocysteinases-Ribosylhomocysteinase |
| S-adenosylhomocysteinedeaminase(EC3 | 1260 | 5 | 14.65 | 0.38 | -1.38 | GTP Pyrophosphokinasegtp |
| FIG01114476-hypotheticalprotein | 138 | 0 | 1.6 | 0.38 | -1.38 | FIG00627694: Hypothetical Proteinfig00627694: |
| INV10415380 | 1482 | 6 | 17.23 | 0.38 | -1.38 | Putative Uncharacterized Protein Putative |
| aroF | 1032 | 4 | 12 | 0.38 | -1.38 | Shikimate 5-Dehydrogenaseshikimate |
| INV10418740 | 807 | 3 | 9.38 | 0.39 | -1.38 | ABC Transporter Permease Protein ABC |
| N-ethylammelinechlorohydrolase | 582 | 2 | 6.77 | 0.39 | -1.37 | Membrane Proteins Related To Metalloendopeptidasesmembrane |
| INV10404770 | 804 | 3 | 9.35 | 0.39 | -1.37 | PTS Transporter, IIBPTS |
| INV10415690 | 1692 | 7 | 19.67 | 0.39 | -1.37 | Putative Membrane Protein Putative |
| ilvC | 1023 | 4 | 11.89 | 0.39 | -1.37 | Hit Family Proteinhit |
| INV10410920 | 1023 | 4 | 11.89 | 0.39 | -1.37 | Pneumococcal Histidine Triad Proteinpneumococcal |
| INV10412440 | 357 | 1 | 4.15 | 0.39 | -1.36 | Putative Myo-Inositol-1(Or 4)-Monophosphatase Putative |
| INV10409320 | 135 | 0 | 1.57 | 0.39 | -1.36 | Gtra-Like Proteingtra-Like |
| Membraneproteinsrelatedtometalloendopeptidases | 576 | 2 | 6.7 | 0.39 | -1.36 | Fes Assembly Nifu-Like Proteinfes |
| fabF | 1236 | 5 | 14.37 | 0.39 | -1.36 | Elongation Factor P (EF-P)Elongation |
| INV10419200 | 795 | 3 | 9.24 | 0.39 | -1.36 | C4-Dicarboxylate Anaerobic Carrier Proteinc4-Dicarboxylate |
| INV10411770 | 1455 | 6 | 16.92 | 0.39 | -1.36 | Putative Membrane Protein Putative |
| INV10415950 | 354 | 1 | 4.12 | 0.39 | -1.36 | Putative Transglysylase-Associated Membrane Protein Putative |
| FIG01114146-hypotheticalprotein | 573 | 2 | 6.66 | 0.39 | -1.35 | Signal Recognition Particle Proteinsignal |
| INV10400860 | 573 | 2 | 6.66 | 0.39 | -1.35 | Bacteriocin Transport/Processing ATP-Binding Proteinbacteriocin |
| INV10413240 | 792 | 3 | 9.21 | 0.39 | -1.35 | Polysaccharide Deacetylase Family Proteinpolysaccharide |
| INV10415770 | 1227 | 5 | 14.27 | 0.39 | -1.35 | Conserved Hypothetical Proteinconserved |
| INV10410910 | 789 | 3 | 9.17 | 0.39 | -1.35 | Sugar Phosphotransferase System (PTS), Fructose Family, IIA Componentsugar |
| lgt | 789 | 3 | 9.17 | 0.39 | -1.35 | Conserved Hypothetical Proteinconserved |
| rbfA | 351 | 1 | 4.08 | 0.39 | -1.34 | Pneumolysin (Thiol-Activated Cytolysin)Pneumolysin |
| INV10417380 | 132 | 0 | 1.53 | 0.39 | -1.34 | Lytr Family Regulatory Proteinlytr |
| INV10404670 | 785 | 3 | 9.13 | 0.4 | -1.34 | Glutamine ABC Transporter, Glutamine-Binding Protein/Permease Proteinglutamine |
| INV10406750 | 564 | 2 | 6.56 | 0.4 | -1.33 | Conserved Hypothetical Proteinconserved |
| deoB | 1212 | 5 | 14.09 | 0.4 | -1.33 | D-Alanine--D-Alanine Ligased-Alanine--D-Alanine |
| efp | 561 | 2 | 6.52 | 0.4 | -1.33 | Putative Primosomal Protein Putative |
| FIG01117889-hypotheticalprotein | 345 | 1 | 4.01 | 0.4 | -1.32 | FIG01115840: Hypothetical Proteinfig01115840: |
| FIG139598-Potentialribosomalprotein | 345 | 1 | 4.01 | 0.4 | -1.32 | FIG01116966: Hypothetical Proteinfig01116966: |
| INV10401080 | 1207 | 5 | 14.03 | 0.4 | -1.32 | Putative Uncharacterized Protein Putative |
| INV10418660 | 774 | 3 | 9 | 0.4 | -1.32 | Degenerate Transposasedegenerate |
| recO | 771 | 3 | 8.96 | 0.4 | -1.32 | ABC Transporter ATP Binding Domain Pncp (CAAX Protease)ABC |
| sufC | 771 | 3 | 8.96 | 0.4 | -1.32 | 50S Ribosomal Protein L1650S |
| clpE | 2259 | 10 | 26.26 | 0.4 | -1.31 | Cina-Like Proteincina-Like |
| INV10419340 | 340 | 1 | 3.95 | 0.4 | -1.31 | PTS System, Iia Componentpts |
| ABC-typemultidrugtransportsystem\_permeasecomponent | 766 | 3 | 8.91 | 0.4 | -1.31 | ABC-Type Multidrug Transport System, Permease Componentabc-Type |
| INV10400540 | 339 | 1 | 3.94 | 0.4 | -1.3 | Integral Membrane Proteinintegral |
| INV10406490 | 339 | 1 | 3.94 | 0.4 | -1.3 | Amino-Acid ABC Transporter Integral Membrane Proteinamino-Acid |
| INV10411680 | 339 | 1 | 3.94 | 0.4 | -1.3 | Putative 3-Isopropylmalate Dehydratase Small Subunit Putative |
| INV10412990 | 1401 | 6 | 16.29 | 0.4 | -1.3 | ABC Transporter ATP-Binding Protein ABC |
| comC2 | 126 | 0 | 1.46 | 0.41 | -1.3 | Phosphopantetheine Adenylyltransferasephosphopantetheine |
| putativemethyltransferase | 126 | 0 | 1.46 | 0.41 | -1.3 | Phage Transcriptional Regulator, Cro/CI Familyphage |
| INV10403490 | 549 | 2 | 6.38 | 0.41 | -1.3 | Putative Permease Putative |
| INV10406720 | 2451 | 11 | 28.5 | 0.41 | -1.3 | Putative Fatty-Acid Binding Protein Putative |
| pstB1 | 759 | 3 | 8.82 | 0.41 | -1.3 | Xaa-Pro Dipeptidyl-Peptidasexaa-Pro |
| INV10402750 | 336 | 1 | 3.91 | 0.41 | -1.3 | Putative Regulator Putative |
| ADP-ribosepyrophosphatase(EC3 | 546 | 2 | 6.35 | 0.41 | -1.29 | ADP-Ribose Pyrophosphatase (EC 3.6.1.13)ADP-Ribose |
| INV10401110 | 546 | 2 | 6.35 | 0.41 | -1.29 | Cell Wall Surface Anchor Family Protein (Pseudogene)Cell |
| pgsA | 546 | 2 | 6.35 | 0.41 | -1.29 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10407360 | 966 | 4 | 11.23 | 0.41 | -1.29 | Putative Peptidoglycan Biosynthesis Membrane Protein Putative |
| asnB | 963 | 4 | 11.2 | 0.41 | -1.29 | Aspartate-Semialdehyde Dehydrogenaseaspartate-Semialdehyde |
| hpt | 543 | 2 | 6.31 | 0.41 | -1.28 | GTP-Binding Protein Eragtp-Binding |
| INV10411020 | 543 | 2 | 6.31 | 0.41 | -1.28 | Putative Sugar Phosphotransferase System (PTS), IIB Component (Pseudogene) Putative |
| prsA2 | 960 | 4 | 11.16 | 0.41 | -1.28 | Peptide Methionine Sulfoxide Reductase Msra (EC 1.8.4.11) / Peptide Methionine Sulfoxide Reductase Msrb (EC 1.8.4.12)Peptide |
| INV10400090 | 123 | 0 | 1.43 | 0.41 | -1.28 | Hypothetical Proteinhypothetical |
| INV10413800 | 750 | 3 | 8.72 | 0.41 | -1.28 | Cation Transporting Atpasecation |
| INV10416700 | 957 | 4 | 11.13 | 0.41 | -1.28 | Gntr Family Regulatory Proteingntr |
| CompetenceproteinCoiA | 956 | 4 | 11.11 | 0.41 | -1.28 | Putative Late Competence Protein Putative |
| INV10402070 | 747 | 3 | 8.68 | 0.41 | -1.28 | Putative ABC Transporter System Permease Protein Putative |
| Degenerativetransposase | 330 | 1 | 3.84 | 0.41 | -1.28 | Dihydrodipicolinate Synthasedihydrodipicolinate |
| INV10411160 | 330 | 1 | 3.84 | 0.41 | -1.28 | Conserved Hypothetical Proteinconserved |
| INV10406520 | 537 | 2 | 6.24 | 0.41 | -1.27 | Putative Coenzyme Putative |
| atpA | 1365 | 6 | 15.87 | 0.41 | -1.27 | Aspartyl-Trna Synthetase (EC 6.1.1.12)Aspartyl-Trna |
| INV10400790 | 327 | 1 | 3.8 | 0.42 | -1.26 | Putative Coa-Binding Protein Putative |
| INV10416310 | 1977 | 9 | 22.98 | 0.42 | -1.26 | ABC Transporter, ATP-Binding/Permease Protein ABC |
| INV10417870 | 1768 | 8 | 20.55 | 0.42 | -1.26 | Putative Beta-Glucosidase Putative |
| INV10403190 | 528 | 2 | 6.14 | 0.42 | -1.25 | Putative Pyruvate Formate-Lyase Activating Enzyme Putative |
| aldB | 732 | 3 | 8.51 | 0.42 | -1.25 | Alpha-Acetolactate Decarboxylasealpha-Acetolactate |
| ppaC | 936 | 4 | 10.88 | 0.42 | -1.25 | Putative Penicillin-Binding Protein 1A Putative |
| 333456\_354568 | 21112 | 103 | 245.45 | 0.42 | -1.24 |  |
| INV10406580 | 321 | 1 | 3.73 | 0.42 | -1.24 | Putative Coenzyme Putative |
| ORF17 | 321 | 1 | 3.73 | 0.42 | -1.24 | Peptide Methionine Sulfoxide Reductasepeptide |
| INV10416860 | 1332 | 6 | 15.49 | 0.42 | -1.24 | Putative RNA Methyltransferase Putative |
| INV10402370 | 723 | 3 | 8.41 | 0.43 | -1.23 | Putative Carboxypeptidase, Possible Microcin Immunity Protein Putative |
| dpr | 519 | 2 | 6.03 | 0.43 | -1.23 | DNA Primasedna |
| rimM | 519 | 2 | 6.03 | 0.43 | -1.23 | Preprotein Translocase Subunit Secg (TC 3.A.5.1.1)Preprotein |
| INV10412240 | 1722 | 8 | 20.02 | 0.43 | -1.22 | Putative Membrane Protein Putative |
| FIG00627241-hypotheticalprotein | 315 | 1 | 3.66 | 0.43 | -1.22 | Biotin Carboxyl Carrier Protein Of Acetyl-Coa Carboxylasebiotin |
| Glyceratekinase(EC2 | 1116 | 5 | 12.97 | 0.43 | -1.22 | Putative Glutamine Synthetase Putative |
| INV10412580 | 714 | 3 | 8.3 | 0.43 | -1.22 | Putative Membrane Protein Putative |
| INV10411120 | 1305 | 6 | 15.17 | 0.43 | -1.21 | Putative Formate/Nitrate Transport Protein Putative |
| INV10404830 | 510 | 2 | 5.93 | 0.43 | -1.21 | ABC Transporter ATP-Binding Protein ABC |
| INV10418820 | 906 | 4 | 10.53 | 0.43 | -1.21 | Putative DNA-Binding Protein (Pseudogene) Putative |
| murB | 906 | 4 | 10.53 | 0.43 | -1.21 | Lipid A Export ATP-Binding/Permease Protein Msbalipid |
| INV10417890 | 1695 | 8 | 19.71 | 0.43 | -1.2 | Putative Lactose-Specific Phosphotransferase System (PTS), IIA Component 2 Putative |
| INV10402110 | 1299 | 6 | 15.1 | 0.43 | -1.2 | Response Regulator Proteinresponse |
| vicR | 705 | 3 | 8.2 | 0.43 | -1.2 | Putative IS630-Spn1 Transposase (Pseudogene) Putative |
| rpsJ | 309 | 1 | 3.59 | 0.44 | -1.2 | Uracil Permeaseuracil |
| htpX | 900 | 4 | 10.46 | 0.44 | -1.2 | Inosine-5'-Monophosphate Dehydrogenaseinosine-5'-Monophosphate |
| INV10400580 | 111 | 0 | 1.29 | 0.44 | -1.2 | Integraseintegrase |
| acoL | 1686 | 8 | 19.6 | 0.44 | -1.19 | Dihydrolipoamide Dehydrogenasedihydrolipoamide |
| pepXP | 2274 | 11 | 26.44 | 0.44 | -1.19 | 3-Hydroxy-3-Methylglutaryl Coenzyme A Synthase3-Hydroxy-3-Methylglutaryl |
| INV10414350 | 700 | 3 | 8.14 | 0.44 | -1.19 | NIF3 (NGG1p Interacting Factor 3) Family Proteinnif3 |
| INV10405380 | 306 | 1 | 3.56 | 0.44 | -1.19 | Putative Uncharacterized Protein Putative |
| rplX | 306 | 1 | 3.56 | 0.44 | -1.19 | Adenylosuccinate Lyaseadenylosuccinate |
| gldA | 1089 | 5 | 12.66 | 0.44 | -1.19 | UDP-Glucose 4-Epimeraseudp-Glucose |
| INV10406630 | 501 | 2 | 5.82 | 0.44 | -1.18 | Putative Metal Transporting P-Type Atpase Putative |
| INV10410600 | 501 | 2 | 5.82 | 0.44 | -1.18 | Conserved Hypothetical Proteinconserved |
| INV10410310 | 305 | 1 | 3.55 | 0.44 | -1.19 | Putative DNA-Binding Protein Putative |
| INV10412260 | 696 | 3 | 8.09 | 0.44 | -1.18 | Putative Glycosyl Transferase Putative |
| Ribulose-phosphate3-epimerase(EC5 | 696 | 3 | 8.09 | 0.44 | -1.18 | Putative Inorganic Polyphosphate/ATP-NAD Kinase Putative |
| INV10409370 | 1278 | 6 | 14.86 | 0.44 | -1.18 | Conserved Hypothetical Proteinconserved |
| INV10406010 | 693 | 3 | 8.06 | 0.44 | -1.18 | Putative Radical SAM Superfamily Protein (Pseudogene) Putative |
| Metal-dependenthydrolaseYbeY\_involvedinrRNAandorribosomematurationandassembly | 498 | 2 | 5.79 | 0.44 | -1.18 | Dimethyladenosine Transferasedimethyladenosine |
| gatC | 303 | 1 | 3.52 | 0.44 | -1.18 | Cell Division Protein Ftszcell |
| INV10403480 | 303 | 1 | 3.52 | 0.44 | -1.18 | Putative Haloacid Dehalogenase-Like Hydrolase Putative |
| polA | 2634 | 13 | 30.62 | 0.44 | -1.18 | Orf46Orf46 |
| INV10419180 | 495 | 2 | 5.75 | 0.44 | -1.17 | Putative Fucosidase Putative |
| pyrC | 1269 | 6 | 14.75 | 0.44 | -1.17 | Phosphatidate Cytidylyltransferase (EC 2.7.7.41)Phosphatidate |
| FIG01116089-hypotheticalprotein | 301 | 1 | 3.5 | 0.44 | -1.17 | FIG01114899: Hypothetical Proteinfig01114899: |
| INV10402270 | 3771 | 19 | 43.84 | 0.45 | -1.16 | Putative Membrane Protein Putative |
| potD | 1071 | 5 | 12.45 | 0.45 | -1.16 | Topoisomerase IV Subunit Btopoisomerase |
| INV10406820 | 684 | 3 | 7.95 | 0.45 | -1.16 | Branched-Chain Amino Acid Transport ATP-Binding Proteinbranched-Chain |
| INV10416280 | 1068 | 5 | 12.42 | 0.45 | -1.16 | Sortase-Sorted Surface Anchored Proteinsortase-Sorted |
| cysD | 1260 | 6 | 14.65 | 0.45 | -1.16 | Conserved Domain Proteinconserved |
| gla | 870 | 4 | 10.11 | 0.45 | -1.15 | Elongation Factor G (EF-G)Elongation |
| GlpGprotein(membraneproteinofglpregulon) | 678 | 3 | 7.88 | 0.45 | -1.15 | Glycerol Facilitator-Aquaporinglycerol |
| INV10401490 | 678 | 3 | 7.88 | 0.45 | -1.15 |  |
| INV10401610 | 1251 | 6 | 14.54 | 0.45 | -1.15 |  |
| INV10407020 | 1059 | 5 | 12.31 | 0.45 | -1.15 | Putative Cyclophilin Type Peptidyl-Prolyl Cis-Trans Isomerase Putative |
| fabE | 486 | 2 | 5.65 | 0.45 | -1.15 | Dihydrofolate Reductasedihydrofolate |
| INV10402720 | 294 | 1 | 3.42 | 0.45 | -1.14 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10404610 | 294 | 1 | 3.42 | 0.45 | -1.14 | Hypothetical Proteinhypothetical |
| FIG01116802-hypotheticalprotein | 672 | 3 | 7.81 | 0.45 | -1.14 | FIG01115489: Hypothetical Proteinfig01115489: |
| INV10414160 | 672 | 3 | 7.81 | 0.45 | -1.14 | Putative Aminotransferase Putative |
| Beta-1\_3-glucosyltransferase | 861 | 4 | 10.01 | 0.45 | -1.14 | Bacteriocin-Like Peptide O Blpobacteriocin-Like |
| OligoendopeptidaseF(EC3 | 1803 | 9 | 20.96 | 0.46 | -1.13 | Multiple Sugar-Binding Protein Precursormultiple |
| rmlA | 858 | 4 | 9.98 | 0.46 | -1.13 | Peptide Chain Release Factor 2peptide |
| 2\_3-butanedioldehydrogenase\_R-alcoholforming\_(R)-and(S)-acetoin-specific(EC1 | 1044 | 5 | 12.14 | 0.46 | -1.13 | 2,3-Butanediol Dehydrogenase, R-Alcohol Forming, (R)- And (S)-Acetoin-Specific (EC 1.1.1.4)2,3-Butanediol |
| INV10416500 | 102 | 0 | 1.19 | 0.46 | -1.13 | Cation Efflux Family Proteincation |
| INV10401170 | 666 | 3 | 7.74 | 0.46 | -1.13 | Binding-Protein-Dependent Transport System Membrane Proteinbinding-Protein-Dependent |
| rpiA | 666 | 3 | 7.74 | 0.46 | -1.13 | Prophage Lambdasa2, Site-Specific Recombinase, Phage Integrase Familyprophage |
| aroK | 477 | 2 | 5.55 | 0.46 | -1.13 | Phospho-2-Dehydro-3-Deoxyheptonate Aldolase, Tyr-Sensitivephospho-2-Dehydro-3-Deoxyheptonate |
| INV10400220 | 477 | 2 | 5.55 | 0.46 | -1.13 | Hypothetical Proteinhypothetical |
| INV10404370 | 288 | 1 | 3.35 | 0.46 | -1.12 | Marr Family Regulatory Proteinmarr |
| INV10414600 | 474 | 2 | 5.51 | 0.46 | -1.12 | Putative Membrane Protein (Pseudogene) Putative |
| INV10405060 | 660 | 3 | 7.67 | 0.46 | -1.12 | ABC Transporter Protein Ecsbabc |
| ftsH | 1959 | 10 | 22.78 | 0.46 | -1.11 | Methionyl-Trna Formyltransferasemethionyl-Trna |
| INV10418670 | 471 | 2 | 5.48 | 0.46 | -1.11 | ABC Transporter ATP-Binding Membrane Protein ABC |
| ssb | 471 | 2 | 5.48 | 0.46 | -1.11 | 50S Ribosomal Protein L1150S |
| bacteriocin\_ putative | 285 | 1 | 3.31 | 0.46 | -1.11 | Putative ATP Synthase Delta Chain Putative |
| groES | 285 | 1 | 3.31 | 0.46 | -1.11 | Serine Hydroxymethyltransferaseserine |
| INV10418390 | 285 | 1 | 3.31 | 0.46 | -1.11 | Putative Competence Protein Putative |
| ung | 654 | 3 | 7.6 | 0.46 | -1.1 | Putative Transketolase Putative |
| INV10406170 | 468 | 2 | 5.44 | 0.47 | -1.1 | Putative Gtpase Putative |
| INV10410620 | 468 | 2 | 5.44 | 0.47 | -1.1 | Conserved Hypothetical Proteinconserved |
| INV10417310 | 837 | 4 | 9.73 | 0.47 | -1.1 | Putative Uncharacterized Protein Putative |
| arcB | 1017 | 5 | 11.82 | 0.47 | -1.1 | Ornithine Carbamoyltransferaseornithine |
| INV10410490 | 648 | 3 | 7.53 | 0.47 | -1.09 | Adenylate Cyclase Family Proteinadenylate |
| purR | 828 | 4 | 9.63 | 0.47 | -1.09 | Phage Terminase Large Subunitphage |
| pcp | 645 | 3 | 7.5 | 0.47 | -1.09 | Putative Peptidoglycan Branched Peptide Synthesis Protein Putative |
| adhE | 2652 | 14 | 30.83 | 0.47 | -1.09 | Aldehyde-Alcohol Dehydrogenase 2 [Includes: Alcohol Dehydrogenase; Acetaldehyde Dehydrogenase]Aldehyde-Alcohol |
| INV10416820 | 279 | 1 | 3.24 | 0.47 | -1.08 | Sucrose Phosphorylasesucrose |
| ftsA | 1374 | 7 | 15.97 | 0.47 | -1.08 | FIG139598: Potential Ribosomal Proteinfig139598: |
| pfk | 1008 | 5 | 11.72 | 0.47 | -1.08 | N-Acetylglucosamine-1-Phosphate Uridyltransferase (EC 2.7.7.23) / Glucosamine-1-Phosphate N-Acetyltransferase (EC 2.3.1.157)N-Acetylglucosamine-1-Phosphate |
| ABCtransporterATP-bindingprotein | 642 | 3 | 7.46 | 0.47 | -1.08 | ABC Transporter ATP-Binding Protein ABC |
| DNAreplicationproteinDnaC | 642 | 3 | 7.46 | 0.47 | -1.08 | Replication Initiation And Membrane Attachment Proteinreplication |
| accC | 1368 | 7 | 15.9 | 0.47 | -1.08 | Biotin Carboxylase Subunit Of Acetyl-Coa Carboxylasebiotin |
| ezrA | 1728 | 9 | 20.09 | 0.47 | -1.08 | Putative Pantothenate Metabolism Flavoprotein Putative |
| INV10415660 | 1002 | 5 | 11.65 | 0.47 | -1.08 | Putative Mechanosensitive Ion Channel Protein Putative |
| hlpA | 276 | 1 | 3.21 | 0.48 | -1.07 | Transcription Elongation Factortranscription |
| INV10409660 | 1181 | 6 | 13.73 | 0.48 | -1.07 | Putative Uncharacterized Protein Putative |
| trpE | 1362 | 7 | 15.83 | 0.48 | -1.07 | Beta-N-Acetylhexosaminidase Precursor (Ec 3.2.1.52) (Sortase-Sorted)Beta-N-Acetylhexosaminidase |
| INV10406410 | 1542 | 8 | 17.93 | 0.48 | -1.07 | Putative Membrane Protein Putative |
| INV10404580 | 636 | 3 | 7.39 | 0.48 | -1.07 | Putative Phosphatase Putative |
| INV10415300 | 453 | 2 | 5.27 | 0.48 | -1.06 | ATP-Binding Proteinatp-Binding |
| rplI | 453 | 2 | 5.27 | 0.48 | -1.06 | Phosphate Import ATP-Binding Protein 2phosphate |
| Ferrochelatase\_protohemeferro-lyase(EC4 | 273 | 1 | 3.17 | 0.48 | -1.06 | Putative Competence Associated Protein Putative |
| agaS | 1167 | 6 | 13.57 | 0.48 | -1.06 | Putative Tagatose-6-Phosphate Aldose/Ketose Isomerase Putative |
| INV10407310 | 1167 | 6 | 13.57 | 0.48 | -1.06 | Putative PEP-Utilizing Enzyme Putative |
| pstB2 | 804 | 4 | 9.35 | 0.48 | -1.05 | 6-Phosphofructokinase6-Phosphofructokinase |
| tRNA-Ser-TGA | 91 | 0 | 1.06 | 0.49 | -1.04 | Putative Arginine Decarboxylase Putative |
| fabK | 975 | 5 | 11.34 | 0.49 | -1.04 | Putative GTP-Binding Protein Putative |
| INV10416770 | 621 | 3 | 7.22 | 0.49 | -1.04 | Putative Oligopeptide Transporter ATP-Binding Protein Putative |
| INV10411180 | 267 | 1 | 3.1 | 0.49 | -1.04 | Putative Membrane Protein Putative |
| veg | 267 | 1 | 3.1 | 0.49 | -1.04 | Tn916, Hypothetical Proteintn916, |
| parE | 1854 | 10 | 21.55 | 0.49 | -1.04 | UDP-N-Acetylmuramate--Alanine Ligaseudp-N-Acetylmuramate--Alanine |
| INV10416170 | 972 | 5 | 11.3 | 0.49 | -1.04 | Hypothetical Proteinhypothetical |
| glr | 795 | 4 | 9.24 | 0.49 | -1.03 | 1,4-Alpha-Glucan Branching Enzyme1,4-Alpha-Glucan |
| pflC | 795 | 4 | 9.24 | 0.49 | -1.03 | N-Acetylmannosamine Kinase (EC 2.7.1.60)N-Acetylmannosamine |
| INV10401690 | 618 | 3 | 7.18 | 0.49 | -1.03 | Asparagine Synthase Family Proteinasparagine |
| INV10401360 | 441 | 2 | 5.13 | 0.49 | -1.03 | Leader Peptidaseleader |
| INV10418760 | 441 | 2 | 5.13 | 0.49 | -1.03 | Phosphate Transport System Proteinphosphate |
| INV10402330 | 264 | 1 | 3.07 | 0.49 | -1.03 | Putative DNA-Binding Protein Putative |
| INV10410500 | 264 | 1 | 3.07 | 0.49 | -1.03 | Conserved Hypothetical Proteinconserved |
| MutatormutTprotein(7\_8-dihydro-8-oxoguanine-triphosphatase)(EC3 | 264 | 1 | 3.07 | 0.49 | -1.03 | Lysyl-Trna Synthetaselysyl-Trna |
| Plasmidaddictionsystempoisonprotein | 264 | 1 | 3.07 | 0.49 | -1.03 | Putative Endonuclease Iii Putative |
| INV10414120 | 789 | 4 | 9.17 | 0.49 | -1.02 | DEAD Box Helicase Family Proteindead |
| nusA | 1137 | 6 | 13.22 | 0.49 | -1.02 | S-Adenosyl-Methyltransferase Mraws-Adenosyl-Methyltransferase |
| 747532\_754257 | 6725 | 38 | 78.19 | 0.49 | -1.02 |  |
| tRNA-Ser-GCT | 88 | 0 | 1.02 | 0.49 | -1.01 | Superoxide Dismutase [Mn]Superoxide |
| INV10415420 | 609 | 3 | 7.08 | 0.5 | -1.01 | Putative Protein Phosphatase Putative |
| metG | 1998 | 11 | 23.23 | 0.5 | -1.01 | Tagatose-6-Phosphate Kinase 2tagatose-6-Phosphate |
| pheS | 1128 | 6 | 13.11 | 0.5 | -1.01 | Glucosamine-6-Phosphate Isomeraseglucosamine-6-Phosphate |
| mvaD | 954 | 5 | 11.09 | 0.5 | -1.01 | Putative Maltose/Maltodextrin-Binding Protein Precursor Putative |
| purB | 1299 | 7 | 15.1 | 0.5 | -1.01 | Phage Integrase: Site-Specific Recombinasephage |
| INV10404300 | 2335 | 13 | 27.15 | 0.5 | -1.01 | Conserved Hypothetical Proteinconserved |
| pbp1A | 2160 | 12 | 25.11 | 0.5 | -1.01 | UDP-N-Acetylmuramoylalanine--D-Glutamate Ligaseudp-N-Acetylmuramoylalanine--D-Glutamate |
| INV10408580 | 432 | 2 | 5.02 | 0.5 | -1 | Putative Permease Putative |
| tRNA-Leu-TAA | 86 | 0 | 1 | 0.5 | -1 | Sialic Acid-Induced Transmembrane Protein Yjht(Nanm), Possible Mutarotasesialic |
| INV10417130 | 774 | 4 | 9 | 0.5 | -1 | Putative Uncharacterized Protein Putative |
| MutTnudixfamilyprotein | 429 | 2 | 4.99 | 0.5 | -1 | Putative Maltose/Maltodextrin ABC Transport System Permease Protein Putative |
| putativeparvulintypepeptidyl-prolylisomerase\_similaritywithPrsAfoldase | 942 | 5 | 10.95 | 0.5 | -0.99 | Prephenate Dehydrataseprephenate |
| rex | 426 | 2 | 4.95 | 0.5 | -0.99 | Positive Transcriptional Regulator, Mutr Familypositive |
| INV10405460 | 255 | 1 | 2.96 | 0.5 | -0.99 | ABC Transporter, Permease Protein ABC |
| INV10406240 | 765 | 4 | 8.89 | 0.51 | -0.98 | Putative Membrane Protein Putative |
| tRNA-Leu-CAA | 84 | 0 | 0.98 | 0.51 | -0.99 | Seryl-Trna Synthetaseseryl-Trna |
| fabZ | 423 | 2 | 4.92 | 0.51 | -0.98 | Probable Gtpase Engc (Pseudogene)Probable |
| INV10400100 | 1269 | 7 | 14.75 | 0.51 | -0.98 | Hypothetical Proteinhypothetical |
| INV10406710 | 930 | 5 | 10.81 | 0.51 | -0.98 | Conserved Hypothetical Proteinconserved |
| rpsT | 252 | 1 | 2.93 | 0.51 | -0.97 | DNA Repair Protein Recodna |
| INV10413080 | 759 | 4 | 8.82 | 0.51 | -0.97 | Putative Pyridoxine Biosynthesis Protein Putative |
| INV10416270 | 927 | 5 | 10.78 | 0.51 | -0.97 | Hypotheical Proteinhypotheical |
| Argininosuccinatesynthase(EC6 | 420 | 2 | 4.88 | 0.51 | -0.97 | Argininosuccinate Synthase (EC 6.3.4.5)Argininosuccinate |
| INV10407100 | 924 | 5 | 10.74 | 0.51 | -0.97 | Conserved Hypothetical Proteinconserved |
| tRNA-Tyr-GTA | 82 | 0 | 0.95 | 0.51 | -0.96 | Spn1 Transposasespn1 |
| INV10411850 | 753 | 4 | 8.75 | 0.51 | -0.96 | SMF Family Proteinsmf |
| INV10413950 | 416 | 2 | 4.84 | 0.51 | -0.96 | P-Loop Atpase Protein Family Proteinp-Loop |
| INV10402440 | 1420 | 8 | 16.51 | 0.51 | -0.96 | Cora-Like Mg2+ Transporter Proteincora-Like |
| INV10412490 | 582 | 3 | 6.77 | 0.52 | -0.96 | Putative Acyl-ACP Thioesterase Putative |
| pepQ | 1083 | 6 | 12.59 | 0.52 | -0.96 | Putative A/G-Specific Adenine Glycosylase Putative |
| FIG01117917-hypotheticalprotein | 1245 | 7 | 14.47 | 0.52 | -0.95 | FIG01115961: Hypothetical Proteinfig01115961: |
| INV10405210 | 579 | 3 | 6.73 | 0.52 | -0.95 | Conserved Hypothetical Proteinconserved |
| INV10417400 | 1410 | 8 | 16.39 | 0.52 | -0.95 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| 1676971\_1677217 | 246 | 1 | 2.86 | 0.52 | -0.95 |  |
| INV10415440 | 246 | 1 | 2.86 | 0.52 | -0.95 | Putative Phosphohydrolase Putative |
| INV10400520 | 906 | 5 | 10.53 | 0.52 | -0.94 | Translation Initiation Factor IF-2translation |
| INV10402760 | 243 | 1 | 2.83 | 0.52 | -0.94 | Conserved Hypothetical Proteinconserved |
| INV10400760 | 1065 | 6 | 12.38 | 0.52 | -0.93 | Putative Carbonic Anhydrase Putative |
| csdB | 1227 | 7 | 14.27 | 0.52 | -0.93 | Conserved Domain Proteinconserved |
| INV10401570 | 570 | 3 | 6.63 | 0.52 | -0.93 | Putative Membrane Protein Putative |
| INV10409480 | 570 | 3 | 6.63 | 0.52 | -0.93 | Putative Regulatory Protein Putative |
| scpB | 570 | 3 | 6.63 | 0.52 | -0.93 | Riboflavin Biosynthesis Protein [Includes: Diaminohydroxyphosphoribosylaminopyrimidine Deaminase And 5-Amino-6-(5- Phosphoribosylamino)Uracil Reductase]Riboflavin |
| wzh | 732 | 4 | 8.51 | 0.53 | -0.93 | Transcriptional Regulatortranscriptional |
| INV10412290 | 241 | 1 | 2.8 | 0.53 | -0.93 | Cell Envelope-Related Transcriptional Attenuator Domain Proteincell |
| Mobileelementprotein | 241 | 1 | 2.8 | 0.53 | -0.93 | 6-Phospho-Beta-Galactosidase 26-Phospho-Beta-Galactosidase |
| INV10406450 | 240 | 1 | 2.79 | 0.53 | -0.92 | ABC Transporter Amino Acid-Binding Protein ABC |
| INV10406510 | 240 | 1 | 2.79 | 0.53 | -0.92 | Putative L-Lactate Oxidase-Related Protein Putative |
| rpsR | 240 | 1 | 2.79 | 0.53 | -0.92 | ATP-Dependent DNA Helicaseatp-Dependent |
| INV10418400 | 2031 | 12 | 23.61 | 0.53 | -0.92 | Putative Competence Protein Putative |
| INV10417120 | 561 | 3 | 6.52 | 0.53 | -0.91 | Conserved Hypothetical Proteinconserved |
| LipidAexportATP-bindingpermeaseproteinMsbA | 561 | 3 | 6.52 | 0.53 | -0.91 | IS3-Spn1 Transposaseis3-Spn1 |
| INV10406610 | 237 | 1 | 2.76 | 0.53 | -0.91 | Putative Regulator Putative |
| tRNA-Ile-GAT | 75 | 0 | 0.87 | 0.53 | -0.9 | Preprotein Translocase Secy Subunitpreprotein |
| tRNA-Met-CAT | 75 | 0 | 0.87 | 0.53 | -0.9 | Putative Chromosome Partition Protein Putative |
| atpG | 879 | 5 | 10.22 | 0.53 | -0.9 | ATP Synthase C Chainatp |
| truB | 879 | 5 | 10.22 | 0.53 | -0.9 | Tellurite Resistance Protein Tehbtellurite |
| INV10415990 | 1521 | 9 | 17.68 | 0.54 | -0.9 | Csbd-Like Proteincsbd-Like |
| INV10406360 | 1038 | 6 | 12.07 | 0.54 | -0.9 | Putative Membrane Protein Putative |
| fps | 876 | 5 | 10.18 | 0.54 | -0.9 | FIG01119302: Hypothetical Proteinfig01119302: |
| tRNA-Arg-TCT | 74 | 0 | 0.86 | 0.54 | -0.9 | Segregation And Condensation Protein Bsegregation |
| tRNA-Phe-GAA | 74 | 0 | 0.86 | 0.54 | -0.9 | Putative DNA Repair Protein Putative |
| tRNA-Pro-TGG | 74 | 0 | 0.86 | 0.54 | -0.9 | SNF2 Family Proteinsnf2 |
| INV10400980 | 234 | 1 | 2.72 | 0.54 | -0.9 | Sugar Phosphotransferase System (PTS), Fructose Family, IIA Componentsugar |
| gidB | 714 | 4 | 8.3 | 0.54 | -0.9 | Fuscose Operon Fucu Proteinfuscose |
| INV10419350 | 714 | 4 | 8.3 | 0.54 | -0.9 | Putative Fucose Phosphotransferase System Repressor Putative |
| tRNA-His-GTG | 73 | 0 | 0.85 | 0.54 | -0.89 | Putative Preprotein Seca Subunit Putative |
| tRNA-Thr-GGT | 73 | 0 | 0.85 | 0.54 | -0.89 | Putative Spermidine Synthase Putative |
| INV10413180 | 550 | 3 | 6.39 | 0.54 | -0.89 | Putative Uncharacterized Protein Putative |
| cysS | 1344 | 8 | 15.63 | 0.54 | -0.89 | Response Regulator Proteinresponse |
| INV10413260 | 1185 | 7 | 13.78 | 0.54 | -0.89 | Putative Transposase (Pseudogene) Putative |
| INV10410930 | 708 | 4 | 8.23 | 0.54 | -0.88 | Putative Ribonucleoside-Diphosphate Reductase Alpha Chain Putative |
| nagB | 708 | 4 | 8.23 | 0.54 | -0.88 | 5-Methyltetrahydropteroyltriglutamate--Homocyst Eine Methyltransferase5-Methyltetrahydropteroyltriglutamate--Homocyst |
| purM | 1023 | 6 | 11.89 | 0.54 | -0.88 | Phage Tail Length Tape-Measure Proteinphage |
| INV10402050 | 72 | 0 | 0.84 | 0.54 | -0.88 | Putative Peptidase Putative |
| tRNA-Arg-CCG | 72 | 0 | 0.84 | 0.54 | -0.88 | Metal-Dependent Transcriptional Regulatormetal-Dependent |
| tRNA-Arg-CCT | 72 | 0 | 0.84 | 0.54 | -0.88 | Segregation And Condensation Protein Asegregation |
| tRNA-Gln-TTG | 72 | 0 | 0.84 | 0.54 | -0.88 | Fructokinasefructokinase |
| tRNA-Gly-GCC | 72 | 0 | 0.84 | 0.54 | -0.88 | Putative L-Serine Dehydratase, Alpha Chain Putative |
| tRNA-Gly-TCC | 72 | 0 | 0.84 | 0.54 | -0.88 | Putative L-Serine Dehydratase, Beta Chain Putative |
| INV10409380 | 861 | 5 | 10.01 | 0.54 | -0.88 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10414060 | 702 | 4 | 8.16 | 0.55 | -0.87 | Putative DNA Replication Protein Dnad Putative |
| zwf | 1488 | 9 | 17.3 | 0.55 | -0.87 | Transposasetransposase |
| folD | 858 | 5 | 9.98 | 0.55 | -0.87 | FIG01117917: Hypothetical Proteinfig01117917: |
| tRNA-Cys-GCA | 71 | 0 | 0.83 | 0.55 | -0.87 | Putative Sucrose-6-Phosphate Hydrolase Putative |
| tRNA-Trp-CCA | 71 | 0 | 0.83 | 0.55 | -0.87 | Putative Signal Peptidase I Putative |
| INV10408130 | 228 | 1 | 2.65 | 0.55 | -0.87 | CAAX Amino Protease Family Proteincaax |
| lytB | 2109 | 13 | 24.52 | 0.55 | -0.87 | IS1167, Transposaseis1167, |
| CatabolitecontrolproteinA | 1011 | 6 | 11.75 | 0.55 | -0.87 | Carbamoyl-Phosphate Synthase Small Chaincarbamoyl-Phosphate |
| INV10412040 | 384 | 2 | 4.46 | 0.55 | -0.86 | Putative DNA-Binding Protein Putative |
| clpL | 2106 | 13 | 24.48 | 0.55 | -0.86 | Putative Stress Response-Related Clp Atpase Putative |
| INV10414150 | 540 | 3 | 6.28 | 0.55 | -0.86 | Mur Ligase Family Proteinmur |
| INV10414620 | 696 | 4 | 8.09 | 0.55 | -0.86 | Putative Membrane Protein (Pseudogene) Putative |
| INV10403350 | 538 | 3 | 6.25 | 0.55 | -0.86 | Putative Surface-Anchored Pullulanase Putative |
| INV10409230 | 1005 | 6 | 11.68 | 0.55 | -0.86 | Putative Uncharacterized Protein (Pseudogene) Putative |
| pheA | 849 | 5 | 9.87 | 0.55 | -0.86 | NH(3)-Dependent NAD(+) Synthetasenh(3)-Dependent |
| INV10412410 | 225 | 1 | 2.62 | 0.55 | -0.86 | Putative Phosphate ABC Transporter Permease Protein Putative |
| INV10406150 | 846 | 5 | 9.84 | 0.55 | -0.85 | Hypothetical Proteinhypothetical |
| csrR | 690 | 4 | 8.02 | 0.55 | -0.85 | Conserved Domain Proteinconserved |
| rplA | 690 | 4 | 8.02 | 0.55 | -0.85 | Prophage Pi2 Protein 37prophage |
| INV10415190 | 222 | 1 | 2.58 | 0.56 | -0.84 | Putative Permease Component Of ABC Transporter Putative |
| 165155\_167375 | 2220 | 14 | 25.81 | 0.56 | -0.84 |  |
| INV10401050 | 2220 | 14 | 25.81 | 0.56 | -0.84 | Phosphorylase Family Proteinphosphorylase |
| INV10418640 | 2220 | 14 | 25.81 | 0.56 | -0.84 | Putative Peptidase Putative |
| manL | 990 | 6 | 11.51 | 0.56 | -0.84 | IS630-Spn1, Transposase Orf1IS630-Spn1, |
| INV10414380 | 834 | 5 | 9.7 | 0.56 | -0.83 | Putative Cation-Transporting Atpase Putative |
| INV10401290 | 1599 | 10 | 18.59 | 0.56 | -0.83 | Putative Glycosyl Transferase Putative |
| INV10404100 | 831 | 5 | 9.66 | 0.56 | -0.83 | Putative DNA Alkylation Repair Enzyme (Pseudogene) Putative |
| aroD | 678 | 4 | 7.88 | 0.56 | -0.83 | 3-Dehydroquinate Synthase3-Dehydroquinate |
| Transcriptionalregulator\_ArsRfamily | 678 | 4 | 7.88 | 0.56 | -0.83 | 30S Ribosomal Protein S930S |
| INV10403980 | 219 | 1 | 2.55 | 0.56 | -0.83 | Group II Intron Maturasegroup |
| INV10411880 | 828 | 5 | 9.63 | 0.56 | -0.83 | Putative Kinase Putative |
| murA1 | 1284 | 8 | 14.93 | 0.57 | -0.82 | Lipid A Export ATP-Binding/Permease Protein Msbalipid |
| nadE | 825 | 5 | 9.59 | 0.57 | -0.82 | Metal-Dependent Hydrolase Ybey, Involved In Rrna And/Or Ribosome Maturation And Assemblymetal-Dependent |
| LSUribosomalproteinL7L12(P1P2) | 369 | 2 | 4.29 | 0.57 | -0.82 | Iron Compound ABC Uptake Transporter Substrate-Binding Protein Piaairon |
| cmk | 672 | 4 | 7.81 | 0.57 | -0.82 | Putative ATP-Dependent Clp Protease Proteolytic Subunit Putative |
| INV10409490 | 672 | 4 | 7.81 | 0.57 | -0.82 | Putative Iron-Siderophore Binding Lipoprotein Putative |
| fabH | 975 | 6 | 11.34 | 0.57 | -0.82 | GTP-Binding Protein Engagtp-Binding |
| INV10408100 | 216 | 1 | 2.51 | 0.57 | -0.81 | Putative Type I Restriction Modification System Restriction Protein Putative |
| INV10405290 | 215 | 1 | 2.5 | 0.57 | -0.81 | Putative Uncharacterized Protein Putative |
| prfA | 1569 | 10 | 18.24 | 0.57 | -0.81 | Putative Xanthine Permease Putative |
| idnO | 816 | 5 | 9.49 | 0.57 | -0.81 | Ferrochelataseferrochelatase |
| INV10413720 | 213 | 1 | 2.48 | 0.58 | -0.8 | Cyclophilin Type Peptidyl-Prolyl Cis-Trans Isomerase Proteincyclophilin |
| rpoD | 1110 | 7 | 12.9 | 0.58 | -0.8 | Putative Transposon Integrase; Tn916 ORF3-Like Putative |
| Prolyl-tRNAsynthetase(EC6 | 1854 | 12 | 21.55 | 0.58 | -0.79 | Putative Lysyl-Aminopeptidase Putative |
| INV10406260 | 657 | 4 | 7.64 | 0.58 | -0.79 | Bipa Family Gtpasebipa |
| ilvA | 1251 | 8 | 14.54 | 0.58 | -0.79 | Histidyl-Trna Synthetase (EC 6.1.1.21)Histidyl-Trna |
| INV10407790 | 1987 | 13 | 23.1 | 0.58 | -0.78 | Putative Branched-Chain-Amino-Acid Aminotransferase Putative |
| INV10405180 | 801 | 5 | 9.31 | 0.58 | -0.78 | Conserved Hypothetical Proteinconserved |
| Phagelysin\_glycosylhydrolase\_family25 | 801 | 5 | 9.31 | 0.58 | -0.78 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| aliA | 1983 | 13 | 23.05 | 0.58 | -0.78 | Putative Extracellular Oligopeptide-Binding Protein Putative |
| glnR | 357 | 2 | 4.15 | 0.58 | -0.78 | Glucose Inhibited Division Protein Aglucose |
| INV10403870 | 357 | 2 | 4.15 | 0.58 | -0.78 | Membrane Proteinmembrane |
| INV10419060 | 1969 | 13 | 22.89 | 0.59 | -0.77 | Putative PTS Multi-Domain Regulator Putative |
| INV10414870 | 354 | 2 | 4.12 | 0.59 | -0.77 | Mutt/NUDIX Hydrolase Family Proteinmutt/NUDIX |
| blpO | 207 | 1 | 2.41 | 0.59 | -0.77 | Peptide Pheromone Blpc (Bacteriocin-Like Peptide)Peptide |
| INV10419130 | 60 | 0 | 0.7 | 0.59 | -0.77 | Putative Glycosyl Hydrolase Putative |
| pepT | 1228 | 8 | 14.28 | 0.59 | -0.76 | Mevalonate Diphosphate Decarboxylasemevalonate |
| codY | 789 | 5 | 9.17 | 0.59 | -0.76 | Putative Phosphopantothenoylcysteine Decarboxylase Putative |
| INV10407040 | 642 | 4 | 7.46 | 0.59 | -0.76 | Conserved Hypothetical Proteinconserved |
| INV10412460 | 495 | 3 | 5.75 | 0.59 | -0.75 | Conserved Hypothetical Proteinconserved |
| INV10412270 | 1366 | 9 | 15.88 | 0.59 | -0.76 | Putative Glycosyl Transferase Putative |
| INV10401060 | 930 | 6 | 10.81 | 0.59 | -0.75 | Trkh-Family Cation Transport Proteintrkh-Family |
| 24224\_59696 | 35472 | 246 | 412.4 | 0.6 | -0.74 |  |
| INV10413320 | 1353 | 9 | 15.73 | 0.6 | -0.74 | Putative Uncharacterized Protein Putative |
| fabD | 921 | 6 | 10.71 | 0.6 | -0.74 | Dps-Like Peroxide Resistance Protein Dprdps-Like |
| pyrE | 633 | 4 | 7.36 | 0.6 | -0.74 | Phosphoglycerate Mutase Family 5Phosphoglycerate |
| INV10410630 | 489 | 3 | 5.69 | 0.6 | -0.74 | Putative Membrane Protein Putative |
| rplV | 345 | 2 | 4.01 | 0.6 | -0.74 | Putative Purine Nucleoside Phosphorylase Putative |
| INV10407130 | 1203 | 8 | 13.99 | 0.6 | -0.74 | Putative Exported Protein Putative |
| INV10413580 | 1344 | 9 | 15.63 | 0.6 | -0.73 | Putative Cystathionine Beta-Lyase Putative |
| FIG01114767-hypotheticalprotein | 198 | 1 | 2.3 | 0.61 | -0.72 | FIG01114010: Hypothetical Proteinfig01114010: |
| gp9 | 198 | 1 | 2.3 | 0.61 | -0.72 | Glycerol Kinaseglycerol |
| INV10416650 | 198 | 1 | 2.3 | 0.61 | -0.72 | Conserved Hypothetical Proteinconserved |
| INV10417570 | 624 | 4 | 7.25 | 0.61 | -0.72 | Putative Acylphosphatase Putative |
| INV10416010 | 766 | 5 | 8.91 | 0.61 | -0.72 | Putative Membrane Protein Putative |
| INV10405390 | 1476 | 10 | 17.16 | 0.61 | -0.72 | Putative Acetyltransferase, GNAT Family Protein Putative |
| INV10412210 | 1191 | 8 | 13.85 | 0.61 | -0.72 | Putative ABC Transporter ATP-Binding Protein Putative |
| INV10414840 | 1614 | 11 | 18.76 | 0.61 | -0.72 | Conserved Hypothetical Proteinconserved |
| INV10414330 | 1329 | 9 | 15.45 | 0.61 | -0.72 | Membrane Glycosyl Transferasemembrane |
| pepO | 1893 | 13 | 22.01 | 0.61 | -0.72 | Mutator Mutx Protein (7,8-Dihydro-8-Oxoguanine-Triphosphatase)Mutator |
| zmpB | 5568 | 39 | 64.73 | 0.61 | -0.72 | Transketolase (Ec 2.2.1.1)Transketolase |
| GTP-bindingproteinEra | 900 | 6 | 10.46 | 0.61 | -0.71 | Glycerophosphoryl Diester Phosphodiesterase (EC 3.1.4.46)Glycerophosphoryl |
| INV10409070 | 759 | 5 | 8.82 | 0.61 | -0.71 | Phoh-Like Proteinphoh-Like |
| INV10414660 | 618 | 4 | 7.18 | 0.61 | -0.71 | ABC Transporter ATP-Binding Protein ABC |
| INV10414750 | 336 | 2 | 3.91 | 0.61 | -0.71 | Integral Membrane Proteinintegral |
| aga | 2163 | 15 | 25.15 | 0.61 | -0.71 | Alpha-Galactosidasealpha-Galactosidase |
| FIG01119302-hypotheticalprotein | 195 | 1 | 2.27 | 0.61 | -0.71 | FIG01116389: Hypothetical Proteinfig01116389: |
| INV10410180 | 2160 | 15 | 25.11 | 0.61 | -0.71 | Putative Membrane Protein Putative |
| INV10406140 | 1176 | 8 | 13.67 | 0.61 | -0.7 |  |
| INV10401280 | 615 | 4 | 7.15 | 0.61 | -0.7 | Putative Major Facilitator Superfamily Protein (Pseudogene) Putative |
| INV10413220 | 1596 | 11 | 18.56 | 0.61 | -0.7 | Aldo/Keto Reductase Family Proteinaldo/Keto |
| hrcA | 1035 | 7 | 12.03 | 0.61 | -0.7 | GMP Synthase [Glutamine-Hydrolyzing]GMP |
| INV10414650 | 894 | 6 | 10.39 | 0.61 | -0.7 | ABC Transporter Permease Protein (Permease)ABC |
| rpsD | 612 | 4 | 7.12 | 0.62 | -0.7 | Dihydroorotate Dehydrogenase, Catalytic Subunitdihydroorotate |
| INV10401320 | 471 | 3 | 5.48 | 0.62 | -0.7 | Lysm Domain Proteinlysm |
| INV10414390 | 885 | 6 | 10.29 | 0.62 | -0.69 | Putative Acyltransferase Putative |
| INV10409280 | 330 | 2 | 3.84 | 0.62 | -0.69 | Putative Amino Acid Permease Putative |
| INV10406210 | 1161 | 8 | 13.5 | 0.62 | -0.69 | Short Chain Dehydrogenaseshort |
| INV10412930 | 466 | 3 | 5.42 | 0.62 | -0.68 | Haloacid Dehalogenase-Like Hydrolasehaloacid |
| comYC | 327 | 2 | 3.8 | 0.62 | -0.68 | Competence-Specific Sigma Factor Comxcompetence-Specific |
| INV10415570 | 1152 | 8 | 13.39 | 0.63 | -0.68 | Putative Hydrolase Putative |
| INV10409060 | 189 | 1 | 2.2 | 0.63 | -0.68 | Conserved Hypothetical Proteinconserved |
| guaA | 1563 | 11 | 18.17 | 0.63 | -0.68 | Glycyl-Trna Synthetase Alpha Chainglycyl-Trna |
| INV10404960 | 600 | 4 | 6.98 | 0.63 | -0.67 | Putative Endo-Beta-N-Acetylglucosaminidase Putative |
| Two-componentresponseregulator | 600 | 4 | 6.98 | 0.63 | -0.67 | Phosphomethylpyrimidine Kinasephosphomethylpyrimidine |
| INV10401620 | 462 | 3 | 5.37 | 0.63 | -0.67 | Putative Transposase (Pseudogene) Putative |
| INV10418900 | 873 | 6 | 10.15 | 0.63 | -0.67 | Putative Membrane Protein Putative |
| INV10404940 | 324 | 2 | 3.77 | 0.63 | -0.67 | Putative Uncharacterized Protein Putative |
| INV10418490 | 870 | 6 | 10.11 | 0.63 | -0.67 | Putative N-Acetylglucosamine-6-Phosphate Deacetylase Putative |
| INV10401010 | 187 | 1 | 2.17 | 0.63 | -0.66 | Glyoxalase/Bleomycin Resistance Protein/Dioxygenase Superfamily Proteinglyoxalase/Bleomycin |
| deoA | 1278 | 9 | 14.86 | 0.63 | -0.67 | Putative Dihydrodipicolinate Reductase Putative |
| msmF | 867 | 6 | 10.08 | 0.63 | -0.66 | L-Lactate Dehydrogenasel-Lactate |
| INV10404850 | 1002 | 7 | 11.65 | 0.63 | -0.66 | Putative Transport Protein Putative |
| INV10416000 | 729 | 5 | 8.48 | 0.63 | -0.66 | Putative Transposase (Pseudogene) Putative |
| INV10416780 | 864 | 6 | 10.04 | 0.63 | -0.66 | Putative Oligopeptide Transporter Permease Protein Putative |
| INV10415480 | 1135 | 8 | 13.2 | 0.63 | -0.66 | Putative Methyltransferase Putative |
| DNApolymeraseIIIalphasubunit(EC2 | 591 | 4 | 6.87 | 0.64 | -0.65 | Chromosomal Replication Initiator Proteinchromosomal |
| INV10401330 | 1266 | 9 | 14.72 | 0.64 | -0.65 | Hypothetical Protein (Pseudogene)Hypothetical |
| INV10415530 | 1263 | 9 | 14.68 | 0.64 | -0.65 | Conserved Hypothetical Proteinconserved |
| asnA | 993 | 7 | 11.54 | 0.64 | -0.65 | Putative Shikimate Kinase Putative |
| INV10413340 | 858 | 6 | 9.98 | 0.64 | -0.65 | Conserved Hypothetical Proteinconserved |
| engB | 588 | 4 | 6.84 | 0.64 | -0.65 | Chaperone Protein Dnak (Heat Shock Protein 70)Chaperone |
| msmE | 1260 | 9 | 14.65 | 0.64 | -0.65 | L-Lactate Oxidasel-Lactate |
| INV10404680 | 183 | 1 | 2.13 | 0.64 | -0.65 | Putative Membrane Protein Putative |
| Methylaseinvolvedinubiquinonemenaquinonebiosynthesis | 183 | 1 | 2.13 | 0.64 | -0.65 | Tagatose 1,6-Diphosphate Aldolase 2tagatose |
| INV10410010 | 990 | 7 | 11.51 | 0.64 | -0.65 | ABC Transporter Permease Protein ABC |
| INV10414250 | 852 | 6 | 9.91 | 0.64 | -0.64 | IS3-Spn1 Orf A (Pseudogene)IS3-Spn1 |
| pfl | 2325 | 17 | 27.03 | 0.64 | -0.64 | N-Acetylmannosamine-6-Phosphate 2-Epimerase (EC 5.1.3.9)N-Acetylmannosamine-6-Phosphate |
| INV10415200 | 315 | 2 | 3.66 | 0.64 | -0.64 | Putative ABC Transport Protein, Solute-Binding Component Putative |
| rpoZ | 315 | 2 | 3.66 | 0.64 | -0.64 | Aspartate Carbamoyltransferaseaspartate |
| xpt | 582 | 4 | 6.77 | 0.64 | -0.64 | Transcriptional Regulator, Merr Familytranscriptional |
| INV10410880 | 849 | 6 | 9.87 | 0.64 | -0.63 | Putative Uncharacterized Protein Putative |
| dltB | 1246 | 9 | 14.49 | 0.65 | -0.63 | Thymidine Phosphorylasethymidine |
| INV10404200 | 846 | 6 | 9.84 | 0.65 | -0.63 | Conserved Hypothetical Proteinconserved |
| INV10403270 | 180 | 1 | 2.09 | 0.65 | -0.63 | Sugar Phosphotransferase System (PTS), IIC Componentsugar |
| glpK | 1509 | 11 | 17.54 | 0.65 | -0.63 | Glycerol Dehydrogenaseglycerol |
| INV10404970 | 578 | 4 | 6.72 | 0.65 | -0.63 | Putative Membrane Protein Putative |
| INV10414910 | 312 | 2 | 3.63 | 0.65 | -0.63 | Putative Uncharacterized Protein Putative |
| purC | 708 | 5 | 8.23 | 0.65 | -0.62 | Phage Lysin, Glycosyl Hydrolase, Family 25Phage |
| tyrA | 1104 | 8 | 12.84 | 0.65 | -0.62 | Thiamin-Phosphate Pyrophosphorylasethiamin-Phosphate |
| iscU | 441 | 3 | 5.13 | 0.65 | -0.62 | Putative Two-Component System, Response Regulator Putative |
| INV10402740 | 966 | 7 | 11.23 | 0.65 | -0.61 | 30S Ribosomal Protein S1430S |
| INV10406550 | 702 | 5 | 8.16 | 0.65 | -0.61 | Putative ABC Transporter, ATP-Binding Protein Putative |
| INV10416050 | 702 | 5 | 8.16 | 0.65 | -0.61 | Sugar Phosphotransferase System (PTS), Lactose/Cellobiose-Specific Family, IIB Componentsugar |
| 553904\_554080 | 176 | 1 | 2.05 | 0.66 | -0.61 |  |
| INV10404980 | 176 | 1 | 2.05 | 0.66 | -0.61 | Type I Restriction-Modification System M Proteintype |
| INV10405440 | 958 | 7 | 11.14 | 0.66 | -0.6 | Putative Uncharacterized Protein (Pseudogene) Putative |
| aliB | 174 | 1 | 2.02 | 0.66 | -0.59 | Putative Oligopeptide-Binding Protein Alib (Pseudogene) Putative |
| 1507612\_1517795 | 10183 | 78 | 118.39 | 0.66 | -0.6 |  |
| INV10417650 | 303 | 2 | 3.52 | 0.66 | -0.59 | Hypothetical Protein (Pseudogene)Hypothetical |
| INV10414400 | 1338 | 10 | 15.56 | 0.66 | -0.59 | Conserved Hypothetical Protein (Pseudogene)Conserved |
| INV10407090 | 690 | 5 | 8.02 | 0.67 | -0.59 | Conserved Hypothetical Proteinconserved |
| INV10409420 | 690 | 5 | 8.02 | 0.67 | -0.59 | Putative Membrane Protein Putative |
| INV10417860 | 690 | 5 | 8.02 | 0.67 | -0.59 | Putative Nucleotide-Binding Protein Putative |
| ppnK | 819 | 6 | 9.52 | 0.67 | -0.59 | Penicillin-Binding Protein 2apenicillin-Binding |
| INV10415410 | 172 | 1 | 2 | 0.67 | -0.58 | Putative Membrane Protein Putative |
| INV10406390 | 688 | 5 | 8 | 0.67 | -0.58 | ABC Transporter ATP-Binding Protein ABC |
| INV10406160 | 558 | 4 | 6.49 | 0.67 | -0.58 | Putative Exported Protein Putative |
| INV10409040 | 1588 | 12 | 18.46 | 0.67 | -0.58 | Protein Gid Homologprotein |
| 1955335\_1955635 | 300 | 2 | 3.49 | 0.67 | -0.58 |  |
| INV10406780 | 300 | 2 | 3.49 | 0.67 | -0.58 | Branched-Chain Amino Acid ABC Transporter, Amino Acid-Binding Proteinbranched-Chain |
| INV10413070 | 300 | 2 | 3.49 | 0.67 | -0.58 | SNO Glutamine Amidotransferase Family Proteinsno |
| INV10418010 | 300 | 2 | 3.49 | 0.67 | -0.58 | L-Ribulose 5-Phosphate 4-Epimerasel-Ribulose |
| infA | 171 | 1 | 1.99 | 0.67 | -0.58 | Hypoxanthine-Guanine Phosphoribosyltransferasehypoxanthine-Guanine |
| INV10409300 | 1326 | 10 | 15.42 | 0.67 | -0.58 | Pneumococcal Histidine Triad Protein E (Pseudogene)Pneumococcal |
| pepA | 1065 | 8 | 12.38 | 0.67 | -0.57 | Putative DNA Mismatch Repair Protein Putative |
| wzg | 1446 | 11 | 16.81 | 0.67 | -0.57 | Transcriptional Antiterminator Of Lichenan Operon, Bglg Familytranscriptional |
| INV10418360 | 933 | 7 | 10.85 | 0.68 | -0.57 | Putative Membrane Protein Putative |
| FIG011945-O-methyltransferasefamilyprotein | 678 | 5 | 7.88 | 0.68 | -0.57 | FIG01116415: Hypothetical Proteinfig01116415: |
| INV10406420 | 804 | 6 | 9.35 | 0.68 | -0.56 | Putative Membrane Protein Putative |
| INV10417180 | 294 | 2 | 3.42 | 0.68 | -0.56 | Putative Uncharacterized Protein Putative |
| INV10401070 | 547 | 4 | 6.36 | 0.68 | -0.56 | Trka Family Cation Transport Proteintrka |
| INV10409330 | 1305 | 10 | 15.17 | 0.68 | -0.56 | Putative Membrane Protein Putative |
| parC | 2436 | 19 | 28.32 | 0.68 | -0.55 | UDP-N-Acetylenolpyruvoylglucosamine Reductaseudp-N-Acetylenolpyruvoylglucosamine |
| 906385\_910327 | 3942 | 31 | 45.83 | 0.68 | -0.55 |  |
| nanH | 918 | 7 | 10.67 | 0.69 | -0.54 | Methylase Involved In Ubiquinone/Menaquinone Biosynthesismethylase |
| ndk | 414 | 3 | 4.81 | 0.69 | -0.54 | S-Adenosylmethionine Synthetases-Adenosylmethionine |
| fruK | 912 | 7 | 10.6 | 0.69 | -0.54 | FIG011945: O-Methyltransferase Family Proteinfig011945: |
| manN | 912 | 7 | 10.6 | 0.69 | -0.54 | IS861, Transposase (Orf1), IS3 Family, Truncatedis861, |
| INV10414130 | 786 | 6 | 9.14 | 0.69 | -0.53 | Major Facilitator Superfamily Protein (Pseudogene)Major |
| INV10418840 | 661 | 5 | 7.68 | 0.69 | -0.53 | 5-Formyltetrahydrofolate Cyclo-Ligase Family Protein5-Formyltetrahydrofolate |
| INV10415720 | 660 | 5 | 7.67 | 0.69 | -0.53 | Putative Thioredoxin Putative |
| INV10406880 | 411 | 3 | 4.78 | 0.69 | -0.53 | Conserved Hypothetical Proteinconserved |
| dltA | 1527 | 12 | 17.75 | 0.69 | -0.53 | Degenerative Transposasedegenerative |
| INV10401310 | 534 | 4 | 6.21 | 0.69 | -0.53 | Putative 5'-Nucleotidase Putative |
| INV10400110 | 1278 | 10 | 14.86 | 0.69 | -0.53 | Hypothetical Proteinhypothetical |
| queA | 1029 | 8 | 11.96 | 0.69 | -0.53 | Glyceraldehyde-3-Phosphate Dehydrogenase, Plasmin Receptorglyceraldehyde-3-Phosphate |
| INV10403990 | 285 | 2 | 3.31 | 0.7 | -0.52 | Conserved Hypothetical Proteinconserved |
| dltD | 1269 | 10 | 14.75 | 0.7 | -0.52 | Deoxyribose-Phosphate Aldolasedeoxyribose-Phosphate |
| IS630-Spn1\_transposaseOrf1 | 160 | 1 | 1.86 | 0.7 | -0.52 | 33 Kda Chaperonin (Heat Shock Protein 33 Homolog)33 |
| INV10417200 | 1389 | 11 | 16.15 | 0.7 | -0.52 | Putative Uncharacterized Protein Putative |
| INV10412000 | 774 | 6 | 9 | 0.7 | -0.51 | Putative Uncharacterized Protein (Pseudogene) Putative |
| scaR | 651 | 5 | 7.57 | 0.7 | -0.51 | Riboflavin Biosynthesis Proteinriboflavin |
| INV10404260 | 528 | 4 | 6.14 | 0.7 | -0.51 | Putative Decarboxylase Putative |
| INV10414930 | 528 | 4 | 6.14 | 0.7 | -0.51 | Putative Transport System Permease Putative |
| INV10417660 | 405 | 3 | 4.71 | 0.7 | -0.51 | ABC Transporter ATP-Binding Protein ABC |
| INV10400650 | 1017 | 8 | 11.82 | 0.7 | -0.51 | Putative Septum Formation Initiator Protein Putative |
| INV10409340 | 159 | 1 | 1.85 | 0.7 | -0.51 | Putative 4-Oxalocrotonate Tautomerase Putative |
| rplU | 159 | 1 | 1.85 | 0.7 | -0.51 | PTS System, Nitrogen Regulatory Component IIA, Putativepts |
| 916657\_917306 | 649 | 5 | 7.55 | 0.7 | -0.51 |  |
| INV10404230 | 1627 | 13 | 18.92 | 0.7 | -0.51 | Putative Bacteriocin Production Protein Putative |
| N-acetylglucosamine-1-phosphateuridyltransferase(EC2 | 1380 | 11 | 16.04 | 0.7 | -0.51 | Maturase-Related Proteinmaturase-Related |
| INV10411220 | 402 | 3 | 4.67 | 0.71 | -0.5 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| msmK | 1131 | 9 | 13.15 | 0.71 | -0.5 | Putative 2-Isopropylmalate Synthase (Pseudogene) Putative |
| INV10416970 | 279 | 2 | 3.24 | 0.71 | -0.5 | Putative Thioredoxin Putative |
| INV10413930 | 521 | 4 | 6.06 | 0.71 | -0.5 | Conserved Hypothetical Proteinconserved |
| trpD | 1005 | 8 | 11.68 | 0.71 | -0.49 | Serine/Threonine-Protein Kinaseserine/Threonine-Protein |
| TypeIrestriction-modificationsystem\_specificitysubunitS(EC3 | 641 | 5 | 7.45 | 0.71 | -0.49 | Thiamine-Phosphate Pyrophosphorylasethiamine-Phosphate |
| lacR1 | 762 | 6 | 8.86 | 0.71 | -0.49 | Putative Transposase Putative |
| INV10402640 | 1002 | 8 | 11.65 | 0.71 | -0.49 | Putative Cardiolipin Synthetase Putative |
| INV10413500 | 759 | 6 | 8.82 | 0.71 | -0.49 | Putative Aminodeoxychorismate Lyase Putative |
| INV10414760 | 759 | 6 | 8.82 | 0.71 | -0.49 | Putative Cell-Division Protein Diviva Putative |
| INV10405580 | 999 | 8 | 11.61 | 0.71 | -0.49 | Putative Glutamine-Binding Protein Precursor Putative |
| INV10405710 | 1842 | 15 | 21.42 | 0.71 | -0.49 | Uracil DNA Glycosylase Superfamily Proteinuracil |
| nadC | 873 | 7 | 10.15 | 0.72 | -0.48 | Homoserine O-Succinyltransferasehomoserine |
| INV10405850 | 753 | 6 | 8.75 | 0.72 | -0.48 | Putative Membrane Protein Putative |
| apt | 513 | 4 | 5.96 | 0.72 | -0.48 | Adenine Phosphoribosyltransferaseadenine |
| INV10402350 | 153 | 1 | 1.78 | 0.72 | -0.48 | Putative Protease Putative |
| 434957\_435826 | 869 | 7 | 10.1 | 0.72 | -0.47 |  |
| INV10403930 | 869 | 7 | 10.1 | 0.72 | -0.47 | IS1167 Transposase (Pseudogene)IS1167 |
| ilvD | 1704 | 14 | 19.81 | 0.72 | -0.47 | DNA-Binding Protein HUDNA-Binding |
| asnS | 1344 | 11 | 15.63 | 0.72 | -0.47 | Aspartate--Ammonia Ligaseaspartate--Ammonia |
| INV10412030 | 390 | 3 | 4.53 | 0.72 | -0.47 | Lema Family Proteinlema |
| strH | 3939 | 33 | 45.79 | 0.73 | -0.46 | 50S Ribosomal Protein L1450S |
| TelluriteresistanceproteinTehB | 861 | 7 | 10.01 | 0.73 | -0.46 | 50S Ribosomal Protein L2050S |
| INV10414780 | 741 | 6 | 8.61 | 0.73 | -0.46 | Conserved Hypothetical Proteinconserved |
| ccs1 | 150 | 1 | 1.74 | 0.73 | -0.45 | Cytochrome C-Type Biogenesis Protein Ccdacytochrome |
| rpmG1 | 150 | 1 | 1.74 | 0.73 | -0.45 | Phosphoribosylformylglycinamidine Cyclo-Ligasephosphoribosylformylglycinamidine |
| INV10404090 | 1683 | 14 | 19.57 | 0.73 | -0.46 | Response Regulator Proteinresponse |
| INV10408880 | 975 | 8 | 11.34 | 0.73 | -0.46 | Putative Carboxynorspermidine Decarboxylase Putative |
| INV10400490 | 739 | 6 | 8.59 | 0.73 | -0.45 | Impb/Mucb/Samb Family Proteinimpb/Mucb/Samb |
| Phosphoglyceratemutasefamily5 | 621 | 5 | 7.22 | 0.73 | -0.45 | NADH Oxidasenadh |
| unknown | 384 | 3 | 4.46 | 0.73 | -0.45 | Thymidylate Kinasethymidylate |
| INV10412630 | 1083 | 9 | 12.59 | 0.74 | -0.44 | Putative ABC Transporter ATP-Binding Protein (Pseudogene) Putative |
| cadD | 615 | 5 | 7.15 | 0.74 | -0.44 | Blpz Protein, Fusionblpz |
| ptsH | 264 | 2 | 3.07 | 0.74 | -0.44 | Putative Phosphomannomutase Putative |
| INV10414200 | 613 | 5 | 7.13 | 0.74 | -0.44 | IS3-Spn1 Orf BIS3-Spn1 |
| INV10412390 | 729 | 6 | 8.48 | 0.74 | -0.44 | Gntr Family Regulatory Proteingntr |
| INV10412340 | 726 | 6 | 8.44 | 0.74 | -0.43 | ABC Transporter ATP-Binding Protein ABC |
| INV10406230 | 957 | 8 | 11.13 | 0.74 | -0.43 | Conserved Hypothetical Proteinconserved |
| INV10416070 | 957 | 8 | 11.13 | 0.74 | -0.43 | Putative ROK-Family Repressor Protein Putative |
| INV10403710 | 725 | 6 | 8.43 | 0.74 | -0.43 | Pfkb Family Carbohydrate Kinasepfkb |
| INV10414310 | 840 | 7 | 9.77 | 0.74 | -0.43 | Putative Membrane Protein Putative |
| thyA | 840 | 7 | 9.77 | 0.74 | -0.43 | 50S Ribosomal Protein L3250S |
| rluB | 724 | 6 | 8.42 | 0.74 | -0.43 | Peptide Chain Release Factor 1peptide |
| INV10410000 | 1071 | 9 | 12.45 | 0.74 | -0.43 | Putative ABC Transporter Substrate Binding Protein Putative |
| INV10412160 | 375 | 3 | 4.36 | 0.75 | -0.42 | Crcb-Like Proteincrcb-Like |
| INV10418890 | 1410 | 12 | 16.39 | 0.75 | -0.42 | Putative Transferase Putative |
| INV10400600 | 144 | 1 | 1.67 | 0.75 | -0.42 | Integrase/Recombinase (Xerc/Codv Family)Integrase/Recombinase |
| INV10401250 | 1062 | 9 | 12.35 | 0.75 | -0.42 | Putative Exported Protein Putative |
| INV10416580 | 717 | 6 | 8.34 | 0.75 | -0.42 | Putative UDP-Glucose 4-Epimerase Putative |
| INV10418020 | 487 | 4 | 5.66 | 0.75 | -0.41 | Putative Hexulose-6-Phosphate Isomerase (Pseudogene) Putative |
| metA | 945 | 8 | 10.99 | 0.75 | -0.41 | Putative KHG/KDPG Aldolase [Includes: 4-Hydroxy-2-Oxoglutarate Aldolase; 2- Dehydro-3-Deoxy-Phosphogluconate Aldolase] Putative |
| INV10401120 | 601 | 5 | 6.99 | 0.75 | -0.41 | Response Regulator Proteinresponse |
| aroA | 1284 | 11 | 14.93 | 0.75 | -0.41 | Arginyl-Trna Synthetasearginyl-Trna |
| endA | 825 | 7 | 9.59 | 0.76 | -0.4 | DNA Integration/Recombination/Invertion Proteindna |
| INV10415680 | 711 | 6 | 8.27 | 0.76 | -0.41 | Putative Sodium:Dicarboxylate Symporter Family Protein Putative |
| recU | 597 | 5 | 6.94 | 0.76 | -0.4 | DNA Polymerase IDNA |
| INV10413450 | 1506 | 13 | 17.51 | 0.76 | -0.4 | IS1239 Transposaseis1239 |
| fmt | 936 | 8 | 10.88 | 0.76 | -0.4 | FIG01117121: Hypothetical Proteinfig01117121: |
| INV10416560 | 822 | 7 | 9.56 | 0.76 | -0.4 | Putative Marr-Family Transcriptional Regulator Putative |
| rpoB | 3429 | 30 | 39.87 | 0.76 | -0.4 | Putative Parvulin Type Peptidyl-Prolyl Isomerase, Similarity With Prsa Foldase Putative |
| agaD | 819 | 7 | 9.52 | 0.76 | -0.4 | Putative N-Acetylgalactosamine-Specific Phosphotransferase System (PTS), IID Component Putative |
| alaS | 2619 | 23 | 30.45 | 0.76 | -0.39 | Alanyl-Trna Synthetasealanyl-Trna |
| INV10413610 | 477 | 4 | 5.55 | 0.76 | -0.39 | Putative Extracellular Oligopeptide-Binding Protein Putative |
| INV10405150 | 702 | 6 | 8.16 | 0.76 | -0.39 | Putative Membrane Protein (Pseudogene) Putative |
| INV10402930 | 1485 | 13 | 17.26 | 0.77 | -0.38 | Putative Extracellular Solute-Binding Protein (Pseudogene) Putative |
| INV10406560 | 1260 | 11 | 14.65 | 0.77 | -0.38 | Putative Membrane Protein Putative |
| vicX | 810 | 7 | 9.42 | 0.77 | -0.38 | Putative IS1167 Transposase (Pseudogene) Putative |
| INV10414730 | 249 | 2 | 2.89 | 0.77 | -0.37 | Conserved Hypothetical Proteinconserved |
| INV10413090 | 360 | 3 | 4.19 | 0.77 | -0.38 | Apbe Family Proteinapbe |
| rplT | 360 | 3 | 4.19 | 0.77 | -0.38 | PTS System, IIA Componentpts |
| INV10417100 | 2031 | 18 | 23.61 | 0.77 | -0.37 | Putative ABC Transporter, ATP-Binding/Permease Protein Putative |
| 5'-methylthioadenosinenucleosidase(EC3 | 693 | 6 | 8.06 | 0.77 | -0.37 | 5'-Methylthioadenosine Nucleosidase (EC 3.2.2.16) / S-Adenosylhomocysteine Nucleosidase (EC 3.2.2.9)5'-Methylthioadenosine |
| INV10402000 | 693 | 6 | 8.06 | 0.77 | -0.37 | CAAX Amino Terminal Protease Family Proteincaax |
| dnaJ | 1137 | 10 | 13.22 | 0.77 | -0.37 | Putative D-Alanyl-Lipoteichoic Acid Biosynthesis Protein Putative |
| INV10412430 | 801 | 7 | 9.31 | 0.78 | -0.37 | NOL1/NOP2/Sun Family Proteinnol1/NOP2/Sun |
| pyrK | 801 | 7 | 9.31 | 0.78 | -0.37 | Pneumococcal Histidine Triad Protein E Alternate (Pseudogene)Pneumococcal |
| INV10400660 | 2574 | 23 | 29.93 | 0.78 | -0.37 | Conserved Hypothetical Proteinconserved |
| INV10415810 | 246 | 2 | 2.86 | 0.78 | -0.36 | Phage-Like Proteinphage-Like |
| galE | 1020 | 9 | 11.86 | 0.78 | -0.36 | Putative Cell Division Protein Putative |
| INV10407910 | 909 | 8 | 10.57 | 0.78 | -0.36 | DNA Translocase Ftskdna |
| INV10413530 | 576 | 5 | 6.7 | 0.78 | -0.36 | Acetyltransferase, Gnat Family Protein. Acetyltransferase, Gnat Family Proteinacetyltransferase, |
| glnA | 1347 | 12 | 15.66 | 0.78 | -0.36 | Glutamyl-Trna Amidotransferase Subunit Bglutamyl-Trna |
| INV10418380 | 1347 | 12 | 15.66 | 0.78 | -0.36 | Putative Competence Protein Putative |
| INV10400700 | 24 | 0 | 0.28 | 0.78 | -0.36 | Putative IS630-Spn1 Transposase Putative |
| FIG00630611-hypotheticalprotein | 354 | 3 | 4.12 | 0.78 | -0.36 | (3R)-Hydroxymyristoyl-[Acyl Carrier Protein] Dehydratase(3R)-Hydroxymyristoyl-[Acyl |
| radC | 684 | 6 | 7.95 | 0.78 | -0.35 | Fatty Acid/Phospholipid Synthesis Proteinfatty |
| INV10416100 | 243 | 2 | 2.83 | 0.78 | -0.35 | Putative DNA-Binding Protein Putative |
| rpmE | 243 | 2 | 2.83 | 0.78 | -0.35 | Bifunctional Purine Biosynthesis Protein Purh [Includes: Phosphoribosylaminoimidazolecarboxamide Formyltransferase; IMP Cyclohydrolase]Bifunctional |
| arcA | 1230 | 11 | 14.3 | 0.78 | -0.35 | Arginine Deiminasearginine |
| INV10404020 | 1887 | 17 | 21.94 | 0.78 | -0.35 | Putative RNA Methylase Family Protein Putative |
| INV10416150 | 462 | 4 | 5.37 | 0.78 | -0.35 | Conserved Hypothetical Proteinconserved |
| INV10418410 | 1008 | 9 | 11.72 | 0.79 | -0.35 | Conserved Hypothetical Proteinconserved |
| INV10418910 | 1008 | 9 | 11.72 | 0.79 | -0.35 | Putative Cation Transporting Atpase Putative |
| INV10401160 | 678 | 6 | 7.88 | 0.79 | -0.34 | Binding-Protein-Dependent Transport System Membrane Proteinbinding-Protein-Dependent |
| INV10413880 | 678 | 6 | 7.88 | 0.79 | -0.34 | Putative Phosphoglucosamine Mutase Putative |
| INV10418810 | 132 | 1 | 1.53 | 0.79 | -0.34 | Putative Transposase Fragment Putative |
| dltC | 240 | 2 | 2.79 | 0.79 | -0.34 | Phosphopentomutasephosphopentomutase |
| INV10413590 | 783 | 7 | 9.1 | 0.79 | -0.34 | ABC Transporter ATP-Binding Protein (Pseudogene)ABC |
| INV10406100 | 348 | 3 | 4.05 | 0.79 | -0.34 | Response Regulator Proteinresponse |
| agaW | 780 | 7 | 9.07 | 0.79 | -0.33 | Putative N-Acetylgalactosamine-Specific Phosphotransferase System (PTS), IIC Component Putative |
| INV10405310 | 993 | 9 | 11.54 | 0.8 | -0.33 | Putative Type III Restriction Endonuclease Putative |
| INV10409090 | 885 | 8 | 10.29 | 0.8 | -0.33 | Putative Competence-Related Protein Putative |
| hypotheticalprotein | 345 | 3 | 4.01 | 0.8 | -0.32 | UTP-Glucose-1-Phosphate Uridylyltransferaseutp-Glucose-1-Phosphate |
| INV10410290 | 345 | 3 | 4.01 | 0.8 | -0.32 | Conserved Hypothetical Proteinconserved |
| INV10401100 | 236 | 2 | 2.74 | 0.8 | -0.32 | Putative Glycosyl Transferase (Pseudogene) Putative |
| Transposase | 343 | 3 | 3.99 | 0.8 | -0.32 | 30S Ribosomal Protein S1830S |
| INV10419140 | 21 | 0 | 0.24 | 0.8 | -0.31 | Conserved Hypothetical Proteinconserved |
| infC | 342 | 3 | 3.98 | 0.8 | -0.32 | Putative Protease Htpx Homolog Putative |
| 120011\_120352 | 341 | 3 | 3.96 | 0.81 | -0.31 |  |
| BlpZprotein\_fusion | 234 | 2 | 2.72 | 0.81 | -0.31 | Regulatory Protein Blpsregulatory |
| INV10406850 | 873 | 8 | 10.15 | 0.81 | -0.31 | Branched-Chain Amino Acid Transport ATP-Binding Proteinbranched-Chain |
| INV10413370 | 978 | 9 | 11.37 | 0.81 | -0.31 | Putative Amino Acid ABC Transporter Permease Protein Putative |
| oxidoreductase\_GfoIdhMocAfamily | 978 | 9 | 11.37 | 0.81 | -0.31 | Metal Cation ABC Transporter ATP-Binding Proteinmetal |
| INV10413960 | 445 | 4 | 5.17 | 0.81 | -0.3 | Endoribonuclease L-PSP Family Proteinendoribonuclease |
| INV10405880 | 869 | 8 | 10.1 | 0.81 | -0.3 | Putative Uncharacterized Protein Putative |
| INV10416020 | 444 | 4 | 5.16 | 0.81 | -0.3 | Sugar Phosphotransferase System (PTS), IIC Componentsugar |
| INV10416760 | 444 | 4 | 5.16 | 0.81 | -0.3 | Putative Oligopeptide Transporter ATP-Binding Protein Putative |
| cca | 1185 | 11 | 13.78 | 0.81 | -0.3 | Choline Binding Protein Gcholine |
| INV10416900 | 231 | 2 | 2.69 | 0.81 | -0.3 | Recx Family Proteinrecx |
| INV10412200 | 548 | 5 | 6.37 | 0.81 | -0.3 | Putative Uncharacterized Protein (Pseudogene) Putative |
| INV10401300 | 1287 | 12 | 14.96 | 0.81 | -0.3 | Polysaccharide Biosynthesis Proteinpolysaccharide |
| INV10412600 | 1392 | 13 | 16.18 | 0.81 | -0.3 | Putative Membrane Protein (Pseudogene) Putative |
| INV10415540 | 1179 | 11 | 13.71 | 0.82 | -0.29 | Putative Nicotinate-Nucleotide Adenylyltransferase Putative |
| INV10416090 | 966 | 9 | 11.23 | 0.82 | -0.29 | Type IV Prepilin Peptidase Family Proteintype |
| INV10410940 | 1488 | 14 | 17.3 | 0.82 | -0.29 | Putative Ribonucleoside-Diphosphate Reductase Beta Chain Putative |
| INV10410190 | 963 | 9 | 11.2 | 0.82 | -0.29 | Putative GTP-Binding Protein Putative |
| 1258405\_1278977 | 20572 | 196 | 239.17 | 0.82 | -0.29 |  |
| INV10413900 | 438 | 4 | 5.09 | 0.82 | -0.28 | Putative Membrane Protein Putative |
| INV10409080 | 857 | 8 | 9.96 | 0.82 | -0.28 | Putative Acetyltransferase (Pseudogene) Putative |
| INV10402670 | 435 | 4 | 5.06 | 0.83 | -0.28 | Conserved Hypothetical Proteinconserved |
| INV10413300 | 849 | 8 | 9.87 | 0.83 | -0.27 | Cell Wall Surface Anchored Proteincell |
| mtsC | 849 | 8 | 9.87 | 0.83 | -0.27 | PTS System, Lichenan-Specific Iic Componentpts |
| INV10415260 | 744 | 7 | 8.65 | 0.83 | -0.27 | ABC Transporter, ATP-Binding Protein ABC |
| transcriptionalregulator\_XREfamily | 225 | 2 | 2.62 | 0.83 | -0.27 | 30S Ribosomal Protein S1230S |
| fucA | 639 | 6 | 7.43 | 0.83 | -0.27 | Formamidopyrimidine-DNA Glycosylase (EC 3.2.2.23)Formamidopyrimidine-DNA |
| arcC | 948 | 9 | 11.02 | 0.83 | -0.27 | Carbamate Kinasecarbamate |
| INV10407230 | 741 | 7 | 8.61 | 0.83 | -0.26 | Putative Membrane Protein Putative |
| INV10400380 | 3726 | 36 | 43.32 | 0.83 | -0.26 | Acetolactate Synthase Small Subunitacetolactate |
| FIG01116303-hypotheticalprotein | 531 | 5 | 6.17 | 0.84 | -0.26 | FIG01114970: Hypothetical Proteinfig01114970: |
| INV10406430 | 222 | 2 | 2.58 | 0.84 | -0.25 | Putative Membrane Protein Putative |
| INV10412330 | 936 | 9 | 10.88 | 0.84 | -0.25 | Putative Membrane Protein (Pseudogene) Putative |
| INV10415800 | 1746 | 17 | 20.3 | 0.85 | -0.24 | Conserved Hypothetical Proteinconserved |
| lacC2 | 931 | 9 | 10.82 | 0.85 | -0.24 | DHH Family Proteindhh |
| INV10408060 | 1236 | 12 | 14.37 | 0.85 | -0.24 | Phage/Plasmid Maintenance Toxin/Antidote System Protein (Toxin)Phage/Plasmid |
| aroF1 | 1032 | 10 | 12 | 0.85 | -0.24 | Chorismate Synthasechorismate |
| INV10400710 | 930 | 9 | 10.81 | 0.85 | -0.24 | Putative IS1167 Transposase (Pseudogene) Putative |
| mtsA | 930 | 9 | 10.81 | 0.85 | -0.24 | Prolipoprotein Diacylglyceryl Transferaseprolipoprotein |
| INV10418070 | 1131 | 11 | 13.15 | 0.85 | -0.24 | Sugar Phosphotransferase System (PTS), Lactose/Cellobiose-Specific Family, IIB Subunit Proteinsugar |
| INV10416160 | 522 | 5 | 6.07 | 0.85 | -0.24 | Putative Laci-Family Transcriptional Regulator (Catabolite Control Protein) Putative |
| trsA | 1026 | 10 | 11.93 | 0.85 | -0.23 | Fes Assembly Protein Sufdfes |
| ftsL | 318 | 3 | 3.7 | 0.85 | -0.23 | Isopentenyl-Diphosphate Delta-Isomeraseisopentenyl-Diphosphate |
| INV10407070 | 1023 | 10 | 11.89 | 0.85 | -0.23 | Putative Uncharacterized Protein Putative |
| trpB | 1224 | 12 | 14.23 | 0.85 | -0.23 | Sortase Srtasortase |
| coaA | 921 | 9 | 10.71 | 0.85 | -0.23 | ATP-Dependent Clp Protease ATP-Binding Subunit Clpxatp-Dependent |
| INV10409440 | 216 | 2 | 2.51 | 0.85 | -0.23 | Putative Exported Protein Putative |
| INV10412950 | 618 | 6 | 7.18 | 0.86 | -0.22 | Putative Membrane Protein (Pseudogene) Putative |
| INV10404810 | 1416 | 14 | 16.46 | 0.86 | -0.22 | Putative Membrane Protein Putative |
| INV10413550 | 1113 | 11 | 12.94 | 0.86 | -0.22 | Putative ATP-Binding Protein Putative |
| INV10413050 | 513 | 5 | 5.96 | 0.86 | -0.21 | Haemolysin-III Related Membrane Proteinhaemolysin-III |
| INV10415700 | 1011 | 10 | 11.75 | 0.86 | -0.21 | Putative Marr-Family Transcriptional Regulator Putative |
| INV10416220 | 711 | 7 | 8.27 | 0.86 | -0.21 | Putative Iron ABC Transporter, ATP-Binding Protein Putative |
| vanZ | 511 | 5 | 5.94 | 0.86 | -0.21 | Tn5252, Relaxasetn5252, |
| INV10415350 | 909 | 9 | 10.57 | 0.86 | -0.21 | Putative Membrane Protein Putative |
| plr | 1008 | 10 | 11.72 | 0.86 | -0.21 | N Utilization Substance Protein B Homolog (Nusb Protein)N |
| Tn916\_transcriptionalregulator\_ putative | 1206 | 12 | 14.02 | 0.87 | -0.21 | 30S Ribosomal Protein S230S |
| INV10416230 | 804 | 8 | 9.35 | 0.87 | -0.2 | Putative Iron ABC Transporter, Solute-Binding Protein Putative |
| INV10401670 | 507 | 5 | 5.89 | 0.87 | -0.2 | Hypothetical Protein (Fragment)Hypothetical |
| INV10417420 | 309 | 3 | 3.59 | 0.87 | -0.2 | Putative P-Loop Hydrolase Putative |
| INV10417430 | 309 | 3 | 3.59 | 0.87 | -0.2 | Putative Membrane Protein Putative |
| scrA | 1884 | 19 | 21.9 | 0.87 | -0.2 | Riboflavin Synthase Alpha Chainriboflavin |
| INV10404110 | 504 | 5 | 5.86 | 0.87 | -0.19 | Hypothetical Proteinhypothetical |
| INV10408120 | 501 | 5 | 5.82 | 0.88 | -0.18 | Putative IS4-Family Transposase (Pseudogene) Putative |
| INV10413380 | 891 | 9 | 10.36 | 0.88 | -0.18 | Conserved Hypothetical Proteinconserved |
| Transcriptionalregulator\_CroCIfamily | 207 | 2 | 2.41 | 0.88 | -0.18 | 30S Ribosomal Protein S1030S |
| INV10410750 | 987 | 10 | 11.47 | 0.88 | -0.18 | Putative Glycogen Biosynthesis Protein Putative |
| INV10410410 | 303 | 3 | 3.52 | 0.88 | -0.18 | Conserved Hypothetical Proteinconserved |
| INV10404920 | 885 | 9 | 10.29 | 0.89 | -0.18 | PAP2 Superfamily Proteinpap2 |
| clpP | 591 | 6 | 6.87 | 0.89 | -0.17 | Putative ATP-Dependent Clp Protease ATP-Binding Subunit Putative |
| pta | 975 | 10 | 11.34 | 0.89 | -0.17 | Glucose-6-Phosphate Isomeraseglucose-6-Phosphate |
| INV10413330 | 780 | 8 | 9.07 | 0.89 | -0.16 | Putative Transposase (Pseudogene) Putative |
| 1158723\_1159406 | 683 | 7 | 7.94 | 0.89 | -0.16 |  |
| INV10410300 | 683 | 7 | 7.94 | 0.89 | -0.16 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10400590 | 297 | 3 | 3.45 | 0.9 | -0.15 | Integraseintegrase |
| INV10404310 | 201 | 2 | 2.34 | 0.9 | -0.15 | Putative Aspartokinase Putative |
| cbpD | 1347 | 14 | 15.66 | 0.9 | -0.15 | Catabolite Control Protein Acatabolite |
| INV10407370 | 3351 | 35 | 38.96 | 0.9 | -0.15 | DJ-1/Pfpi Family Proteindj-1/Pfpi |
| INV10406960 | 582 | 6 | 6.77 | 0.9 | -0.15 | SAM-Dependent Methyltransferasesam-Dependent |
| INV10411790 | 486 | 5 | 5.65 | 0.9 | -0.15 | Putative Membrane Protein Putative |
| INV10409240 | 867 | 9 | 10.08 | 0.9 | -0.15 | Putative Cytochrome C-Type Biogenesis Protein Putative |
| 680188\_681241 | 1053 | 11 | 12.24 | 0.91 | -0.14 |  |
| INV10406400 | 483 | 5 | 5.62 | 0.91 | -0.14 | Putative Uncharacterized Protein Putative |
| INV10405350 | 198 | 2 | 2.3 | 0.91 | -0.14 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10402730 | 1902 | 20 | 22.11 | 0.91 | -0.14 | Putative Phosphoribulokinase Putative |
| INV10418370 | 858 | 9 | 9.98 | 0.91 | -0.13 | Putative Membrane Protein Putative |
| INV10400570 | 855 | 9 | 9.94 | 0.91 | -0.13 | Integraseintegrase |
| Tn5252\_Orf23 | 855 | 9 | 9.94 | 0.91 | -0.13 | DNA-Directed RNA Polymerase Beta' Chaindna-Directed |
| IS861\_transposase(orf1)\_IS3family\_truncated | 196 | 2 | 2.28 | 0.91 | -0.13 | Isoprenylcysteine Carboxyl Methyltransferase (ICMT) Family Proteinisoprenylcysteine |
| ftsW | 1230 | 13 | 14.3 | 0.92 | -0.13 | Putative Putative Folylpolyglutamate Synthase Putative |
| INV10418570 | 1512 | 16 | 17.58 | 0.92 | -0.13 | Marr Family Regulatory Proteinmarr |
| INV10410870 | 945 | 10 | 10.99 | 0.92 | -0.12 | Putative Multidrug Resistance Protein Putative |
| INV10401270 | 570 | 6 | 6.63 | 0.92 | -0.12 | Padr-Like Family Regulatory Proteinpadr-Like |
| Transketolase(EC2 | 1971 | 21 | 22.91 | 0.92 | -0.12 | 30S Ribosomal Protein S1730S |
| gloA | 381 | 4 | 4.43 | 0.92 | -0.12 | Methyltransferase Gidbmethyltransferase |
| INV10415180 | 381 | 4 | 4.43 | 0.92 | -0.12 | Putative Permease Component Of ABC Transporter Putative |
| bacA | 846 | 9 | 9.84 | 0.92 | -0.12 | ATP Synthase Gamma Chainatp |
| INV10414050 | 2709 | 29 | 31.49 | 0.92 | -0.12 | Putative Exported Choline-Binding Glycosyl Hydrolase Putative |
| INV10412100 | 750 | 8 | 8.72 | 0.93 | -0.11 | Conserved Hypothetical Proteinconserved |
| INV10410830 | 657 | 7 | 7.64 | 0.93 | -0.11 | Voltage Gated Chloride Channel Family Proteinvoltage |
| phtE | 564 | 6 | 6.56 | 0.93 | -0.11 | Glutaredoxin-Like Proteinglutaredoxin-Like |
| ppc | 2697 | 29 | 31.36 | 0.93 | -0.11 | Penicillin-Binding Protein 1Bpenicillin-Binding |
| INV10408600 | 1392 | 15 | 16.18 | 0.93 | -0.1 | Sprt-Like Proteinsprt-Like |
| srtA | 744 | 8 | 8.65 | 0.93 | -0.1 | 50S Ribosomal Protein L950S |
| INV10413310 | 375 | 4 | 4.36 | 0.93 | -0.1 |  |
| INV10408140 | 1112 | 12 | 12.93 | 0.93 | -0.1 | Putative Repressor Protein (Pseudogene) Putative |
| INV10404130 | 651 | 7 | 7.57 | 0.93 | -0.1 | Ribonuclease Hiiiribonuclease |
| INV10405340 | 282 | 3 | 3.28 | 0.93 | -0.1 | 6-Phospho-Beta-Glucosidase6-Phospho-Beta-Glucosidase |
| INV10405450 | 558 | 6 | 6.49 | 0.93 | -0.1 | Putative Transposase (Fragment) Putative |
| INV10414640 | 1200 | 13 | 13.95 | 0.94 | -0.09 | Metallo-Beta-Lactamase Superfamily Proteinmetallo-Beta-Lactamase |
| ccmA | 648 | 7 | 7.53 | 0.94 | -0.09 | CCA-Adding Enzymecca-Adding |
| INV10404800 | 1839 | 20 | 21.38 | 0.94 | -0.09 | Conserved Hypothetical Proteinconserved |
| INV10404590 | 372 | 4 | 4.32 | 0.94 | -0.09 | Hypothetical Protein (Pseudogene)Hypothetical |
| INV10412360 | 828 | 9 | 9.63 | 0.94 | -0.09 | Conserved Hypothetical Proteinconserved |
| INV10416800 | 2016 | 22 | 23.44 | 0.94 | -0.09 | Putative Extracellular Oligopeptide-Binding Protein Putative |
| INV10413640 | 462 | 5 | 5.37 | 0.94 | -0.09 | Conserved Hypothetical Protein (Pseudogene)Conserved |
| INV10417090 | 642 | 7 | 7.46 | 0.95 | -0.08 | Putative ABC Transporter, ATP-Binding/Permease Protein (Pseudogene) Putative |
| trcF | 3511 | 39 | 40.82 | 0.96 | -0.06 | 30S Ribosomal Protein S2030S |
| INV10410840 | 633 | 7 | 7.36 | 0.96 | -0.06 | Tyrosine Recombinase Xerctyrosine |
| metE | 2250 | 25 | 26.16 | 0.96 | -0.06 | Galactose-6-Phosphate Isomerase Laca Subunitgalactose-6-Phosphate |
| INV10416540 | 363 | 4 | 4.22 | 0.96 | -0.06 | ABC-Type Glycine Betaine Transport System ATP-Binding Protein ABC-Type |
| INV10404240 | 4941 | 55 | 57.44 | 0.96 | -0.06 | Sodium:Alanine Symporter Family Proteinsodium:Alanine |
| punA | 810 | 9 | 9.42 | 0.96 | -0.06 | Phage Holinphage |
| INV10409740 | 541 | 6 | 6.29 | 0.96 | -0.06 | Alpha-Amylase (Pseudogene)Alpha-Amylase |
| trmD | 720 | 8 | 8.37 | 0.96 | -0.06 | Holliday Junction DNA Helicase Ruvaholliday |
| INV10400740 | 987 | 11 | 11.47 | 0.96 | -0.06 | Deoxyuridine 5'-Triphosphate Nucleotidohydrolasedeoxyuridine |
| INV10414340 | 1518 | 17 | 17.65 | 0.97 | -0.05 | FAD Dependent Oxidoreductasefad |
| fms | 270 | 3 | 3.14 | 0.97 | -0.05 | FIG01116987: Hypothetical Proteinfig01116987: |
| nfsA | 715 | 8 | 8.31 | 0.97 | -0.05 | Trna Delta(2)-Isopentenylpyrophosphate Transferasetrna |
| INV10412470 | 447 | 5 | 5.2 | 0.97 | -0.05 | Putative Membrane Protein Putative |
| scrK | 888 | 10 | 10.32 | 0.97 | -0.04 | Ribosomal RNA Large Subunit Methyltransferase N (EC 2.1.1.-)Ribosomal |
| INV10404030 | 1413 | 16 | 16.43 | 0.98 | -0.04 | Putative Membrane Protein Putative |
| INV10416550 | 972 | 11 | 11.3 | 0.98 | -0.04 | Conserved Hypothetical Proteinconserved |
| INV10404010 | 1323 | 15 | 15.38 | 0.98 | -0.03 | Conserved Hypothetical Proteinconserved |
| INV10405670 | 969 | 11 | 11.27 | 0.98 | -0.03 | Putative Protease Putative |
| INV10414190 | 705 | 8 | 8.2 | 0.98 | -0.03 | Putative Acetyltransferase (GNAT) Family Protein Putative |
| cbpA | 1752 | 20 | 20.37 | 0.98 | -0.03 | Carbamoyl-Phosphate Synthase Large Chaincarbamoyl-Phosphate |
| Phagehyaluronidase | 613 | 7 | 7.13 | 0.98 | -0.02 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10407670 | 873 | 10 | 10.15 | 0.99 | -0.02 | Putative Amino Acid ABC Transporter Permease Protein Putative |
| Cytidinedeoxycytidylatedeaminasefamilyprotein | 435 | 5 | 5.06 | 0.99 | -0.01 | Serine Acetyltransferaseserine |
| INV10409450 | 348 | 4 | 4.05 | 0.99 | -0.01 | Putative RNA Methyltransferase Putative |
| tRNA-Leu-AAG | 87 | 1 | 1.01 | 0.99 | -0.01 | Sensor Histidine Kinasesensor |
| INV10416750 | 519 | 6 | 6.03 | 1 | -0.01 | Putative Substrate-Binding Protein (Pseudogene) Putative |
| INV10415270 | 951 | 11 | 11.06 | 1 | -0.01 | Putative Membrane Protein Putative |
| INV10408860 | 432 | 5 | 5.02 | 1 | 0 | Saccharopine Dehydrogenase Family Proteinsaccharopine |
| INV10414550 | 345 | 4 | 4.01 | 1 | 0 | Putative Metallophosphoesterase Protein Putative |
| Glucosamine--fructose-6-phosphateaminotransferase[isomerizing](EC2 | 1809 | 21 | 21.03 | 1 | 0 | Putative Glycogen Phosphorylase Putative |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposasetransposase |
|  |  |  | 0 | 1 | 0 | Transposase And Inactivated Derivativetransposase |
|  |  |  | 0 | 1 | 0 | Transposase And Inactivated Derivativetransposase |
|  |  |  | 0 | 1 | 0 | Putative Putative Transcription-Repair Coupling Factor Putative |
|  |  |  | 0 | 1 | 0 | Putative Trehalose-6-Phosphate Hydrolase Putative |
|  |  |  | 0 | 1 | 0 | Gntr-Family Transcriptional Regulatorgntr-Family |
|  |  |  | 0 | 1 | 0 | Trna (Guanine-N(1)-)-Methyltransferasetrna |
|  |  |  | 0 | 1 | 0 | Trna Modification Gtpase Trmetrna |
|  |  |  | 0 | 1 | 0 | Trna-Arg-Acgtrna-Arg-ACG |
|  |  |  | 0 | 1 | 0 | Trna-Arg-Acgtrna-Arg-ACG |
|  |  |  | 0 | 1 | 0 | Trna-Arg-Ccgtrna-Arg-CCG |
|  |  |  | 0 | 1 | 0 | Trna-Arg-Ccttrna-Arg-CCT |
|  |  |  | 0 | 1 | 0 | Trna-Arg-Tcttrna-Arg-TCT |
|  |  |  | 0 | 1 | 0 | Trna-Asn-Gtttrna-Asn-GTT |
|  |  |  | 0 | 1 | 0 | Trna-Asn-Gtttrna-Asn-GTT |
|  |  |  | 0 | 1 | 0 | Trna-Cys-Gcatrna-Cys-GCA |
|  |  |  | 0 | 1 | 0 | Trna-Gln-Ttgtrna-Gln-TTG |
|  |  |  | 0 | 1 | 0 | Trna-Gln-Ttgtrna-Gln-TTG |
|  |  |  | 0 | 1 | 0 | Trna-Glu-Ttctrna-Glu-TTC |
|  |  |  | 0 | 1 | 0 | Trna-Glu-Ttctrna-Glu-TTC |
|  |  |  | 0 | 1 | 0 | Trna-Glu-Ttctrna-Glu-TTC |
|  |  |  | 0 | 1 | 0 | Trna-Gly-Gcctrna-Gly-GCC |
|  |  |  | 0 | 1 | 0 | Trna-Gly-Gcctrna-Gly-GCC |
|  |  |  | 0 | 1 | 0 | Trna-Gly-Tcctrna-Gly-TCC |
|  |  |  | 0 | 1 | 0 | Trna-Gly-Tcctrna-Gly-TCC |
|  |  |  | 0 | 1 | 0 | Trna-His-Gtgtrna-His-GTG |
|  |  |  | 0 | 1 | 0 | Trna-Ile-Gattrna-Ile-GAT |
|  |  |  | 0 | 1 | 0 | Trna-Ile-Gattrna-Ile-GAT |
|  |  |  | 0 | 1 | 0 | Trna-Leu-Aagtrna-Leu-AAG |
|  |  |  | 0 | 1 | 0 | Trna-Leu-Caatrna-Leu-CAA |
|  |  |  | 0 | 1 | 0 | Trna-Leu-Taatrna-Leu-TAA |
|  |  |  | 0 | 1 | 0 | Trna-Leu-Taatrna-Leu-TAA |
|  |  |  | 0 | 1 | 0 | Trna-Met-Cattrna-Met-CAT |
|  |  |  | 0 | 1 | 0 | Trna-Met-Cattrna-Met-CAT |
|  |  |  | 0 | 1 | 0 | Trna-Met-Cattrna-Met-CAT |
|  |  |  | 0 | 1 | 0 | Trna-Phe-Gaatrna-Phe-GAA |
|  |  |  | 0 | 1 | 0 | Trna-Phe-Gaatrna-Phe-GAA |
|  |  |  | 0 | 1 | 0 | Trna-Pro-Tggtrna-Pro-TGG |
|  |  |  | 0 | 1 | 0 | Trna-Pro-Tggtrna-Pro-TGG |
|  |  |  | 0 | 1 | 0 | Trna-Ser-Gcttrna-Ser-GCT |
|  |  |  | 0 | 1 | 0 | Trna-Ser-Tgatrna-Ser-TGA |
|  |  |  | 0 | 1 | 0 | Trna-Ser-Tgatrna-Ser-TGA |
|  |  |  | 0 | 1 | 0 | Trna-Thr-Ggttrna-Thr-GGT |
|  |  |  | 0 | 1 | 0 | Trna-Trp-Ccatrna-Trp-CCA |
|  |  |  | 0 | 1 | 0 | Trna-Tyr-Gtatrna-Tyr-GTA |
|  |  |  | 0 | 1 | 0 | Trna-Tyr-Gtatrna-Tyr-GTA |
|  |  |  | 0 | 1 | 0 | Trna-Val-Tactrna-Val-TAC |
|  |  |  | 0 | 1 | 0 | Tryptophan Synthase Alpha Chaintryptophan |
|  |  |  | 0 | 1 | 0 | Tryptophan Synthase Beta Chaintryptophan |
|  |  |  | 0 | 1 | 0 | Indole-3-Glycerol Phosphate Synthaseindole-3-Glycerol |
|  |  |  | 0 | 1 | 0 | Anthranilate Phosphoribosyltransferaseanthranilate |
|  |  |  | 0 | 1 | 0 | Anthranilate Synthase Component Ianthranilate |
|  |  |  | 0 | 1 | 0 | N-(5'-Phosphoribosyl)Anthranilate Isomerasen-(5'-Phosphoribosyl)Anthranilate |
|  |  |  | 0 | 1 | 0 | Anthranilate Synthase Component Iianthranilate |
|  |  |  | 0 | 1 | 0 | Tryptophanyl-Trna Synthetasetryptophanyl-Trna |
|  |  |  | 0 | 1 | 0 | Trse-Like Proteintrse-Like |
|  |  |  | 0 | 1 | 0 | Trna Pseudouridine Synthase Atrna |
|  |  |  | 0 | 1 | 0 | Trna Pseudouridine Synthase Btrna |
|  |  |  | 0 | 1 | 0 | Elongation Factor Tselongation |
|  |  |  | 0 | 1 | 0 | Elongation Factor Tu (EF-Tu)Elongation |
|  |  |  | 0 | 1 | 0 | Two-Component Response Regulatortwo-Component |
|  |  |  | 0 | 1 | 0 | Type I Restriction-Modification System, DNA-Methyltransferase Subunit M (EC 2.1.1.72)Type |
|  |  |  | 0 | 1 | 0 | Type I Restriction-Modification System, Specificity Subunit S (EC 3.1.21.3)Type |
|  |  |  | 0 | 1 | 0 | Type I Restriction-Modification System, Specificity Subunit S (EC 3.1.21.3)Type |
|  |  |  | 0 | 1 | 0 | Prephenate Dehydrogenaseprephenate |
|  |  |  | 0 | 1 | 0 | Putative Tyrosyl-Trna Synthetase Putative |
|  |  |  | 0 | 1 | 0 | Uridine Kinaseuridine |
|  |  |  | 0 | 1 | 0 | UDP-Glucose 4-Epimerase (EC 5.1.3.2)UDP-Glucose |
|  |  |  | 0 | 1 | 0 | UDP-Glucose 6-Dehydrogenaseudp-Glucose |
|  |  |  | 0 | 1 | 0 | UDP-Glucose 6-Dehydrogenase Ugdudp-Glucose |
|  |  |  | 0 | 1 | 0 | Putative Unsaturated Glucuronyl Hydrolase Putative |
|  |  |  | 0 | 1 | 0 | Undecaprenyl Pyrophosphate Phosphataseundecaprenyl |
|  |  |  | 0 | 1 | 0 | Undecaprenyl Pyrophosphate Synthetase (EC 2.5.1.31)Undecaprenyl |
|  |  |  | 0 | 1 | 0 | Uracil-DNA Glycosylaseuracil-DNA |
|  |  |  | 0 | 1 | 0 | Unknownunknown |
|  |  |  | 0 | 1 | 0 | Unknownunknown |
|  |  |  | 0 | 1 | 0 | Uracil Phosphoribosyltransferaseuracil |
|  |  |  | 0 | 1 | 0 | USG Proteinusg |
|  |  |  | 0 | 1 | 0 | Uvrabc System Protein A (Uvra Protein)Uvrabc |
|  |  |  | 0 | 1 | 0 | Uvrabc System Protein B (Uvrb Protein)Uvrabc |
|  |  |  | 0 | 1 | 0 | Uvrabc DNA Repair System Protein Cuvrabc |
|  |  |  | 0 | 1 | 0 | Valyl-Trna Synthetasevalyl-Trna |
|  |  |  | 0 | 1 | 0 | Putative Vanz-Family Resistance Protein Putative |
|  |  |  | 0 | 1 | 0 | Conserved Hypothetical Proteinconserved |
|  |  |  | 0 | 1 | 0 | Sensor Histidine Kinasesensor |
|  |  |  | 0 | 1 | 0 | Response Regulator Proteinresponse |
|  |  |  | 0 | 1 | 0 | Metallo-Beta-Lactamase Superfamily Proteinmetallo-Beta-Lactamase |
|  |  |  | 0 | 1 | 0 | Galacturonosyl Transferasegalacturonosyl |
|  |  |  | 0 | 1 | 0 | Galacturonic Acid Acetyl Transferasegalacturonic |
|  |  |  | 0 | 1 | 0 | Putative Glycosyl Transferase Putative |
|  |  |  | 0 | 1 | 0 | Capsular Polysaccharide Biosynthesis Protein Wzdcapsular |
|  |  |  | 0 | 1 | 0 | Tyrosine-Protein Kinase Wzetyrosine-Protein |
|  |  |  | 0 | 1 | 0 | Integral Membrane Regulatory Protein Wzgintegral |
|  |  |  | 0 | 1 | 0 | Protein-Tyrosine Phosphatase Wzhprotein-Tyrosine |
|  |  |  | 0 | 1 | 0 | Flippase Wzxflippase |
|  |  |  | 0 | 1 | 0 | Oligosaccharide Repeat Unit Polymerase Wzyoligosaccharide |
|  |  |  | 0 | 1 | 0 | Tyrosine Recombinase Xerdtyrosine |
|  |  |  | 0 | 1 | 0 | Putative Xanthine Phosphoribosyltransferase Putative |
|  |  |  | 0 | 1 | 0 | Putative Exodeoxyribonuclease VII Large Subunit Putative |
|  |  |  | 0 | 1 | 0 | Putative Exodeoxyribonuclease VII Small Subunit Putative |
|  |  |  | 0 | 1 | 0 | Zeta Toxinzeta |
|  |  |  | 0 | 1 | 0 | Zeta Toxinzeta |
|  |  |  | 0 | 1 | 0 | Zinc Metalloprotease Zmpb Precursor (EC 3.4.24.-)Zinc |
|  |  |  | 0 | 1 | 0 | Iga-Proteaseiga-Protease |
|  |  |  | 0 | 1 | 0 | Zinc Metalloprotease Bzinc |
|  |  |  | 0 | 1 | 0 | Glucose-6-Phosphate 1-Dehydrogenaseglucose-6-Phosphate |
| INV10412550 | 258 | 3 | 3 | 1 | 0 | Nicotinate Phosphoribosyltransferase (Naprtase) Family Proteinnicotinate |
| INV10405470 | 1461 | 17 | 16.99 | 1 | 0 | ABC Transporter, ATP-Binding Protein ABC |
| INV10416250 | 945 | 11 | 10.99 | 1 | 0 | Hypotheical Proteinhypotheical |
| INV10408910 | 1632 | 19 | 18.97 | 1 | 0 | Haloacid Dehalogenase-Like Hydrolasehaloacid |
| INV10401240 | 1374 | 16 | 15.97 | 1 | 0 | Putative Membrane Protein Putative |
| INV10416710 | 1372 | 16 | 15.95 | 1 | 0 | ABC Transporter ATP-Binding Protein ABC |
| MultidrugresistanceeffluxpumpPmrA | 1200 | 14 | 13.95 | 1 | 0 | DNA Ligasedna |
| Positivetranscriptionalregulator\_MutRfamily | 854 | 10 | 9.93 | 1.01 | 0.01 | Oxygen-Insensitive NAD(P)H Nitroreductase (EC 1.-.-.-) / Dihydropteridine Reductase (EC 1.5.1.34)Oxygen-Insensitive |
| groEL | 1623 | 19 | 18.87 | 1.01 | 0.01 | Glucosamine--Fructose-6-Phosphate Aminotransferase [Isomerizing] (EC 2.6.1.16)Glucosamine--Fructose-6-Phosphate |
| accA | 768 | 9 | 8.93 | 1.01 | 0.01 | Acetyl-Coenzyme A Carboxylase Carboxyl Transferase Subunit Alphaacetyl-Coenzyme |
| FIG01114020-hypotheticalprotein | 597 | 7 | 6.94 | 1.01 | 0.01 | Ferrochelatase, Protoheme Ferro-Lyase (EC 4.99.1.1)Ferrochelatase, |
| INV10400870 | 170 | 2 | 1.98 | 1.01 | 0.01 | Bacteriocin Transport Accessory Proteinbacteriocin |
| INV10405720 | 255 | 3 | 2.96 | 1.01 | 0.01 | Putative Uncharacterized Protein Putative |
| INV10405840 | 765 | 9 | 8.89 | 1.01 | 0.02 | ABC Transporter ATP-Binding Protein ABC |
| INV10413690 | 339 | 4 | 3.94 | 1.01 | 0.02 | Conserved Hypothetical Proteinconserved |
| aspC | 1188 | 14 | 13.81 | 1.01 | 0.02 | Asparaginyl-Trna Synthetaseasparaginyl-Trna |
| nusB | 423 | 5 | 4.92 | 1.01 | 0.02 | Phospho-N-Acetylmuramoyl-Pentapeptide-Transfera Sephospho-N-Acetylmuramoyl-Pentapeptide-Transfera |
| INV10407800 | 504 | 6 | 5.86 | 1.02 | 0.03 | Putative Extracellular Oligopeptide-Binding Protein Putative |
| INV10416530 | 504 | 6 | 5.86 | 1.02 | 0.03 | ABC-Type Glycine Betaine Transport System Protein ABC-Type |
| ZincmetalloproteasezmpBprecursor(EC3 | 5214 | 62 | 60.62 | 1.02 | 0.03 | Transcription Regulator, Probabletranscription |
| INV10412250 | 585 | 7 | 6.8 | 1.03 | 0.04 | Putative Membrane Protein Putative |
| INV10416660 | 585 | 7 | 6.8 | 1.03 | 0.04 | Putative Phosphoesterase Putative |
| nanB | 2093 | 25 | 24.33 | 1.03 | 0.04 | Methionyl-Trna Synthetasemethionyl-Trna |
| INV10416600 | 333 | 4 | 3.87 | 1.03 | 0.04 | Putative Iron Compound ABC Transporter, Permease Protein Putative |
| INV10417930 | 249 | 3 | 2.89 | 1.03 | 0.04 | Putative Membrane Protein Putative |
| INV10412230 | 1755 | 21 | 20.4 | 1.03 | 0.04 | Putative Uncharacterized Protein Putative |
| INV10413840 | 165 | 2 | 1.92 | 1.03 | 0.04 | ABC Transporter ATP-Binding Protein ABC |
| INV10415390 | 165 | 2 | 1.92 | 1.03 | 0.04 | Putative IS1381 Transposase Orfa (Pseudogene) Putative |
| INV10413940 | 414 | 5 | 4.81 | 1.03 | 0.05 | Conserved Hypothetical Proteinconserved |
| INV10412420 | 744 | 9 | 8.65 | 1.04 | 0.05 | Putative Phosphate ABC Transporter Permease Protein Putative |
| INV10414940 | 909 | 11 | 10.57 | 1.04 | 0.05 | Putative Transport System Permease Putative |
| ABCtransporterpermeaseprotein | 738 | 9 | 8.58 | 1.04 | 0.06 | ABC Transporter Permease Protein ABC |
| INV10418600 | 900 | 11 | 10.46 | 1.05 | 0.07 | Multi Antimicrobial Extrusion (MATE) Family Transportermulti |
| scpA | 729 | 9 | 8.48 | 1.06 | 0.08 | Putative Riboflavin Biosynthesis Protein Putative |
| INV10402090 | 321 | 4 | 3.73 | 1.06 | 0.08 | Putative Membrane Protein Putative |
| INV10406500 | 321 | 4 | 3.73 | 1.06 | 0.08 | Putative Amino-Acid ABC Transporter Integral Membrane Protein Putative |
| INV10410950 | 804 | 10 | 9.35 | 1.06 | 0.09 | Putative Aldose 1-Epimerase 2 (Pseudogene) Putative |
| hemH | 721 | 9 | 8.38 | 1.07 | 0.09 | Gp5gp5 |
| INV10402600 | 477 | 6 | 5.55 | 1.07 | 0.1 | Conserved Hypothetical Proteinconserved |
| INV10413710 | 477 | 6 | 5.55 | 1.07 | 0.1 | Putative S1 RNA Binding Domain Protein Putative |
| INV10406540 | 1200 | 15 | 13.95 | 1.07 | 0.1 | Putative Membrane Protein Putative |
| INV10416910 | 1038 | 13 | 12.07 | 1.07 | 0.1 | Conserved Hypothetical Proteinconserved |
| FIG01115377-hypotheticalprotein | 315 | 4 | 3.66 | 1.07 | 0.1 | FIG01114205: Hypothetical Proteinfig01114205: |
| folE | 555 | 7 | 6.45 | 1.07 | 0.1 | FIG01118148: Hypothetical Proteinfig01118148: |
| tRNA-Asn-GTT | 74 | 1 | 0.86 | 1.08 | 0.1 | Putative Sucrose-Specific Phosphotransferase System (PTS), IIABC Component Putative |
| tRNA-Val-TAC | 74 | 1 | 0.86 | 1.08 | 0.1 | Regulatory Protein Spxregulatory |
| INV10416810 | 633 | 8 | 7.36 | 1.08 | 0.11 | Putative Polysaccharide Repeat Unit Polymerase Putative |
| INV10408660 | 553 | 7 | 6.43 | 1.08 | 0.11 | Putative Membrane Protein Putative |
| kgdA | 630 | 8 | 7.32 | 1.08 | 0.11 | ABC Transporter, ATP-Binding Protein ABC |
| INV10414920 | 1107 | 14 | 12.87 | 1.08 | 0.11 | Conserved Hypothetical Proteinconserved |
| INV10415450 | 708 | 9 | 8.23 | 1.08 | 0.12 | Conserved Hypothetical Proteinconserved |
| INV10403160 | 5304 | 67 | 61.66 | 1.09 | 0.12 | Putative Arac-Family Transcriptional Regulator Putative |
| FIG01114689-hypotheticalprotein | 231 | 3 | 2.69 | 1.09 | 0.12 | FIG00630611: Hypothetical Proteinfig00630611: |
| gmk | 627 | 8 | 7.29 | 1.09 | 0.12 | Merr Family Regulatory Proteinmerr |
| tRNA-Glu-TTC | 72 | 1 | 0.84 | 1.09 | 0.12 | Putative Sucrose Operon Repressor Putative |
| lysS | 1491 | 19 | 17.33 | 1.09 | 0.13 | IS1167, Transposaseis1167, |
| pspA | 1956 | 25 | 22.74 | 1.1 | 0.13 | Putative Xaa-His Dipeptidase Putative |
| INV10405860 | 699 | 9 | 8.13 | 1.1 | 0.13 | Putative Membrane Protein Putative |
| INV10412310 | 699 | 9 | 8.13 | 1.1 | 0.13 | Conserved Hypothetical Proteinconserved |
| INV10405950 | 540 | 7 | 6.28 | 1.1 | 0.14 | Sugar Phosphotransferase System (PTS), Galactitol-Specific Family, IIC Componentsugar |
| INV10401350 | 459 | 6 | 5.34 | 1.1 | 0.14 |  |
| recG | 2016 | 26 | 23.44 | 1.1 | 0.14 | Putative Immunity Protein Pncm Putative |
| nanA | 3183 | 41 | 37.01 | 1.11 | 0.14 | 5,10-Methylenetetrahydrofolate Reductase5,10-Methylenetetrahydrofolate |
| INV10405890 | 769 | 10 | 8.94 | 1.11 | 0.15 | Putative Uncharacterized Protein Putative |
| INV10418850 | 147 | 2 | 1.71 | 1.11 | 0.15 | Putative Peptidase Putative |
| INV10412590 | 844 | 11 | 9.81 | 1.11 | 0.15 | Putative DNA-Binding Protein Putative |
| INV10413910 | 843 | 11 | 9.8 | 1.11 | 0.15 | Pyridine Nucleotide-Disulphide Oxidoreductase Family Proteinpyridine |
| INV10408570 | 301 | 4 | 3.5 | 1.11 | 0.15 | Putative Membrane Protein Putative |
| lmb | 918 | 12 | 10.67 | 1.11 | 0.16 | Putative Membrane Protein Putative |
| nox | 1380 | 18 | 16.04 | 1.11 | 0.16 | Mobile Element Proteinmobile |
| INV10408620 | 2532 | 33 | 29.44 | 1.12 | 0.16 | Putative Membrane Protein Putative |
| INV10406900 | 1679 | 22 | 19.52 | 1.12 | 0.16 | Putative Glucose-Specific Phosphotransferase System (PTS), IIABC Component Putative |
| INV10414790 | 1065 | 14 | 12.38 | 1.12 | 0.16 | Putative Membrane Protein Putative |
| INV10416030 | 297 | 4 | 3.45 | 1.12 | 0.17 | Putative Lactose/Cellobiose-Specific Phosphotransferase System (PTS), IIA Component Putative |
| INV10405900 | 678 | 9 | 7.88 | 1.13 | 0.17 | Putative Surface-Anchored Serine Protease Putative |
| INV10416210 | 1968 | 26 | 22.88 | 1.13 | 0.18 | Putative Inner Membrane Component Of ABC Transporter Putative |
| INV10407300 | 825 | 11 | 9.59 | 1.13 | 0.18 | Putative NUDIX Family Protein Putative |
| 1879127\_1879496 | 369 | 5 | 4.29 | 1.13 | 0.18 |  |
| INV10400080 | 369 | 5 | 4.29 | 1.13 | 0.18 | Hypothetical Proteinhypothetical |
| INV10417340 | 369 | 5 | 4.29 | 1.13 | 0.18 | Putative DNA-Binding Protein Putative |
| INV10417770 | 369 | 5 | 4.29 | 1.13 | 0.18 | Haloacid Dehalogenase-Like Hydrolasehaloacid |
| INV10407900 | 672 | 9 | 7.81 | 1.13 | 0.18 | Deor Family Regulatory Proteindeor |
| INV10409510 | 897 | 12 | 10.43 | 1.14 | 0.19 | Ferric Siderophore ABC Transporter, Permease Proteinferric |
| INV10412320 | 897 | 12 | 10.43 | 1.14 | 0.19 | Conserved Hypothetical Proteinconserved |
| INV10412010 | 738 | 10 | 8.58 | 1.15 | 0.2 | ABC Transporter, ATP-Binding Protein ABC |
| phpA | 2535 | 34 | 29.47 | 1.15 | 0.2 | Putative Anaerobic Ribonucleoside-Triphosphate Reductase Activating Protein Putative |
| pepC | 1335 | 18 | 15.52 | 1.15 | 0.2 | Mutt/Nudix Family Proteinmutt/Nudix |
| xseB | 213 | 3 | 2.48 | 1.15 | 0.2 | Transcriptional Regulator Orfxtranscriptional |
| INV10414260 | 885 | 12 | 10.29 | 1.15 | 0.2 | Putative Membrane Protein Putative |
| glnQ3 | 735 | 10 | 8.55 | 1.15 | 0.2 | NADP-Specific Glutamate Dehydrogenasenadp-Specific |
| alr | 1104 | 15 | 12.84 | 1.16 | 0.21 | Alanine Racemasealanine |
| pepV | 1401 | 19 | 16.29 | 1.16 | 0.21 | Phosphomevalonate Kinasephosphomevalonate |
| INV10410790 | 360 | 5 | 4.19 | 1.16 | 0.21 | Putative Uncharacterized Protein Putative |
| INV10410850 | 360 | 5 | 4.19 | 1.16 | 0.21 | Putative Lipoate-Protein Ligase A Putative |
| Tn5252\_Orf10protein | 358 | 5 | 4.16 | 1.16 | 0.22 | DNA-Directed RNA Polymerase Beta Chaindna-Directed |
| leuA | 1097 | 15 | 12.75 | 1.16 | 0.22 | Putative Membrane Protein Putative |
| INV10415760 | 2127 | 29 | 24.73 | 1.17 | 0.22 | Putative Oligopeptidase Putative |
| dexB | 1608 | 22 | 18.69 | 1.17 | 0.22 | Degenerate Transposasedegenerate |
| INV10410110 | 576 | 8 | 6.7 | 1.17 | 0.23 | Putative Glycosyltransferase Putative |
| mtsB | 723 | 10 | 8.41 | 1.17 | 0.23 | CTP:Phosphocholine Cytidylyltransferasectp:Phosphocholine |
| INV10400640 | 205 | 3 | 2.38 | 1.18 | 0.24 | S4 Domain Containing Proteins4 |
| INV10413890 | 1074 | 15 | 12.49 | 1.19 | 0.25 | Putative Exported Protein Putative |
| INV10406250 | 711 | 10 | 8.27 | 1.19 | 0.25 | Putative Ribosomal Small Subunit Pseudouridine Synthase A Putative |
| agaV | 492 | 7 | 5.72 | 1.19 | 0.25 | Putative N-Acetylgalactosamine-Specific Phosphotransferase System (PTS), IIB Component Putative |
| tpx | 492 | 7 | 5.72 | 1.19 | 0.25 | 30S Ribosomal Protein S630S |
| INV10412350 | 636 | 9 | 7.39 | 1.19 | 0.25 | Putative Alpha-Amylase Putative |
| valS | 2652 | 37 | 30.83 | 1.19 | 0.26 | Tn5252, Relaxasetn5252, |
| INV10416570 | 346 | 5 | 4.02 | 1.19 | 0.26 | Conserved Hypothetical Proteinconserved |
| INV10408560 | 201 | 3 | 2.34 | 1.2 | 0.26 | Putative Uncharacterized Protein Putative |
| INV10418420 | 201 | 3 | 2.34 | 1.2 | 0.26 | Putative Zinc-Binding Alcohol Dehydrogenase Putative |
| INV10408590 | 558 | 8 | 6.49 | 1.2 | 0.26 | Putative Transcription Accessory Protein Putative |
| INV10417080 | 414 | 6 | 4.81 | 1.2 | 0.27 | Conserved Hypothetical Proteinconserved |
| probablyaromaticringhydroxylatingenzyme\_evidencedbyCOGnitorPaaD-likeprotein(DUF59)involvedinFe-Sclusterassembly | 342 | 5 | 3.98 | 1.21 | 0.27 | Putative Glutamyl-Aminopeptidase Putative |
| INV10414520 | 627 | 9 | 7.29 | 1.21 | 0.27 | Response Regulator Proteinresponse |
| INV10413360 | 912 | 13 | 10.6 | 1.21 | 0.27 | Putative Amino Acid ABC Transporter ATP-Binding Protein Putative |
| INV10410800 | 270 | 4 | 3.14 | 1.21 | 0.27 | Putative Gtpase Protein Putative |
| rpsO | 270 | 4 | 3.14 | 1.21 | 0.27 | Ribosome-Binding Factor Aribosome-Binding |
| INV10404400 | 1050 | 15 | 12.21 | 1.21 | 0.28 | Conserved Hypothetical Proteinconserved |
| fucK | 1404 | 20 | 16.32 | 1.21 | 0.28 | Putative Fructose-Specific Phosphotransferase System (PTS), IIABC Component Putative |
| INV10413870 | 975 | 14 | 11.34 | 1.22 | 0.28 | Conserved Hypothetical Proteinconserved |
| INV10404080 | 549 | 8 | 6.38 | 1.22 | 0.29 | Sensor Histidine Kinasesensor |
| hasC | 900 | 13 | 10.46 | 1.22 | 0.29 | Glutathione Reductaseglutathione |
| tpi | 759 | 11 | 8.82 | 1.22 | 0.29 | 30S Ribosomal Protein S530S |
| INV10416080 | 618 | 9 | 7.18 | 1.22 | 0.29 | Acetyltransferase, GNAT Familyacetyltransferase, |
| INV10412130 | 1461 | 21 | 16.99 | 1.22 | 0.29 | Haloacid Dehalogenase-Like Hydrolasehaloacid |
| exoA | 828 | 12 | 9.63 | 1.22 | 0.29 | Dna/Rna Helicase (Dead/Deah Box Family)Dna/Rna |
| INV10413030 | 195 | 3 | 2.27 | 1.22 | 0.29 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10408890 | 615 | 9 | 7.15 | 1.23 | 0.3 | Porphyromonas-Type Peptidyl-Arginine Deiminaseporphyromonas-Type |
| spi | 615 | 9 | 7.15 | 1.23 | 0.3 | 50S Ribosomal Protein L350S |
| INV10418500 | 2646 | 38 | 30.76 | 1.23 | 0.3 | Acyltransferase Family Proteinacyltransferase |
| INV10407770 | 192 | 3 | 2.23 | 1.24 | 0.31 | ABC Transporter Permease Protein ABC |
| INV10413470 | 678 | 10 | 7.88 | 1.24 | 0.31 | Putative Acetyltransferase Putative |
| Dephospho-CoAkinase(EC2 | 606 | 9 | 7.05 | 1.24 | 0.31 | Degenerate Transposasedegenerate |
| adhP | 1020 | 15 | 11.86 | 1.24 | 0.32 | Alcohol Dehydrogenasealcohol |
| INV10408650 | 536 | 8 | 6.23 | 1.24 | 0.32 | Putative Membrane Protein Putative |
| RibosomalRNAlargesubunitmethyltransferaseN(EC2 | 1086 | 16 | 12.63 | 1.25 | 0.32 | Putative Phosphoenolpyruvate Carboxylase Putative |
| lspA | 462 | 7 | 5.37 | 1.26 | 0.33 | Tetr Family Regulatory Proteintetr |
| manM | 804 | 12 | 9.35 | 1.26 | 0.33 | IS630-Spn1, Transposase Orf2IS630-Spn1, |
| INV10413850 | 324 | 5 | 3.77 | 1.26 | 0.33 | Degv Family Proteindegv |
| INV10406650 | 870 | 13 | 10.11 | 1.26 | 0.33 | Putative Glyoxalase Family Protein Putative |
| Bacteriocin-likepeptideMBlpM | 255 | 4 | 2.96 | 1.26 | 0.34 | Undecaprenol Kinase (Bacitracin Resistance Protein)Undecaprenol |
| INV10415790 | 1752 | 26 | 20.37 | 1.26 | 0.34 | Putative Peptidase Putative |
| 3'-to-5'exoribonucleaseRNaseR | 2355 | 35 | 27.38 | 1.27 | 0.34 | 3'-To-5' Exoribonuclease Rnase R3'-To-5' |
| FIG01115706-hypotheticalprotein | 117 | 2 | 1.36 | 1.27 | 0.35 | FIG01114589: Hypothetical Proteinfig01114589: |
| Transcriptionalregulator | 386 | 6 | 4.49 | 1.28 | 0.35 | 30S Ribosomal Protein S830S |
| INV10414410 | 453 | 7 | 5.27 | 1.28 | 0.35 | Putative Membrane Protein Putative |
| INV10402510 | 318 | 5 | 3.7 | 1.28 | 0.35 | Putative Lipoprotein Putative |
| INV10408000 | 318 | 5 | 3.7 | 1.28 | 0.35 | Putative Cysteine Desulfhydrase Putative |
| INV10415500 | 318 | 5 | 3.7 | 1.28 | 0.35 | Putative Isochorismatase Putative |
| 849941\_850659 | 718 | 11 | 8.35 | 1.28 | 0.36 |  |
| INV10407830 | 718 | 11 | 8.35 | 1.28 | 0.36 | Putative Membrane Protein Putative |
| INV10415550 | 447 | 7 | 5.2 | 1.29 | 0.37 | Conserved Hypothetical Proteinconserved |
| INV10413040 | 513 | 8 | 5.96 | 1.29 | 0.37 | Conserved Hypothetical Proteinconserved |
| INV10412170 | 577 | 9 | 6.71 | 1.3 | 0.38 | Chorismate Mutase Type II Proteinchorismate |
| INV10404320 | 510 | 8 | 5.93 | 1.3 | 0.38 | Enoyl-Coa Hydratase/Isomerase Family Proteinenoyl-Coa |
| INV10402650 | 642 | 10 | 7.46 | 1.3 | 0.38 | Putative Membrane Protein Putative |
| INV10418720 | 774 | 12 | 9 | 1.3 | 0.38 | Putative Lipoprotein Putative |
| INV10404790 | 840 | 13 | 9.77 | 1.3 | 0.38 | Putative Cation Transport Protein Putative |
| INV10418750 | 705 | 11 | 8.2 | 1.3 | 0.38 | ABC Transporter Permease Protein ABC |
| fucU | 441 | 7 | 5.13 | 1.31 | 0.38 | Putative 1-Phosphofructokinase Putative |
| licC | 1296 | 20 | 15.07 | 1.31 | 0.39 | ABC Transporter, ATP-Binding Protein ABC |
| dapB | 768 | 12 | 8.93 | 1.31 | 0.39 | Cysteine ABC Transporter, Substrate-Binding Proteincysteine |
| INV10417330 | 963 | 15 | 11.2 | 1.31 | 0.39 | Putative Uncharacterized Protein Putative |
| INV10413790 | 2337 | 36 | 27.17 | 1.31 | 0.39 | Putative Glutathione S-Transferase Putative |
| INV10415840 | 240 | 4 | 2.79 | 1.32 | 0.4 | Beta-Fructofuranosidasebeta-Fructofuranosidase |
| pstI | 1734 | 27 | 20.16 | 1.32 | 0.4 | Pyruvate Formate-Lyase Activating Enzymepyruvate |
| secA | 2514 | 39 | 29.23 | 1.32 | 0.4 | Glucose-1-Phosphate Thymidylyltransferase Rmlaglucose-1-Phosphate |
| INV10413150 | 366 | 6 | 4.26 | 1.33 | 0.41 | Putative NADPH-Dependent FMN Reductase Putative |
| INV10418580 | 1332 | 21 | 15.49 | 1.33 | 0.42 | Putative Exported Protein Putative |
| rrf | 558 | 9 | 6.49 | 1.34 | 0.42 | Putative Recombination Protein U Putative |
| INV10401130 | 750 | 12 | 8.72 | 1.34 | 0.42 | Histidine Kinase Proteinhistidine |
| acpS | 363 | 6 | 4.22 | 1.34 | 0.42 | Holo-[Acyl-Carrier Protein] Synthaseholo-[Acyl-Carrier |
| INV10417780 | 426 | 7 | 4.95 | 1.34 | 0.43 | Putative Preprotein Translocase Sece Subunit Putative |
| rplK | 426 | 7 | 4.95 | 1.34 | 0.43 | Phosphate Import ATP-Binding Protein 3phosphate |
| cysE | 618 | 10 | 7.18 | 1.34 | 0.43 | Conserved Hypothetical Proteinconserved |
| INV10412140 | 489 | 8 | 5.69 | 1.35 | 0.43 | SAP Domain Proteinsap |
| INV10416640 | 552 | 9 | 6.42 | 1.35 | 0.43 | Conserved Hypothetical Proteinconserved |
| fus | 2082 | 33 | 24.21 | 1.35 | 0.43 | Putative Fructose-6-Phosphate Aldolase 1 Putative |
| INV10407330 | 1123 | 18 | 13.06 | 1.35 | 0.43 | Putative Membrane Protein Putative |
| conjugativetransposonmembraneprotein | 231 | 4 | 2.69 | 1.36 | 0.44 | Competence Protein Coiacompetence |
| pepS | 1242 | 20 | 14.44 | 1.36 | 0.44 | 3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase3-Hydroxy-3-Methylglutaryl-Coenzyme |
| INV10404040 | 1680 | 27 | 19.53 | 1.36 | 0.45 | Putative Major Facilitator Superfamily Protein Putative |
| DNAintegrationrecombinationinvertionprotein | 165 | 3 | 1.92 | 1.37 | 0.45 | D-Alanyl Carrier Proteind-Alanyl |
| INV10407760 | 165 | 3 | 1.92 | 1.37 | 0.45 | ABC Transporter Permease Protein ABC |
| treR | 729 | 12 | 8.48 | 1.37 | 0.46 | Ribosome Recycling Factorribosome |
| Maturase-relatedprotein | 351 | 6 | 4.08 | 1.38 | 0.46 | IS861, Transposase (Orf1), IS3 Family, Truncatedis861, |
| priA | 2397 | 39 | 27.87 | 1.39 | 0.47 | Putative Pyruvate Dehydrogenase E1 Component, Alpha Subunit Putative |
| INV10413350 | 969 | 16 | 11.27 | 1.39 | 0.47 | Putative Amino Acid ABC Transporter, Extracellular Amino Acid-Binding Protein Putative |
| INV10415290 | 471 | 8 | 5.48 | 1.39 | 0.47 | Putative Membrane Protein Putative |
| scrR | 966 | 16 | 11.23 | 1.39 | 0.48 | Ribulose-Phosphate 3-Epimerase (EC 5.1.3.1)Ribulose-Phosphate |
| INV10415280 | 1089 | 18 | 12.66 | 1.39 | 0.48 | Putative Membrane Protein Putative |
| INV10415320 | 1272 | 21 | 14.79 | 1.39 | 0.48 | Gntr Family Regulatory Proteingntr |
| glpO | 1827 | 30 | 21.24 | 1.39 | 0.48 | Glycogen Synthaseglycogen |
| 948567\_979552 | 30985 | 504 | 360.23 | 1.4 | 0.48 |  |
| murE | 1446 | 24 | 16.81 | 1.4 | 0.49 | Lipoprotein Signal Peptidaselipoprotein |
| divIB | 1200 | 20 | 13.95 | 1.4 | 0.49 | Degenerate Transposasedegenerate |
| lctO | 1137 | 19 | 13.22 | 1.41 | 0.49 | Putative Cobalt Transport Protein Putative |
| INV10415330 | 1320 | 22 | 15.35 | 1.41 | 0.49 | ABC Transporter ATP-Binding Protein ABC |
| INV10402610 | 3204 | 53 | 37.25 | 1.41 | 0.5 | Putative Folylpolyglutamate Synthase Putative |
| INV10417360 | 1311 | 22 | 15.24 | 1.42 | 0.5 | Putative Cell Wall-Binding Amidase Putative |
| INV10415820 | 458 | 8 | 5.32 | 1.42 | 0.51 | Putative Atpase Putative |
| INV10403890 | 216 | 4 | 2.51 | 1.42 | 0.51 | Putative Membrane Protein Putative |
| pyrD | 939 | 16 | 10.92 | 1.43 | 0.51 | Phosphoenolpyruvate-Dihydroxyacetone Phosphotransferase (EC 2.7.1.121), Subunit Dham; DHA-Specific IIA Componentphosphoenolpyruvate-Dihydroxyacetone |
| thiE | 633 | 11 | 7.36 | 1.44 | 0.52 | 50S Ribosomal Protein L2450S |
| dapA | 573 | 10 | 6.66 | 1.44 | 0.52 | Cysteinyl-Trna Synthetasecysteinyl-Trna |
| ogt | 513 | 9 | 5.96 | 1.44 | 0.52 | Large-Conductance Mechanosensitive Channellarge-Conductance |
| rpsI | 393 | 7 | 4.57 | 1.44 | 0.52 | Dihydroorotate Dehydrogenase Electron Transfer Subunitdihydroorotate |
| INV10404870 | 213 | 4 | 2.48 | 1.44 | 0.52 | Putative Membrane Protein Putative |
| INV10405230 | 93 | 2 | 1.08 | 1.44 | 0.53 | Putative Uncharacterized Protein Putative |
| gcnA | 1881 | 32 | 21.87 | 1.44 | 0.53 | Fuculose-1-Phosphate Aldolasefuculose-1-Phosphate |
| INV10414360 | 1104 | 19 | 12.84 | 1.45 | 0.53 | Conserved Hypothetical Proteinconserved |
| phageprotein | 330 | 6 | 3.84 | 1.45 | 0.53 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10400720 | 924 | 16 | 10.74 | 1.45 | 0.53 | Conserved Hypothetical Proteinconserved |
| INV10407390 | 686 | 12 | 7.98 | 1.45 | 0.53 | Putative Haloacid Dehalogenase-Like Hydrolase Putative |
| 778203\_779542 | 1339 | 23 | 15.57 | 1.45 | 0.53 |  |
| INV10405410 | 626 | 11 | 7.28 | 1.45 | 0.54 | Putative Ribomuclease Putative |
| INV10416960 | 741 | 13 | 8.61 | 1.46 | 0.54 | Putative Trna-Binding Protein Putative |
| pyrH | 738 | 13 | 8.58 | 1.46 | 0.55 | Pneumococcal Histidine Triad Protein E (Bvh-3)Pneumococcal |
| Tn5252\_relaxase | 1830 | 32 | 21.28 | 1.48 | 0.57 | Putative DNA-Directed RNA Polymerase, Delta Subunit Putative |
| INV10408990 | 261 | 5 | 3.03 | 1.49 | 0.57 | Conserved Hypothetical Proteinconserved |
| INV10418680 | 434 | 8 | 5.05 | 1.49 | 0.57 | Conserved Hypothetical Proteinconserved |
| INV10416980 | 894 | 16 | 10.39 | 1.49 | 0.58 | Putative Exported Protein Putative |
| Macrolide-effluxprotein | 1231 | 22 | 14.31 | 1.5 | 0.59 | IS1380-Spn1, Transposaseis1380-Spn1, |
| mvaS | 1173 | 21 | 13.64 | 1.5 | 0.59 | Putative Mannose-Specific Phosphotransferase System (PTS), IID Component Putative |
| 1882167\_1882309 | 142 | 3 | 1.65 | 1.51 | 0.59 |  |
| INV10417370 | 142 | 3 | 1.65 | 1.51 | 0.59 | Putative Drug/Sodium Antiporter Putative |
| INV10415670 | 369 | 7 | 4.29 | 1.51 | 0.6 | Putative Sodium:Dicarboxylate Symporter Family Protein Putative |
| INV10416240 | 878 | 16 | 10.21 | 1.52 | 0.6 | Hypotheical Proteinhypotheical |
| INV10403860 | 365 | 7 | 4.24 | 1.53 | 0.61 | Laci Family Regulatory Proteinlaci |
| purD | 1263 | 23 | 14.68 | 1.53 | 0.61 | Phage Major Tail Proteinphage |
| INV10413830 | 528 | 10 | 6.14 | 1.54 | 0.62 | Cation Efflux Family Proteincation |
| INV10400730 | 1476 | 27 | 17.16 | 1.54 | 0.62 | Putative Deaminase Putative |
| INV10405430 | 360 | 7 | 4.19 | 1.54 | 0.62 |  |
| INV10400750 | 861 | 16 | 10.01 | 1.54 | 0.63 | Putative Phosphoglycerate Mutase Family Protein Putative |
| INV10406920 | 525 | 10 | 6.1 | 1.55 | 0.63 | Putative Helicase Putative |
| INV10408090 | 855 | 16 | 9.94 | 1.55 | 0.64 | Putative Integrase/Recombinase Putative |
| INV10412370 | 1073 | 20 | 12.47 | 1.56 | 0.64 | Putative Membrane Protein Putative |
| epuA | 189 | 4 | 2.2 | 1.56 | 0.64 | DNA Replication Protein Dnacdna |
| dnaI | 897 | 17 | 10.43 | 1.58 | 0.66 | Putative Activated D-Alanine Transport Protein Putative |
| purF | 1443 | 27 | 16.78 | 1.58 | 0.66 | Phage Proteinphage |
| uvrB | 1989 | 37 | 23.12 | 1.58 | 0.66 | Tn5252, Orf23tn5252, |
| INV10417140 | 895 | 17 | 10.41 | 1.58 | 0.66 | Putative Uncharacterized Protein Putative |
| mvaA | 1275 | 24 | 14.82 | 1.58 | 0.66 | Maltose Operon Transcriptional Repressormaltose |
| INV10407930 | 888 | 17 | 10.32 | 1.59 | 0.67 | Putative Membrane Protein Putative |
| aqpZ | 669 | 13 | 7.78 | 1.59 | 0.67 | Aquaporin Zaquaporin |
| INV10414880 | 501 | 10 | 5.82 | 1.61 | 0.69 | Putative Transcription Regulator Putative |
| INV10414440 | 981 | 19 | 11.41 | 1.61 | 0.69 | Conserved Hypothetical Protein (Pseudogene)Conserved |
| INV10412540 | 1246 | 24 | 14.49 | 1.61 | 0.69 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10405370 | 498 | 10 | 5.79 | 1.62 | 0.7 | Putative IS1239 Transposase (Pseudogene) Putative |
| INV10402580 | 177 | 4 | 2.06 | 1.64 | 0.71 | Conserved Hypothetical Proteinconserved |
| INV10419330 | 490 | 10 | 5.7 | 1.64 | 0.72 | Putative PTS System, Mannose-Specific IIAB Component Putative |
| INV10416930 | 540 | 11 | 6.28 | 1.65 | 0.72 | Putative Single Stranded DNA-Binding Protein Putative |
| ProteinofunknownfunctionDUF208 | 328 | 7 | 3.81 | 1.66 | 0.73 | Aminopeptidase Pepsaminopeptidase |
| INV10418590 | 532 | 11 | 6.19 | 1.67 | 0.74 | Putative Haloacid Dehalogenase-Like Hydrolase Putative |
| holB | 891 | 18 | 10.36 | 1.67 | 0.74 | 60 Kda Chaperonin60 |
| dnaG | 1761 | 35 | 20.47 | 1.68 | 0.75 | Putative Cell Division Protein Divib/Ftsq Putative |
| lacT2 | 837 | 17 | 9.73 | 1.68 | 0.75 | Putative Amidase Putative |
| hypotheticalphageprotein | 426 | 9 | 4.95 | 1.68 | 0.75 | DNA Gyrase Subunit BDNA |
| lacA | 426 | 9 | 4.95 | 1.68 | 0.75 | ABC Transporter, Permease Protein ABC |
| INV10402900 | 1345 | 27 | 15.64 | 1.68 | 0.75 | Putative Permease Component Of ABC Transporter (Pseudogene) Putative |
| leuB | 1038 | 21 | 12.07 | 1.68 | 0.75 | Putative Protease Putative |
| bgaA | 6702 | 132 | 77.92 | 1.69 | 0.75 | Beta-1,3-Glucosyltransferasebeta-1,3-Glucosyltransferase |
| INV10405990 | 1387 | 28 | 16.13 | 1.69 | 0.76 | Putative Uncharacterized Protein Putative |
| INV10413560 | 1227 | 25 | 14.27 | 1.7 | 0.77 | Putative SNF-Family Helicase Putative |
| 1000755\_1001830 | 1075 | 22 | 12.5 | 1.7 | 0.77 |  |
| INV10409390 | 1075 | 22 | 12.5 | 1.7 | 0.77 | Conserved Hypothetical Proteinconserved |
| trpG | 567 | 12 | 6.59 | 1.71 | 0.78 | Putative Fes Assembly Atpase Sufc, ABC Transporter, ATP-Binding Protein Putative |
| murG | 1059 | 22 | 12.31 | 1.73 | 0.79 | LSU Ribosomal Protein L21plsu |
| mraW | 951 | 20 | 11.06 | 1.74 | 0.8 | Lactose Phosphotransferase System Repressor 1lactose |
| adcA | 1247 | 26 | 14.5 | 1.74 | 0.8 | Zinc-Binding Protein Adca Precursorzinc-Binding |
| pyrF | 702 | 15 | 8.16 | 1.75 | 0.8 | Putative Phosphate Transport System Protein Putative |
| FIG01115561-hypotheticalprotein | 995 | 21 | 11.57 | 1.75 | 0.81 | FIG01114502: Hypothetical Proteinfig01114502: |
| rnc | 699 | 15 | 8.13 | 1.75 | 0.81 | Putative Glutamate 5-Kinase Putative |
| INV10406460 | 789 | 17 | 9.17 | 1.77 | 0.82 | Amino-Acid ABC Transporter ATP-Binding Protein (Pseudogene)Amino-Acid |
| INV10405750 | 642 | 14 | 7.46 | 1.77 | 0.83 | Putative Uncharacterized Protein Putative |
| FIG01114899-hypotheticalprotein | 591 | 13 | 6.87 | 1.78 | 0.83 | FIG01114045: Hypothetical Proteinfig01114045: |
| gltX | 1461 | 31 | 16.99 | 1.78 | 0.83 | Glucose-1-Phosphate Adenylyltransferaseglucose-1-Phosphate |
| INV10415430 | 204 | 5 | 2.37 | 1.78 | 0.83 | Putative Ribosomal RNA Small Subunit Methyltransferase Putative |
| Integrase | 1509 | 32 | 17.54 | 1.78 | 0.83 | Hypothetical Phage Proteinhypothetical |
| INV10404390 | 732 | 16 | 8.51 | 1.79 | 0.84 | Hypothetical Proteinhypothetical |
| INV10405220 | 153 | 4 | 1.78 | 1.8 | 0.85 | Conserved Hypothetical Proteinconserved |
| INV10410120 | 153 | 4 | 1.78 | 1.8 | 0.85 | Putative Glycosyltransferase Putative |
| INV10415740 | 153 | 4 | 1.78 | 1.8 | 0.85 | Conserved Hypothetical Proteinconserved |
| INV10407080 | 535 | 12 | 6.22 | 1.8 | 0.85 | ATP-Binding Proteinatp-Binding |
| INV10414900 | 630 | 14 | 7.32 | 1.8 | 0.85 | Putative Membrane Protein Putative |
| INV10407700 | 717 | 16 | 8.34 | 1.82 | 0.86 | Putative Cytolysin (Pseudogene) Putative |
| INV10402910 | 995 | 22 | 11.57 | 1.83 | 0.87 | Probable ATP-Binding Component Of ABC Transporterprobable |
| blpA2 | 2158 | 47 | 25.09 | 1.84 | 0.88 | Putative Surface Anchored Beta-Galactosidase Putative |
| rpmH | 54 | 2 | 0.63 | 1.84 | 0.88 | Phosphoribosylglycinamide Formyltransferasephosphoribosylglycinamide |
| INV10413510 | 147 | 4 | 1.71 | 1.85 | 0.88 | Acetyltransferase (GNAT) Family Proteinacetyltransferase |
| INV10416670 | 426 | 10 | 4.95 | 1.85 | 0.89 | HAM1 Protein Homologham1 |
| INV10404410 | 330 | 8 | 3.84 | 1.86 | 0.89 | Putative Glycosyl Transferase (Pseudogene) Putative |
| INV10410140 | 2451 | 54 | 28.5 | 1.86 | 0.9 | Putative Phage Shock Protein Putative |
| 527268\_531467 | 4199 | 92 | 48.82 | 1.87 | 0.9 |  |
| INV10414860 | 741 | 17 | 8.61 | 1.87 | 0.91 | Putative Membrane Protein Putative |
| INV10412110 | 552 | 13 | 6.42 | 1.89 | 0.92 | Putative Phosphohydrolase Putative |
| 527268\_531281 | 4013 | 89 | 46.66 | 1.89 | 0.92 |  |
| IS630-Spn1\_transposaseOrf2 | 141 | 4 | 1.64 | 1.89 | 0.92 | Putative Trna-Dihydrouridine Synthase Putative |
| 1396666\_1397623 | 957 | 22 | 11.13 | 1.9 | 0.92 |  |
| INV10412640 | 957 | 22 | 11.13 | 1.9 | 0.92 | Putative Peptidase Putative |
| INV10403700 | 186 | 5 | 2.16 | 1.9 | 0.93 | Putative Transposase (Pseudogene) Putative |
| engA | 1311 | 30 | 15.24 | 1.91 | 0.93 | Chaperone Protein Dnajchaperone |
| 870453\_871260 | 807 | 19 | 9.38 | 1.93 | 0.95 |  |
| INV10408040 | 807 | 19 | 9.38 | 1.93 | 0.95 | Putative Type I RM Modification Enzyme Putative |
| lacD2 | 981 | 23 | 11.41 | 1.93 | 0.95 | Sigma 54 Modulation Protein / S30EA Ribosomal Proteinsigma |
| INV10405660 | 756 | 18 | 8.79 | 1.94 | 0.96 | Putative Esterase Putative |
| glpF1 | 705 | 17 | 8.2 | 1.96 | 0.97 | Putative Epimerase Putative |
| INV10414140 | 264 | 7 | 3.07 | 1.97 | 0.97 | Pyridine Nucleotide-Disulphide Oxidoreductasepyridine |
| INV10405830 | 351 | 9 | 4.08 | 1.97 | 0.98 | Putative Uncharacterized Protein Putative |
| INV10413740 | 955 | 23 | 11.1 | 1.98 | 0.99 | Conserved Hypothetical Proteinconserved |
| INV10413170 | 432 | 11 | 5.02 | 1.99 | 1 | Conserved Hypothetical Proteinconserved |
| lacB1 | 516 | 13 | 6 | 2 | 1 | Conserved Hypothetical Proteinconserved |
| INV10414530 | 642 | 16 | 7.46 | 2.01 | 1.01 | Conserved Hypothetical Proteinconserved |
| DNARNAHELICASE(DEADDEAHBOXFAMILY) | 2680 | 64 | 31.16 | 2.02 | 1.02 | Replicative DNA Helicasereplicative |
| INV10410760 | 1317 | 32 | 15.31 | 2.02 | 1.02 | Putative Hydrolase (Pseudogene) Putative |
| pheT | 2406 | 58 | 27.97 | 2.04 | 1.03 | Sialidase A (Neuraminidase A)Sialidase |
| INV10410720 | 795 | 20 | 9.24 | 2.05 | 1.04 | Putative Pullulanase Putative |
| INV10408050 | 249 | 7 | 2.89 | 2.05 | 1.04 | Putative Uncharacterized Protein Putative |
| INV10416680 | 249 | 7 | 2.89 | 2.05 | 1.04 | Putative Exported Protein Putative |
| INV10404780 | 81 | 3 | 0.94 | 2.06 | 1.04 | Putative Cation Transport Protein Putative |
| Cellwall-associatedmureinhydrolaseLytA | 957 | 24 | 11.13 | 2.06 | 1.04 | Cell Division Initiation Protein Divivacell |
| INV10414300 | 453 | 12 | 5.27 | 2.07 | 1.05 | Phna Proteinphna |
| INV10415210 | 534 | 14 | 6.21 | 2.08 | 1.06 | Conserved Hypothetical Proteinconserved |
| INV10403910 | 1566 | 39 | 18.21 | 2.08 | 1.06 |  |
| INV10402590 | 2040 | 51 | 23.72 | 2.1 | 1.07 | Putative Holliday Junction Resolvase Putative |
| chlorohydrolase | 159 | 5 | 1.85 | 2.11 | 1.07 | Cell Division Protein Gpsb, Coordinates The Switch Between Cylindrical And Septal Cell Wall Synthesis By Re-Localization Of PBP1Cell |
| INV10412530 | 606 | 16 | 7.05 | 2.11 | 1.08 | Putative Choline Binding Protein (Pseudogene) Putative |
| INV10404120 | 564 | 15 | 6.56 | 2.12 | 1.08 | Conserved Hypothetical Proteinconserved |
| CelldivisioninitiationproteinDivIVA | 117 | 4 | 1.36 | 2.12 | 1.08 | Competence-Induced Protein Ccs1 (Pseudogene)Competence-Induced |
| INV10412650 | 563 | 15 | 6.55 | 2.12 | 1.08 | Putative Peptidase Putative |
| INV10408850 | 603 | 16 | 7.01 | 2.12 | 1.09 | Transposase (Pseudogene)Transposase |
| DNA-cytosinemethyltransferase(EC2 | 1089 | 28 | 12.66 | 2.12 | 1.09 | Putative Purine Nucleoside Phosphorylase Putative |
| INV10406130 | 1369 | 35 | 15.92 | 2.13 | 1.09 | Conserved Hypothetical Proteinconserved |
| dnaE | 3063 | 77 | 35.61 | 2.13 | 1.09 | DNA Polymerase IVDNA |
| IS861\_transposase(orf2)\_IS3family\_truncated | 274 | 8 | 3.19 | 2.15 | 1.1 | Putative Two-Component System, Sensor Histidine Kinase Putative |
| INV10414540 | 792 | 21 | 9.21 | 2.16 | 1.11 | Putative Transcriptional Regulator Protein Putative |
| thrB | 870 | 23 | 10.11 | 2.16 | 1.11 | 50S Ribosomal Protein L3050S |
| cdd | 390 | 11 | 4.53 | 2.17 | 1.12 | Heme Exporter Protein A (Cytochrome C-Type Biogenesis Protein)Heme |
| INV10417020 | 942 | 25 | 10.95 | 2.18 | 1.12 | Putative Membrane Protein Putative |
| INV10407720 | 901 | 24 | 10.48 | 2.18 | 1.12 | Putative Membrane Protein (Pseudogene) Putative |
| glnQ2 | 741 | 20 | 8.61 | 2.18 | 1.13 | N-Acetyl-Beta-D-Glucosaminidasen-Acetyl-Beta-D-Glucosaminidase |
| INV10408900 | 975 | 26 | 11.34 | 2.19 | 1.13 | Carbon-Nitrogen Hydrolase Family Proteincarbon-Nitrogen |
| murD | 1351 | 36 | 15.71 | 2.21 | 1.15 | Laminin Binding Proteinlaminin |
| 1624627\_1625237 | 610 | 17 | 7.09 | 2.22 | 1.15 |  |
| INV10414740 | 610 | 17 | 7.09 | 2.22 | 1.15 | Putative Uncharacterized Protein Putative |
| INV10401180 | 1227 | 33 | 14.27 | 2.23 | 1.15 | Extracellular Solute-Binding Proteinextracellular |
| INV10410900 | 879 | 24 | 10.22 | 2.23 | 1.16 | Haloacid Dehalogenase-Like Hydrolasehaloacid |
| INV10416630 | 261 | 8 | 3.03 | 2.23 | 1.16 | Siderophore Uptake Periplasmic Binding Proteinsiderophore |
| INV10418530 | 1680 | 45 | 19.53 | 2.24 | 1.16 | Putative Membrane Protein Putative |
| INV10417030 | 1257 | 34 | 14.61 | 2.24 | 1.16 | Putative DNA-Binding Protein Putative |
| INV10415750 | 297 | 9 | 3.45 | 2.25 | 1.17 | Conserved Hypothetical Proteinconserved |
| dinB | 1063 | 29 | 12.36 | 2.25 | 1.17 | Degenerate Transposasedegenerate |
| blpB | 1362 | 37 | 15.83 | 2.26 | 1.17 | Bira Bifunctional Protein [Includes: Biotin Operon Repressor; Biotin--[Acetyl-Coa-Carboxylase] Synthetase]Bira |
| INV10407780 | 759 | 22 | 8.82 | 2.34 | 1.23 | Putative Membrane Protein Putative |
| INV10416790 | 171 | 6 | 1.99 | 2.34 | 1.23 | Putative Oligopeptide Transporter Permease Protein Putative |
| 1253454\_1255712 | 2258 | 63 | 26.25 | 2.35 | 1.23 |  |
| Formamidopyrimidine-DNAglycosylase(EC3 | 825 | 24 | 9.59 | 2.36 | 1.24 | FIG01118323: Hypothetical Proteinfig01118323: |
| INV10405910 | 381 | 12 | 4.43 | 2.39 | 1.26 | Putative Sugar Phosphotransferase System (PTS), IIA Component Putative |
| scrB | 1455 | 42 | 16.92 | 2.4 | 1.26 | Riboflavin Synthase Beta Chain (6,7-Dimethyl-8-Ribityllumazine Synthase)Riboflavin |
| mscL | 378 | 12 | 4.39 | 2.41 | 1.27 | Large Subunit Ribosomal RNA; Lsurna; LSU Rrnalarge |
| leuS | 2502 | 72 | 29.09 | 2.43 | 1.28 | Putative Protease Putative |
| TypeIrestriction-modificationsystem\_DNA-methyltransferasesubunitM(EC2 | 1464 | 43 | 17.02 | 2.44 | 1.29 | Putative Phosphomethylpyrimidine Kinase Putative |
| INV10406950 | 405 | 13 | 4.71 | 2.45 | 1.29 | Putative DNA Polymerase III Delta Subunit Putative |
| INV10402770 | 543 | 17 | 6.31 | 2.46 | 1.3 | Phosphoglycerate Mutase Family Proteinphosphoglycerate |
| sufB | 1413 | 42 | 16.43 | 2.47 | 1.3 | 50S Ribosomal Protein L1550S |
| INV10418060 | 540 | 17 | 6.28 | 2.47 | 1.31 | Sugar Phosphotransferase System (PTS), IIA Componentsugar |
| INV10407710 | 816 | 25 | 9.49 | 2.48 | 1.31 | Putative DNA Topology Modulation Protein Putative |
| INV10407890 | 810 | 25 | 9.42 | 2.5 | 1.32 | Putative Membrane Protein Putative |
| Diacylglycerolkinase(EC2 | 396 | 13 | 4.6 | 2.5 | 1.32 | Degenerate Transposasedegenerate |
| FIG086557-Conjugationrelatedprotein | 222 | 8 | 2.58 | 2.51 | 1.33 | FIG01116802: Hypothetical Proteinfig01116802: |
| ImpBMucBSamBfamilyprotein | 1416 | 43 | 16.46 | 2.52 | 1.33 | Holliday Junction DNA Helicase Ruvbholliday |
| INV10414850 | 1098 | 34 | 12.77 | 2.54 | 1.35 | Conserved Hypothetical Proteinconserved |
| INV10408810 | 183 | 7 | 2.13 | 2.56 | 1.35 | Putative Membrane Protein (Pseudogene) Putative |
| INV10405420 | 249 | 9 | 2.89 | 2.57 | 1.36 | Leucine-Rich Proteinleucine-Rich |
| INV10412190 | 1287 | 40 | 14.96 | 2.57 | 1.36 | Conserved Hypothetical Proteinconserved |
| gor | 1347 | 42 | 15.66 | 2.58 | 1.37 | Glycerol Uptake Facilitator Protein 1glycerol |
| INV10405920 | 147 | 6 | 1.71 | 2.58 | 1.37 | Sugar Phosphotransferase System (PTS), IIB Componentsugar |
| ileS | 2793 | 86 | 32.47 | 2.6 | 1.38 | Putative Oxygen-Independent Coproporphyrinogen III Oxidase Putative |
| INV10407730 | 2130 | 66 | 24.76 | 2.6 | 1.38 | Putative Methyltransferase Putative |
| clpX | 1233 | 39 | 14.33 | 2.61 | 1.38 | Putative ATP-Dependent Protease ATP-Binding Subunit Clpl Putative |
| cbpE | 1884 | 59 | 21.9 | 2.62 | 1.39 | Choline-Binding Surface Protein Acholine-Binding |
| INV10400610 | 765 | 25 | 8.89 | 2.63 | 1.39 | Intramembrane Protease Rasp/Yluc, Implicated In Cell Division Based On Ftsl Cleavageintramembrane |
| INV10418510 | 1281 | 41 | 14.89 | 2.64 | 1.4 | Putative Membrane Protein Putative |
| upp | 630 | 21 | 7.32 | 2.64 | 1.4 | Tmrna-Binding Protein Smpbtmrna-Binding |
| lacG2 | 1407 | 45 | 16.36 | 2.65 | 1.41 | Putative Transposase (Pseudogene) Putative |
| FerrousirontransportperoxidaseEfeB | 1004 | 33 | 11.67 | 2.68 | 1.42 | Exodeoxyribonucleaseexodeoxyribonuclease |
| FIG01118323-hypotheticalprotein | 198 | 8 | 2.3 | 2.73 | 1.45 | FIG01116379: Hypothetical Proteinfig01116379: |
| 835603\_835987 | 384 | 14 | 4.46 | 2.75 | 1.46 |  |
| INV10407680 | 384 | 14 | 4.46 | 2.75 | 1.46 | Carbohydrate Kinasecarbohydrate |
| wze | 666 | 23 | 7.74 | 2.75 | 1.46 | Putative Thiol Peroxidase Putative |
| INV10402780 | 195 | 8 | 2.27 | 2.75 | 1.46 | Putative Inner Membrane Component Of ABC Transporter Putative |
| IS1381\_transposaseOrfA | 132 | 6 | 1.53 | 2.76 | 1.47 | Hypothetical Proteinhypothetical |
| INV10406110 | 286 | 11 | 3.33 | 2.77 | 1.47 | Sensor Histidine Kinasesensor |
| tag | 564 | 20 | 6.56 | 2.78 | 1.47 | 50S Ribosomal Protein L1850S |
| potA | 966 | 33 | 11.23 | 2.78 | 1.48 | Putative Chorismate Binding Enzyme Putative |
| INV10414890 | 594 | 21 | 6.91 | 2.78 | 1.48 | ROK Family Proteinrok |
| INV10401020 | 684 | 24 | 7.95 | 2.79 | 1.48 | Conserved Hypothetical Proteinconserved |
| tmRNA-bindingproteinSmpB | 468 | 17 | 5.44 | 2.79 | 1.48 | DNA-Directed RNA Polymerase Alpha Chaindna-Directed |
| 1799135\_1799535 | 400 | 15 | 4.65 | 2.83 | 1.5 |  |
| blpS | 339 | 13 | 3.94 | 2.83 | 1.5 | Bacteriocin Blpobacteriocin |
| INV10415250 | 1797 | 62 | 20.89 | 2.88 | 1.53 | Putative Membrane Protein Putative |
| INV10408840 | 840 | 30 | 9.77 | 2.88 | 1.53 | Putative IS1239 Transposase (Pseudogene) Putative |
| INV10404860 | 445 | 17 | 5.17 | 2.92 | 1.54 | Spou Rrna Methylase Family Proteinspou |
| comEA | 651 | 24 | 7.57 | 2.92 | 1.54 | GTP-Sensing Transcriptional Pleiotropic Repressorgtp-Sensing |
| asd | 1077 | 39 | 12.52 | 2.96 | 1.56 | Putative Phospho-2-Dehydro-3-Deoxyheptonate Aldolase 1 Putative |
| thiN | 663 | 25 | 7.71 | 2.99 | 1.58 | 50S Ribosomal Protein L2950S |
| 980372\_980573 | 201 | 9 | 2.34 | 3 | 1.58 |  |
| INV10409200 | 201 | 9 | 2.34 | 3 | 1.58 | Putative Uncharacterized Protein Putative |
|  |  | 2 | 0 | 3 | 1.58 | Transposasetransposase |
| INV10413420 | 171 | 8 | 1.99 | 3.01 | 1.59 | Conserved Hypothetical Proteinconserved |
| fucI | 1767 | 64 | 20.54 | 3.02 | 1.59 | Putative Geranyltranstransferase Putative |
| FIG01114010-hypotheticalprotein | 141 | 7 | 1.64 | 3.03 | 1.6 | Fructose-Bisphosphate Aldolasefructose-Bisphosphate |
| INV10402500 | 813 | 31 | 9.45 | 3.06 | 1.61 | Regulatory Protein Spxregulatory |
| INV10408920 | 279 | 12 | 3.24 | 3.06 | 1.62 | Putative Membrane Protein Putative |
| INV10412180 | 670 | 26 | 7.79 | 3.07 | 1.62 | Putative Flavodoxin Putative |
| dnaB | 1171 | 44 | 13.61 | 3.08 | 1.62 | Glucan 1,6-Alpha-Glucosidaseglucan |
| lacE2 | 1692 | 63 | 19.67 | 3.1 | 1.63 | Conserved Hypothetical Proteinconserved |
| proC | 798 | 31 | 9.28 | 3.11 | 1.64 | Aminopeptidase Caminopeptidase |
| INV10401030 | 438 | 18 | 5.09 | 3.12 | 1.64 | Conserved Hypothetical Proteinconserved |
| FIG01114768-hypotheticalprotein | 300 | 13 | 3.49 | 3.12 | 1.64 | FIG01114020: Hypothetical Proteinfig01114020: |
| INV10412150 | 240 | 11 | 2.79 | 3.17 | 1.66 | Crcb-Like Proteincrcb-Like |
| INV10405700 | 726 | 29 | 8.44 | 3.18 | 1.67 | Nitroreductase Family Proteinnitroreductase |
| speE | 861 | 34 | 10.01 | 3.18 | 1.67 | 50S Ribosomal Protein L250S |
| INV10418610 | 1152 | 45 | 13.39 | 3.2 | 1.68 | Putative Threonine Synthase Putative |
| 541745\_542197 | 452 | 19 | 5.25 | 3.2 | 1.68 |  |
| 308521\_308755 | 234 | 11 | 2.72 | 3.23 | 1.69 |  |
| INV10402620 | 234 | 11 | 2.72 | 3.23 | 1.69 | Putative Lipoprotein Putative |
| INV10415560 | 660 | 27 | 7.67 | 3.23 | 1.69 | GTP-Binding Proteingtp-Binding |
| 1362675\_1364823 | 2148 | 83 | 24.97 | 3.23 | 1.69 |  |
| INV10409100 | 1740 | 68 | 20.23 | 3.25 | 1.7 | Putative Alanine Dehydrogenase 1 (Pseudogene) Putative |
| proA | 1263 | 50 | 14.68 | 3.25 | 1.7 | Putative Pyruvate Dehydrogenase E1 Component, Beta Subunit Putative |
| INV10417790 | 1179 | 47 | 13.71 | 3.26 | 1.71 | RNA Pseudouridylate Synthaserna |
| TranscriptionalregulatorOrfX | 492 | 21 | 5.72 | 3.27 | 1.71 | 30S Ribosomal Protein S1330S |
| coaD | 489 | 21 | 5.69 | 3.29 | 1.72 | Pantothenate Kinasepantothenate |
| potC | 774 | 32 | 9 | 3.3 | 1.72 | Topoisomerase IV Subunit Atopoisomerase |
| trpC | 768 | 32 | 8.93 | 3.32 | 1.73 | Single Strand Binding Protein (SSB)Single |
| 584299\_586278 | 1979 | 79 | 23.01 | 3.33 | 1.74 |  |
| INV10407660 | 530 | 23 | 6.16 | 3.35 | 1.75 | Conserved Hypothetical Proteinconserved |
| INV10412280 | 195 | 10 | 2.27 | 3.37 | 1.75 | Putative Licd-Family Phosphotransferase Putative |
| INV10411470 | 450 | 20 | 5.23 | 3.37 | 1.75 | Putative Glutamine ABC Transporter, Glutamine-Binding Protein/Permease Protein Putative |
| INV10414630 | 768 | 33 | 8.93 | 3.42 | 1.78 | D-Tyrosyl-Trna(Tyr) Deacylased-Tyrosyl-Trna(Tyr) |
| INV10414950 | 561 | 25 | 6.52 | 3.46 | 1.79 | Extracellular Solute-Binding Lipoproteinextracellular |
| mraY | 981 | 42 | 11.41 | 3.47 | 1.79 | Transcription Antiterminator Lact 2transcription |
| folC | 1323 | 56 | 15.38 | 3.48 | 1.8 | FIG01117889: Hypothetical Proteinfig01117889: |
| INV10403920 | 1890 | 79 | 21.97 | 3.48 | 1.8 | Putative DNA-Binding Protein Putative |
| INV10413570 | 1317 | 56 | 15.31 | 3.49 | 1.81 | Putative Aminotransferase Putative |
| INV10405360 | 6436 | 266 | 74.83 | 3.52 | 1.82 | Putative Integral Membrane Protein (Possible Nuclease Activity) Putative |
| INV10414960 | 157 | 9 | 1.83 | 3.54 | 1.82 | Sugar Phosphotransferase System (PTS), IIBC Componentsugar |
| INV10408150 | 570 | 26 | 6.63 | 3.54 | 1.82 | Putative Lipoprotein Putative |
| FIG00627334-hypotheticalprotein | 2448 | 104 | 28.46 | 3.56 | 1.83 | 3-Oxoacyl-[Acyl-Carrier-Protein] Synthase II3-Oxoacyl-[Acyl-Carrier-Protein] |
| FIG01114970-hypotheticalprotein | 243 | 13 | 2.83 | 3.66 | 1.87 | FIG01114146: Hypothetical Proteinfig01114146: |
| INV10418520 | 2087 | 92 | 24.26 | 3.68 | 1.88 | Putative Pyrrolidone-Carboxylate Peptidase Putative |
| Antirestrictionprotein | 498 | 24 | 5.79 | 3.68 | 1.88 | Antirestriction Proteinantirestriction |
| INV10413270 | 1872 | 83 | 21.76 | 3.69 | 1.88 | Putative Transposase (Pseudogene) Putative |
| INV10405190 | 607 | 29 | 7.06 | 3.72 | 1.9 | Putative Uncharacterized Protein Putative |
| INV10409110 | 7665 | 336 | 89.11 | 3.74 | 1.9 | Putative Acetyltransferase (GNAT) Family Protein Putative |
| INV10418830 | 1025 | 48 | 11.92 | 3.79 | 1.92 | Rhomboid Family Membrane Proteinrhomboid |
| INV10415490 | 318 | 17 | 3.7 | 3.83 | 1.94 | Conserved Hypothetical Proteinconserved |
| INV10407750 | 273 | 15 | 3.17 | 3.83 | 1.94 | ABC Transporter ATP-Binding Protein ABC |
| FIG01116987-hypotheticalprotein | 360 | 19 | 4.19 | 3.86 | 1.95 | FIG01115706: Hypothetical Proteinfig01115706: |
| Oxygen-insensitiveNAD(P)Hnitroreductase(EC1 | 531 | 27 | 6.17 | 3.9 | 1.97 | Metal Cation ABC Transporter Membrane Proteinmetal |
| INV10408190 | 1186 | 57 | 13.79 | 3.92 | 1.97 | Putative Uncharacterized Protein Putative |
| INV10408110 | 882 | 44 | 10.25 | 4 | 2 | Type I Restriction Modification System Proteintype |
| FIG01114502-hypotheticalprotein | 450 | 24 | 5.23 | 4.01 | 2 | FIG00628088: Hypothetical Proteinfig00628088: |
| FIG01116966-hypotheticalprotein | 228 | 14 | 2.65 | 4.11 | 2.04 | FIG01115561: Hypothetical Proteinfig01115561: |
| glyA | 1257 | 64 | 14.61 | 4.16 | 2.06 | Glucokinaseglucokinase |
| INV10407740 | 450 | 25 | 5.23 | 4.17 | 2.06 | Putative Lipoprotein Putative |
| INV10405170 | 798 | 42 | 9.28 | 4.18 | 2.06 | Putative Uncharacterized Protein Putative |
| comEC | 2241 | 113 | 26.05 | 4.21 | 2.08 | Competence-Stimulating Peptide Type 2 Precursor (Csp-2)Competence-Stimulating |
| polC | 4392 | 219 | 51.06 | 4.23 | 2.08 | Oxidoreductase, Gfo/Idh/Moca Familyoxidoreductase, |
| 1052773\_1117795 | 65022 | 3198 | 755.95 | 4.23 | 2.08 |  |
| BacteriocinimmunityproteinBlpL | 372 | 22 | 4.32 | 4.32 | 2.11 | Bacteriocin-Like Peptide N Blpnbacteriocin-Like |
| INV10413760 | 1104 | 59 | 12.84 | 4.34 | 2.12 | Putative Membrane Protein Putative |
| purE | 489 | 28 | 5.69 | 4.34 | 2.12 | Phage Portal Proteinphage |
| deoC | 663 | 37 | 7.71 | 4.36 | 2.13 | Polypeptide Deformylasepolypeptide |
| INV10407690 | 282 | 18 | 3.28 | 4.44 | 2.15 | Conserved Hypothetical Proteinconserved |
| Transposaseandinactivatedderivative | 417 | 25 | 4.85 | 4.45 | 2.15 | 30S Ribosomal Protein S1930S |
| INV10414280 | 645 | 37 | 7.5 | 4.47 | 2.16 | Major Facilitator Superfamily Proteinmajor |
| INV10414970 | 962 | 54 | 11.18 | 4.51 | 2.17 | Putative N-Acetylmannosamine-6-Phosphate 2-Epimerase Putative |
| FIG01114872-hypotheticalprotein | 489 | 30 | 5.69 | 4.64 | 2.21 | FIG01114020: Hypothetical Proteinfig01114020: |
| calcium-bindingprotein\_ putative | 411 | 26 | 4.78 | 4.67 | 2.22 | Putative Branched-Chain Amino Acid Transport System Carrier Protein Putative |
| lacF | 318 | 21 | 3.7 | 4.68 | 2.23 | Putative Transposase Family Protein Putative |
| smc | 3540 | 199 | 41.16 | 4.74 | 2.25 | Ribonuclease Hiiribonuclease |
| tnp | 1031 | 61 | 11.99 | 4.77 | 2.25 | 30S Ribosomal Protein S330S |
| engC | 1310 | 78 | 15.23 | 4.87 | 2.28 | DNA Polymerase III, Beta Chaindna |
| INV10405730 | 405 | 27 | 4.71 | 4.9 | 2.29 | Putative Uncharacterized Protein Putative |
| HitFamilyProtein | 442 | 30 | 5.14 | 5.05 | 2.34 | Glycerol-3-Phosphate Dehydrogenase [NAD(P)+]Glycerol-3-Phosphate |
| INV10402450 | 708 | 46 | 8.23 | 5.09 | 2.35 | Putative Metallopeptidase Putative |
| INV10411440 | 588 | 39 | 6.84 | 5.1 | 2.35 | CAAX Amino Terminal Protease Family Proteincaax |
| blpR | 738 | 48 | 8.58 | 5.11 | 2.35 | Sensor Histidine Kinase Blphsensor |
| Pleiotropicregulatorofexopolysaccharidesynthesis\_competenceandbiofilmformationFtr\_XREfamily | 684 | 46 | 7.95 | 5.25 | 2.39 | Putative Putative N Utilization Substance Protein A Putative |
| conserveddomainprotein | 2815 | 178 | 32.73 | 5.31 | 2.41 | Putative Competence Protein Putative |
| INV10408010 | 870 | 58 | 10.11 | 5.31 | 2.41 |  |
| membraneprotein\_ putative | 2117 | 135 | 24.61 | 5.31 | 2.41 | IS861, Transposase (Orf2), IS3 Family, Truncatedis861, |
| pmi | 945 | 63 | 10.99 | 5.34 | 2.42 | Oligoendopeptidase F (Ec 3.4.24.-)Oligoendopeptidase |
| ksgA | 873 | 59 | 10.15 | 5.38 | 2.43 | ABC Transporter, Substrate-Binding Protein ABC |
| purK | 1092 | 73 | 12.7 | 5.4 | 2.43 | Phage Replication Initiation Proteinphage |
| lipoprotein\_NLPP60family | 1002 | 68 | 11.65 | 5.45 | 2.45 | Putative Membrane Protein Putative |
| FIG01116389-hypotheticalprotein | 1882 | 126 | 21.88 | 5.55 | 2.47 | FIG01115415: Hypothetical Proteinfig01115415: |
| FIG00628965-hypotheticalprotein | 936 | 66 | 10.88 | 5.64 | 2.5 | Enoyl-ACP Reductaseenoyl-ACP |
| RegulatoryproteinrecX | 777 | 57 | 9.03 | 5.78 | 2.53 | DNA Polymerase III Polc-Typedna |
| INV10409250 | 759 | 56 | 8.82 | 5.8 | 2.54 | Putative Redoxin Family Protein Putative |
| INV10408760 | 432 | 34 | 5.02 | 5.81 | 2.54 | ABC Transporter, ATP-Binding Protein ABC |
| INV10413780 | 678 | 51 | 7.88 | 5.85 | 2.55 | Putative Membrane Protein Putative |
| INV10416510 | 675 | 51 | 7.85 | 5.88 | 2.55 | Tetr Family Regulatory Proteintetr |
| potB | 807 | 61 | 9.38 | 5.97 | 2.58 | Putative Chromosome Partitioning Protein Parb Putative |
| INV10414290 | 279 | 25 | 3.24 | 6.13 | 2.62 | Putative Membrane Protein Putative |
| FIG01114468-hypotheticalprotein | 642 | 51 | 7.46 | 6.14 | 2.62 | FIG00627334: Hypothetical Proteinfig00627334: |
| INV10409970 | 852 | 67 | 9.91 | 6.24 | 2.64 |  |
| INV10405740 | 2022 | 152 | 23.51 | 6.24 | 2.64 | M42 Glutamyl Aminopeptidasem42 |
| INV10415230 | 793 | 63 | 9.22 | 6.26 | 2.65 | Acetyl Xylan Esterase (AXE1) Family Proteinacetyl |
| undecaprenylpyrophosphatephosphatase | 130 | 15 | 1.51 | 6.37 | 2.67 | Thymidylate Synthasethymidylate |
| pbp2x | 2253 | 176 | 26.19 | 6.51 | 2.7 | Putative UDP-N-Acetylglucosamine-N-Acetylmuramyl-(Pentapeptide)Pyr Ophosphoryl-Undecaprenol N-Acetylglucosamine Transferase Putative |
| FIG01118149-hypotheticalprotein | 297 | 28 | 3.45 | 6.51 | 2.7 | FIG01116303: Hypothetical Proteinfig01116303: |
| INV10407280 | 1143 | 93 | 13.29 | 6.58 | 2.72 | Putative Short Chain Dehydrogenase Putative |
| INV10409990 | 1551 | 126 | 18.03 | 6.67 | 2.74 | Putative Transposase (Pseudogene) Putative |
| INV10407270 | 429 | 40 | 4.99 | 6.85 | 2.77 | Conserved Hypothetical Proteinconserved |
| INV10405250 | 1039 | 89 | 12.08 | 6.88 | 2.78 | Putative Acetyltransferase Putative |
| Phageholin | 336 | 33 | 3.91 | 6.93 | 2.79 | N-Ethylammeline Chlorohydrolasen-Ethylammeline |
| INV10415710 | 1068 | 92 | 12.42 | 6.93 | 2.79 | Conserved Hypothetical Proteinconserved |
| INV10414980 | 954 | 83 | 11.09 | 6.95 | 2.8 | Putative Oxidoreductase Putative |
| D-alanyl-D-alaninecarboxypeptidase(EC3 | 717 | 65 | 8.34 | 7.07 | 2.82 | Putative Cysteine Synthase Putative |
| INV10416520 | 447 | 43 | 5.2 | 7.1 | 2.83 | Nicotinamide Mononucleotide Transporternicotinamide |
| blpH | 1341 | 117 | 15.59 | 7.11 | 2.83 | ABC Transporter Blpbabc |
| sensorhistidinekinase | 1098 | 97 | 12.77 | 7.12 | 2.83 | Dtdp-4-Keto-6-Deoxy-D-Glucose 3,5-Epimerase Rmlcdtdp-4-Keto-6-Deoxy-D-Glucose |
| SNF2familyprotein | 6232 | 528 | 72.45 | 7.2 | 2.85 | Ribonuclease Zribonuclease |
| INV10408180 | 588 | 59 | 6.84 | 7.66 | 2.94 | Putative IS1381 Transposase (Pseudogene) Putative |
| INV10407410 | 603 | 61 | 7.01 | 7.74 | 2.95 | Putative IS640-Spn1 Transposase (Pseudogene) Putative |
| blpC | 156 | 21 | 1.81 | 7.82 | 2.97 | Putative Bacteriocin Transporter C39 Protease Domain Blpa2 Putative |
| rnh | 780 | 78 | 9.07 | 7.85 | 2.97 | Probably Aromatic Ring Hydroxylating Enzyme, Evidenced By Cognitor; Paad-Like Protein (DUF59) Involved In Fe-S Cluster Assemblyprobably |
| INV10414510 | 154 | 21 | 1.79 | 7.88 | 2.98 | Sensor Histidine Kinase Proteinsensor |
| folP | 981 | 97 | 11.41 | 7.9 | 2.98 | FIG01118149: Hypothetical Proteinfig01118149: |
| thiM | 783 | 82 | 9.1 | 8.22 | 3.04 | 50S Ribosomal Protein L2850S |
| dyr | 507 | 57 | 5.89 | 8.41 | 3.07 | DNA Polymerase III Subunit Gamma/Taudna |
| FIG01115786-hypotheticalprotein | 273 | 36 | 3.17 | 8.86 | 3.15 | FIG01114689: Hypothetical Proteinfig01114689: |
| FIG01116415-hypotheticalprotein | 1086 | 130 | 12.63 | 9.61 | 3.26 | FIG01115489: Hypothetical Proteinfig01115489: |
| tgt | 1143 | 144 | 13.29 | 10.15 | 3.34 | 50S Ribosomal Protein L2250S |
| INV10401150 | 864 | 114 | 10.04 | 10.41 | 3.38 | Putative IS630-Spn1 Transposase (Pseudogene) Putative |
| trpF | 630 | 88 | 7.32 | 10.69 | 3.42 | Fes Assembly Protein Sufbfes |
| Tn5252\_Orf9protein | 228 | 58 | 2.65 | 16.16 | 4.01 | RNA Polymerase Sigma Factor Rpodrna |
| truA | 750 | 178 | 8.72 | 18.42 | 4.2 | Putative Thymidine Kinase Putative |
| tRNA-Arg-ACG | 74 | 44 | 0.86 | 24.19 | 4.6 | S-Adenosylmethionine-Dependent Methyltransferases-Adenosylmethionine-Dependent |
| Tn916\_hypotheticalprotein | 423 | 201 | 4.92 | 34.13 | 5.09 | DNA-Directed RNA Polymerase Omega Chaindna-Directed |
| sodA | 606 | 361 | 7.05 | 44.99 | 5.49 | Ribose 5-Phosphate Isomerase Aribose |
|  |  |  |  |  |  |  |