# Supplementary Figures and Tables

# 1.1 Supplementary Figures

**FIG S1**

**Supplementary Figure 1.** Absorption peaks of truncated CrrB (135-353 amino acids, CrrBT) and its P151L mutant (CrrBTP151L) at 280 nm by using molecular sieve. The dimer protein (D, molecular weight 51 kDa) was located at 15 ml and the monomer (M, molecular weight 25.5 kDa) at 16 ml.

# 1.2 Supplementary Tables

**Supplementary Table 1.** The detailed information of the strains.

|  |  |  |
| --- | --- | --- |
| **Strain** | **Species** | **Source** |
| **ATCC13883** | *Klebsiella pneumoniae* | American Type Culture Collection |
| **ATCC27853** | *Pseudomonas aeruginosa* | American Type Culture Collection |
| **ATCC19606** | *Acinetobacter baumannii* | American Type Culture Collection |
| **P2418-1** | PB-resistant *Klebsiella pneumoniae* | Shenzhen People’s Hospital |
| **666-15r** | spontaneous mutant of ATCC13883 | This work |
| **WT CrrB(P151L)** | artificial mutant of ATCC13883 | This work |

**Supplementary Table 2.** Primers used in CRISPR-Cas9 gene editing.

|  |  |
| --- | --- |
| **Primers** | **Sequence** |
| **CrrB-TF** | CGGAAAAAGCTTGAACATGCC |
| **CrrB-TR** | CAAAACTCGGCAGTATGTGGG |
| **CrrB-HF1** | CGAATTCCTGCAGCCCGGGGGATCCATGAACAAAGAAACGATTCTGAGCC |
| **CrrB-HR1** | ATTGGACGGGTGACCAAGTTCCGGAGTTCATGAGCAATTGC |
| **CrrB-HF2** | AACTTGGTCACCCGTCCAATTGGGAGGCTTCAGGGACTGGTTG |
| **CrrB-HR2** | CCACCGCGGTGGCGGCCGCTCTAGACAGGCCATGAGAGTTTGAAAAGT |
| **crrB-N20F** | ACGCCGGTGACTATCTTACG |
| **Art-CrrB-N20F** | AACTTGGTCACCCGTCCAAT |
| **Infu-crrB-N20F** | ACGCCGGTGACTATCTTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC |
| **Infu-crrB-N20R** | CGTAAGATAGTCACCGGCGTACTAGTATTATACCTAGGACTGAGCTAGC |
| **pSGKP-F1** | TGCAGACTACGGGCCTAAAG |
| **pSGKP-R1** | AGCGCAACGCAATTAATGTG |
| **CT-CrrB-HF2** | ACGCTGGTGACTATCTTACGTGGGAGGCTTCAGGGACTGGTTG |
| **CT-CrrB-HR1** | CGTAAGATAGTCACCAGCGTCCGGAGTTCATGAGCAATTGC |
| **Infu-CTcrrB-N20F** | ACTTGGTCACCCGTCCAAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGC |

**Supplementary Table 3.** Primers used in qRT-PCR.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Forward primers** | **Reverse primers** |
| ***16SrRNA*** | AGGCCTAACACATGCAAGTC | TGCAATATTCCCCACTGCTG |
| ***arnA*** | TAACCCGGAAAACGAAGCGA | CGGTCTCTTCCATCTCGACG |
| ***arnB*** | GGACGCTTATGATCGCCAGA | CGTGGCTCAGTTTTTCCAGC |
| ***arnC*** | CTGGTGACCTGTCTGACCAC | AGGCCCATACCGACAAACTG |
| ***arnD*** | GGTATTGCCTACGCCGATCA | CCAGTTCACCACGAACCACT |
| ***arnE*** | GAGCGTCTGGATCTGTCTGG | GCGATGCTGACCGGAATAGA |
| ***arnF*** | GCTGGTACTTTGCCCTCCAT | CCGGCCAGAAGATGGTCAAT |
| ***arnT*** | CTGAAAAAGACGCCCAGCAC | CGCCACCCAACCTAACAGAT |
| ***pmrA*** | ATCTGCGCCTTAACGTCACT | GGGCATACTCTTTCGGCGTA |
| ***pmrB*** | TGGCATGAGAGCAAAGAGCA | TGCTGATATACAGCGCCAGG |
| ***phoP*** | ATCAAGCTGACCGCCTTTGA | AAGCTGGAGCATCAGCGAAT |
| ***phoQ*** | TGCTGTGGACTCAGATGCTT | ATAGTGCAAATGCCGCTGAA |
| ***crrA*** | GTGAGGTTTCCACGCCAGTA | TTTCTCGGGTTTCTCGCCAA |
| ***crrB*** | GGCGTTTTCGAACCAGAACC | TCCTGAAGAACTCACGACGC |
| ***pmrC*** | GCGAAATGATTGCCGTCCTC | GCGGGCTTACGGATTTTCAC |

**Supplementary Table 4.** The activity of 666-15 combined with different classes of antibiotics.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | ***K. pneumoniae*ATCC13883** | | ***A. baumannii*ATCC19606** | | ***P. aeruginosa*ATCC27853** | |
| **MIC (μg/mL)** | **FICI** | **MIC (μg/mL)** | **FICI** | **MIC (μg/mL)** | **FICI** |
| **Polymyxin B** | 2 | ＜0.094 | 4 | <0.281 | 2 | <0.281 |
| **Ofloxacin** | 0.5 | 2 | 0.125 | 2 | 1 | <1 |
| **Tigecycline** | 0.5 | 2 | 0.125 | 2 | NR | ～ |
| **Rifampicin** | 4 | 2 | 0.5 | 2 | 8 | 2 |
| **Meropenem** | 0.25 | 2 | 1 | 2 | 1 | 2 |
| **Gentamicin** | 2 | 2 | 8 | 2 | 8 | 2 |
| **Ceftazidime** | 0.5 | 2 | 8 | 2 | 4 | 2 |

**NR,** Natural resistance

**Supplementary Table 5.** Information of differentially expressed proteins (DEPs).

|  |  |  |  |
| --- | --- | --- | --- |
| **Protein Name** | **Description** | **Fold Change** | ***p Value*** |
| **GltI** | Amino acid ABC transporter substrate-binding protein | 0.001671 | 0.000004 |
| **Spy** | ATP-independent periplasmic protein-refolding chaperone | 0.00359 | 0.000001 |
| **B4U21\_04180** | DUF1471 domain-containing protein | 0.00583 | 0.000014 |
| **ArtJ\_1** | Arginine ABC transporter | 0.007704 | 0.000241 |
| **BANRA\_00269** | ABC transporter substrate-binding protein | 0.009924 | 0.000013 |
| **FruB\_3** | PTS sugar transporter subunit IIA | 0.010252 | 0.004777 |
| **Sra** | 30S ribosomal protein S22 | 0.010372 | 0.122046 |
| **OsmY** | Molecular chaperone OsmY | 0.011487 | 0.000006 |
| **IpdC** | Indolepyruvate decarboxylase | 0.015016 | 0.000299 |
| **YhbO** | DJ-1/PfpI/YhbO family deglycase/protease | 0.016654 | 0.000245 |
| **KshA\_1** | 3-ketosteroid-9-alpha-hydroxylase oxygenase subunit | 0.020716 | 0.000071 |
| **B4U21\_23685** | YgdI/YgdR family lipoprotein | 0.023962 | 0.000001 |
| **MglB\_2** | D-galactose/ D-glucose-binding protein | 0.025705 | 0.000775 |
| **YdjH\_2** | 2-dehydro-3-deoxygluconokinase | 0.027045 | 0.000082 |
| **UxuA** | Mannonate dehydratase | 0.028611 | 0.313628 |
| **BetB\_1** | Aldehyde dehydrogenase | 0.029722 | 0.004171 |
| **YqjC** | DUF1090 domain-containing protein | 0.030492 | 0.167518 |
| **ArtJ** | Arginine ABC transporter substrate-binding protein | 0.0331 | 0.000001 |
| **BANRA\_01420** | Uncharacterized protein | 0.033212 | 0.000029 |
| **B4U25\_16840** | NAD(P)-dependent oxidoreductase | 0.033274 | 0.005543 |
| **YaiA** | Protein YaiA | 0.035658 | 0.000028 |
| **CobQ** | Cobyric acid synthase | 0.036373 | 0.307798 |
| **DppA\_4** | ABC transporter substrate-binding protein | 0.03683 | 0.000017 |
| **MglB** | D-galactose-binding periplasmic protein | 0.037203 | 0.000217 |
| **ETE82\_04120** | GFA family protein | 0.037358 | 0.007601 |
| **ArtM\_5** | ATP-binding cassette domain-containing protein | 0.039866 | 0.000023 |
| **CybC** | Soluble cytochrome b562 | 0.040267 | 0.000663 |
| **Sad\_2** | Aldehyde dehydrogenase family protein | 0.04058 | 0.000042 |
| **GltJ** | ABC transporter permease subunit | 0.042232 | 0.000314 |
| **GJJ01\_27215** | UPF0229 protein GJJ01\_27215 | 0.045805 | 0.000102 |
| **OtsA** | Trehalose-6-phosphate synthase | 0.04588 | 0.000027 |
| **Acs** | Acetyl-coenzyme A synthetase | 0.046508 | 0.000001 |
| **YbiH** | Putative DNA-binding transcriptional regulator | 0.047451 | 0.000989 |
| **DppA\_2** | ABC transporter substrate-binding protein | 0.048822 | 0.000022 |
| **RbsB\_5** | ABC transporter substrate-binding protein | 0.049067 | 0.000161 |
| **RbsB** | D-ribose ABC transporter substrate-binding protein | 0.049579 | 0.000156 |
| **TusB** | Protein TusB | 0.05003 | 0.00001 |
| **YggG\_1** | Beta-barrel assembly-enhancing protease | 0.050036 | 0.000023 |
| **FadE** | Acyl-coenzyme A dehydrogenase | 0.051341 | 0.000015 |
| **CspD** | Cold shock-like protein CspD | 0.053775 | 0.000182 |
| **SprT** | Protein SprT | 0.054392 | 0.000003 |
| **B4U21\_25295** | Thioredoxin | 0.054549 | 0.000206 |
| **KefG** | Glutathione-regulated potassium-efflux system ancillary protein KefG | 0.056311 | 0.000002 |
| **GJJ01\_07205** | DUF3300 domain-containing protein | 0.06242 | 0.000758 |
| **SodC** | Superoxide dismutase [Cu-Zn] | 0.062479 | 0.000025 |
| **MglB\_3** | D-galactose/ D-glucose-binding protein | 0.062723 | 0.001057 |
| **DsbA** | Thiol:disulfide interchange protein | 0.062776 | 0 |
| **HutU** | Urocanate hydratase | 0.062974 | 0.000049 |
| **MalX** | PTS maltose transporter subunit IICB | 0.063349 | 0.036492 |
| **DsbG** | Thiol:disulfide interchange protein | 0.064375 | 0.000027 |
| **EcnB** | Entericidin B | 0.064636 | 0.000045 |
| **DD583\_25045** | Methyltransferase domain-containing protein | 0.06477 | 0.000222 |
| **PstS** | Phosphate-binding protein PstS | 0.065593 | 0.000098 |
| **MglA\_3** | Ribose import ATP-binding protein RbsA | 0.066066 | 0.000354 |
| **Rmf** | Ribosome modulation factor | 0.066183 | 0.002964 |
| **KatE** | Catalase | 0.06665 | 0.000125 |
| **CsbC** | Galactose-proton symport of transport system | 0.067066 | 0.001607 |
| **FabG\_13** | Dehydrogenase | 0.067371 | 0.000045 |
| **AdhP** | Alcohol dehydrogenase | 0.070142 | 0.000229 |
| **OppA** | Oligopeptide ABC transporter substrate-binding protein OppA | 0.07062 | 0.000011 |
| **GJJ01\_07200** | DUF2950 family protein | 0.071349 | 0.000071 |
| **DM062\_06415** | Putative homeobox protein | 0.072108 | 0.002163 |
| **BANRA\_01686** | DUF2076 domain-containing protein | 0.072407 | 0.005084 |
| **B4U25\_04750** | GNAT family N-acetyltransferase | 0.072425 | 0.000044 |
| **YccX** | Acylphosphatase | 0.075256 | 0.00131 |
| **DppD** | Dipeptide ABC transporter ATP-binding protein | 0.075558 | 0.001422 |
| **FXN67\_18430** | L,D-transpeptidase family protein | 0.076383 | 0.000471 |
| **YciF** | DUF892 family protein | 0.077463 | 0.002821 |
| **CutA** | Divalent-cation tolerance protein CutA | 0.080044 | 0.018194 |
| **YcjI** | Murein peptide amidase A | 0.080784 | 0.000275 |
| **ProY** | Amino acid permease | 0.084507 | 0.000041 |
| **GatZ** | D-tagatose-1,6-bisphosphate aldolase subunit GatZ | 0.084571 | 0.001063 |
| **IolB** | 5-deoxy-glucuronate isomerase | 0.085689 | 0.002406 |
| **IolE** | Inosose dehydratase | 0.08571 | 0.001145 |
| **YhbO\_1** | Cysteine protease YraA | 0.086116 | 0.000008 |
| **XylB\_1** | Benzyl alcohol dehydrogenase | 0.089013 | 0.000049 |
| **Mak** | Fructokinase | 0.089036 | 0.000029 |
| **BANRA\_02377** | DSBA oxidoreductase | 0.089353 | 0.000603 |
| **B4U21\_03210** | PTS maltose transporter subunit IIBC | 0.091029 | 0.005964 |
| **YieL** | Endo-1,4-beta-xylanase A | 0.091695 | 0.000369 |
| **PpiA** | Peptidyl-prolyl cis-trans isomerase | 0.092035 | 0.000586 |
| **IolD** | 3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (Decyclizing) | 0.094213 | 0.000292 |
| **LldP** | L-lactate permease | 0.096046 | 0.000006 |
| **ArgT** | Amino acid ABC transporter substrate-binding protein | 0.096401 | 0.000164 |
| **HiuH** | 5-hydroxyisourate hydrolase | 0.097129 | 0.000828 |
| **HpaE** | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase | 0.097327 | 0.000081 |
| **PhoC\_2** | Acid phosphatase | 0.098212 | 0.000002 |
| **MglA\_3** | Galactose/methyl galactoside import ATP-binding protein MglA | 0.100734 | 0.000192 |
| **GsiA\_12** | Dipeptide ABC transporter ATP binding subunit DppF | 0.101506 | 0.000062 |
| **HtpX** | Protease HtpX | 0.102835 | 0.000087 |
| **RpmF** | 50S ribosomal protein L32 | 0.10318 | 0.061282 |
| **TipA** | Albicidin resistance protein | 0.103597 | 0.000022 |
| **GmuB\_2** | Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component | 0.104376 | 0.000165 |
| **YcbJ** | Chromosome partition protein MukF | 0.105496 | 0.000261 |
| **RcnB\_1** | Nickel/cobalt homeostasis protein RcnB | 0.105548 | 0.000597 |
| **PckA** | Phosphoenolpyruvate carboxykinase (ATP) | 0.106681 | 0.000007 |
| **BhsA\_5** | DUF1471 domain-containing protein | 0.107618 | 0.005024 |
| **YfiI** | 1,5-anhydro-D-fructose reductase | 0.108173 | 0.005291 |
| **YfiN** | Diguanylate cyclase | 0.108336 | 0.402015 |
| **FadM** | 4-hydroxybenzoyl-CoA thioesterase | 0.111258 | 0.000054 |
| **B4U25\_21355** | DUF2511 domain-containing protein | 0.112516 | 0.001778 |
| **YeaP\_1** | Diguanylate cyclase | 0.112853 | 0.000673 |
| **YcgB** | SpoVR family protein | 0.113388 | 0.000009 |
| **MaeB** | NADP-dependent malic enzyme | 0.114726 | 0.000002 |
| **YgaC** | DUF2002 domain-containing protein | 0.115236 | 0.000045 |
| **CitW** | Citrate-sodium symporter | 0.11526 | 0.00009 |
| **GsiB** | Dipeptide-binding ABC transporter, periplasmic substrate-binding component | 0.115466 | 0.00019 |
| **GudX** | Glucarate dehydratase | 0.115741 | 0.000389 |
| **C4Y50\_029165** | Four-carbon acid sugar kinase family protein | 0.116128 | 0.000134 |
| **FkpA\_1** | Peptidyl-prolyl cis-trans isomerase | 0.116178 | 0.000021 |
| **Dps** | DNA protection during starvation protein | 0.116659 | 0.000327 |
| **YbaK** | Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase | 0.118793 | 0.004769 |
| **IolC** | 5-dehydro-2-deoxygluconokinase | 0.118998 | 0.001076 |
| **AmiB** | N-acetylmuramoyl-L-alanine amidase | 0.119422 | 0.000105 |
| **SerA\_3** | D-3-phosphoglycerate dehydrogenase | 0.120051 | 0.000149 |
| **Mdh** | Malate dehydrogenase | 0.120216 | 0.000019 |
| **Zur** | Transcriptional regulator Zur | 0.120285 | 0.047136 |
| **XecA1** | 2-hydroxypropyl-CoM lyase | 0.120714 | 0.002391 |
| **CdsA** | Phosphatidate cytidylyltransferase | 0.121358 | 0.006032 |
| **AmiD** | AmiD protein | 0.122514 | 0.000084 |
| **Blc\_2** | Outer membrane lipoprotein Blc | 0.122542 | 0.000006 |
| **HutI** | Imidazolonepropionase | 0.122636 | 0 |
| **YrdA\_2** | Carbonic anhydrase, family 3 | 0.125688 | 0.005027 |
| **AmpH** | AmpH protein | 0.126059 | 0.001018 |
| **YbbA** | ABC transporter ATP-binding protein | 0.128113 | 0.000029 |
| **NudF\_1** | ADP-ribose pyrophosphatase | 0.12844 | 0.001164 |
| **MepA** | Penicillin-insensitive murein endopeptidase | 0.129974 | 0.000572 |
| **YgcP** | Glycerol uptake operon antiterminator regulatory protein | 0.130497 | 0.002043 |
| **RbsC\_5** | ABC transporter permease | 0.130651 | 0.000359 |
| **ElaA** | Acetyltransferase | 0.131075 | 0.000116 |
| **YbiC\_1** | Malate dehydrogenase | 0.1311 | 0.000053 |
| **DD583\_18315** | Transketolase (Fragment) | 0.132054 | 0.174425 |
| **DksA** | C4-type zinc finger protein, DksA/TraR family | 0.132446 | 0.000014 |
| **UspA** | Universal stress protein | 0.133034 | 0.009668 |
| **CueO** | Multicopper oxidase CueO | 0.133086 | 0.000424 |
| **PaaY** | Acetyltransferase | 0.133751 | 0.000078 |
| **TesA** | Multifunctional acyl-CoA thioesterase I/protease I/lysophospholipase L1 | 0.133803 | 0.00161 |
| **IolG** | Inositol 2-dehydrogenase | 0.133873 | 0.00009 |
| **TreA** | Periplasmic trehalase | 0.134557 | 0.000004 |
| **GJJ01\_10960** | Stress-induced acidophilic repeat motif-containing protein | 0.134566 | 0.003049 |
| **OppA\_2** | Oligopeptide ABC transporter substrate-binding protein OppA | 0.134681 | 0.000134 |
| **AstA** | Arginine N-succinyltransferase | 0.137582 | 0.000919 |
| **GudD** | Glucarate dehydratase | 0.139845 | 0.000321 |
| **DsdA** | D-serine dehydratase | 0.139937 | 0.002971 |
| **NdoA** | Naphthalene 1,2-dioxygenase | 0.14008 | 0.045189 |
| **HutH** | Histidine ammonia-lyase | 0.140706 | 0.000175 |
| **Pldh-t** | 3-ketoacyl-ACP reductase | 0.141067 | 0.000034 |
| **B4U21\_28700** | Transcriptional regulator | 0.141411 | 0.155661 |
| **MlaC** | ABC transporter | 0.142483 | 0.000261 |
| **YciE\_2** | DUF892 family protein | 0.14251 | 0.001616 |
| **Tas** | General stress protein 69 | 0.142588 | 0.000009 |
| **RffA** | dTDP-4-amino-4,6-dideoxygalactose transaminase | 0.143682 | 0.000015 |
| **YsgA** | Carboxymethylenebutenolidase | 0.143698 | 0.000647 |
| **B4U21\_28790** | Lipopolysaccharide core biosynthesis protein RfaZ | 0.143889 | 0.000496 |
| **ElaB\_1** | Bacterial protein of uncharacterized function (DUF883) | 0.14519 | 0.000159 |
| **B4U21\_31695** | Cupin | 0.145315 | 0.000102 |
| **PfkB** | Phosphofructokinase | 0.14532 | 0.000001 |
| **BANRA\_01328** | DUF2291 domain-containing protein | 0.145533 | 0.000007 |
| **CpxP** | Cell-envelope stress modulator CpxP | 0.146387 | 0.000156 |
| **NanE** | Putative N-acetylmannosamine-6-phosphate 2-epimerase | 0.146751 | 0.000201 |
| **YfgJ** | Protein of uncharacterized function (DUF1407) | 0.148253 | 0.003866 |
| **ETE82\_21525** | Transporter substrate-binding domain-containing protein | 0.14851 | 0.001824 |
| **AstD** | N-succinylglutamate 5-semialdehyde dehydrogenase | 0.149129 | 0.000158 |
| **CysW\_4** | ABC transporter permease subunit | 0.149181 | 0.001224 |
| **CydB\_1** | Cytochrome bd oxidase subunit II | 0.150159 | 0.019519 |
| **SlyX** | Protein SlyX | 0.150364 | 0.002582 |
| **BANRA\_04506** | Antibiotic biosynthesis monooxygenase | 0.153105 | 0.005023 |
| **KdpC** | Potassium-transporting ATPase KdpC subunit | 0.153591 | 0.000127 |
| **YfdX** | Protein YfdX | 0.153605 | 0.007436 |
| **HpcE\_1** | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase | 0.157178 | 0.000251 |
| **MppA** | MppA protein | 0.157229 | 0.000459 |
| **GJJ01\_05795** | Nucleotidyltransferase domain-containing protein | 0.157235 | 0.000105 |
| **IolH** | Glyceraldehyde-3-phosphate ketol-isomerase | 0.157266 | 0.000777 |
| **DD581\_13095** | Cupin | 0.157672 | 0.006166 |
| **DksA** | RNA polymerase-binding transcription factor DksA | 0.157811 | 0.002787 |
| **B4U21\_10035** | UPF0509 protein B4U21\_10035 | 0.158519 | 0.000329 |
| **YgdI** | Lipoprotein | 0.159413 | 0.000038 |
| **GJJ01\_03830** | Anaerobic C4-dicarboxylate transporter | 0.159598 | 0.018318 |
| **B4U21\_31020** | Uncharacterized lipoprotein YifL | 0.159652 | 0.013895 |
| **C4Y50\_029935** | Iron-containing redox enzyme family protein | 0.159802 | 0.000104 |
| **PpsA** | Phosphoenolpyruvate synthase | 0.160418 | 0.000004 |
| **RimK** | Probable alpha-L-glutamate ligase | 0.160821 | 0.000106 |
| **ArcB** | Aerobic respiration control sensor protein | 0.161162 | 0.000174 |
| **YniA** | Fructosamine kinase family protein | 0.161339 | 0.000262 |
| **YjbJ** | UPF0337 protein YjbJ | 0.161619 | 0.00009 |
| **Cdh** | CDP-diacylglycerol pyrophosphatase | 0.163426 | 0.00003 |
| **AtkA** | Potassium-transporting ATPase potassium-binding subunit | 0.163661 | 0.000634 |
| **OppB** | Oligopeptide ABC transporter permease OppB | 0.164365 | 0.000861 |
| **Crl** | Sigma factor-binding protein Crl | 0.164884 | 0.000005 |
| **FabG\_3** | 3-oxoacyl-ACP reductase | 0.166466 | 0.003458 |
| **Fpr** | Ferredoxin (flavodoxin):NADP(+) oxidoreductase | 0.167596 | 0.000001 |
| **DctA** | C4-dicarboxylate transport protein | 0.168703 | 0.000531 |
| **CpxR** | Copper-sensing two-component system response regulator CpxR | 0.168853 | 0.001061 |
| **GJJ01\_23975** | DUF1349 domain-containing protein | 0.169705 | 0.001795 |
| **B4U21\_01410** | UPF0325 protein B4U21\_01410 | 0.171515 | 0.00001 |
| **Blc** | Outer membrane lipoprotein Blc | 0.172641 | 0.156284 |
| **LpxO** | Aspartyl beta-hydroxylase | 0.172704 | 0.000167 |
| **AdhC2** | Alcohol dehydrogenase | 0.172728 | 0.000072 |
| **FadB** | Fatty acid oxidation complex subunit alpha | 0.172752 | 0.000007 |
| **YfcH** | Cell division inhibitor | 0.172956 | 0.000138 |
| **AphA** | Class B acid phosphatase | 0.173196 | 0.000232 |
| **MliC** | C-type lysozyme inhibitor | 0.173484 | 0.000257 |
| **ArgC** | N-acetyl-gamma-glutamyl-phosphate reductase | 0.17471 | 0.087388 |
| **AroD** | 3-dehydroquinate dehydratase | 0.174877 | 0.000062 |
| **UspG** | Universal stress protein G | 0.175575 | 0.00104 |
| **YhbH** | Ribosomal subunit interface protein | 0.176724 | 0.001549 |
| **ArnB\_1** | UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase | 0.177693 | 0.000005 |
| **HlyD** | Macrolide export protein MacA | 0.177792 | 0.000008 |
| **TbpA** | Thiamine-binding periplasmic protein | 0.177899 | 0.000349 |
| **GJJ01\_12205** | Lactoylglutathione lyase | 0.178345 | 0.000027 |
| **DpiA** | Transcriptional regulatory protein | 0.178981 | 0.000249 |
| **PhoQ** | Sensor histidine protein kinase/phosphatase PhoQ | 0.180265 | 0.080482 |
| **IaaH** | Amidohydrolase | 0.180965 | 0.000399 |
| **GJJ01\_20800** | Deoxyguanosinetriphosphate triphosphohydrolase | 0.182249 | 0.016328 |
| **GlnH** | GlnH protein | 0.183267 | 0.001043 |
| **HutG** | Formimidoylglutamase | 0.183531 | 0.000008 |
| **Hpd** | 3-dehydroshikimate dehydratase | 0.185409 | 0.005152 |
| **AstC\_2** | Acetylornithine/succinyldiaminopimelate aminotransferase | 0.186125 | 0.000092 |
| **B4U21\_09100** | Manganese catalase | 0.186133 | 0.005206 |
| **BL124\_00004595** | Lipoprotein | 0.186205 | 0.022386 |
| **CurA** | Oxidoreductase YncB | 0.186656 | 0.000002 |
| **Can\_2** | Carbonic anhydrase | 0.187525 | 0.00048 |
| **GhrA\_1** | Glyoxylate/hydroxypyruvate reductase A | 0.187874 | 0.000034 |
| **YceI** | Polyisoprenoid-binding protein | 0.190259 | 0.001523 |
| **RseA** | Anti-sigma-E factor RseA | 0.190875 | 0 |
| **BANRA\_01135** | DUF1176 domain-containing protein | 0.190988 | 0.007425 |
| **GabT** | 4-aminobutyrate--2-oxoglutarate transaminase | 0.191238 | 0.000109 |
| **DhaL** | DhaL protein | 0.191756 | 0.000101 |
| **YbhF\_3** | ABC transporter multidrug efflux pump | 0.191766 | 0.000127 |
| **FadA** | 3-ketoacyl-CoA thiolase | 0.193597 | 0.000004 |
| **Eco** | Ecotin | 0.195276 | 0.000014 |
| **GstA** | Glutathione S-transferase GstA | 0.195536 | 0.007112 |
| **DhaT\_2** | Alcohol dehydrogenase | 0.195795 | 0.000219 |
| **AcrR\_1** | TetR family transcriptional regulator | 0.196003 | 0 |
| **Gmr** | EAL domain-containing protein | 0.196015 | 0.000621 |
| **GlnE** | Bifunctional glutamine synthetase adenylyltransferase/adenylyl-removing enzyme | 0.19752 | 0.000037 |
| **YfcF** | Glutathione S-transferase | 0.198245 | 0.00021 |
| **PncC\_3** | 2-oxo-tetronate isomerase | 0.198708 | 0.000054 |
| **PpsC\_1** | NAD(P)H-quinone oxidoreductase | 0.198802 | 0.000097 |
| **HslJ** | Heat shock protein HslJ | 0.200177 | 0.003696 |
| **PcaC** | 4-carboxymuconolactone decarboxylase | 0.20026 | 0.000019 |
| **B4U25\_32810** | Probable metal-binding protein (DUF2387) | 0.200435 | 0.005886 |
| **GJJ01\_03350** | Uncharacterized protein conserved in bacteria | 0.201863 | 0.000046 |
| **PhoH** | PhoH protein | 0.204794 | 0.000024 |
| **PspF\_2** | PRD domain-containing protein | 0.204834 | 0.001352 |
| **Dpp5** | Tol-Pal system protein TolB | 0.204961 | 0.00006 |
| **ArnA** | Bifunctional polymyxin resistance protein ArnA | 0.206309 | 0.000001 |
| **YjjU** | Patatin family protein | 0.207496 | 0.004987 |
| **KdpC** | KdpC | 0.207596 | 0.000325 |
| **YeaG** | PrkA family serine protein kinase | 0.209041 | 0.000072 |
| **YmrA** | PmrA | 0.209409 | 0.003727 |
| **GlpK** | Glycerol kinase | 0.211418 | 0.000117 |
| **IolS\_2** | Aldo/keto reductase | 0.211684 | 0.000031 |
| **CisY** | Citrate synthase | 0.211705 | 0.00002 |
| **UspC** | Universal stress protein | 0.211731 | 0.006422 |
| **BANRA\_00130** | DUF1338 domain-containing protein | 0.212278 | 0.000278 |
| **NfnB** | NAD(P)H nitroreductase | 0.214879 | 0.000004 |
| **PuuD** | Gamma-glutamyl-gamma-aminobutyrate hydrolase | 0.215005 | 0.01501 |
| **YpdC\_1** | AraC family transcriptional regulator | 0.217708 | 0.007167 |
| **B4U21\_06550** | Asp/Glu/hydantoin racemase | 0.218044 | 0.000083 |
| **B4U21\_28520** | Epimerase KguE | 0.219833 | 0.000095 |
| **YbjP** | Lipoprotein | 0.220158 | 0.00106 |
| **FadJ** | Fatty acid oxidation complex subunit alpha | 0.220983 | 0.00004 |
| **ModA** | Molybdate ABC transporter substrate-binding protein | 0.224048 | 0.013533 |
| **HipA** | HipA protein | 0.224857 | 0.000006 |
| **B4U21\_17675** | UPF0181 protein B4U21\_17675 | 0.225087 | 0.228662 |
| **ChaB** | Cation transport regulator | 0.226142 | 0.000606 |
| **ChbB** | PTS N,N'-diacetylchitobiose transporter subunit IIB | 0.227599 | 0.077862 |
| **B4U25\_26945** | Uncharacterized protein | 0.229336 | 0.000592 |
| **PotA\_5** | ABC transporter ATP-binding protein | 0.229987 | 0.000004 |
| **GJJ01\_06250** | Amino acid deaminase | 0.230386 | 0.017711 |
| **MobB** | Molybdopterin-guanine dinucleotide biosynthesis protein B | 0.230872 | 0.294446 |
| **Azr** | Chromate reductase | 0.231012 | 0.000001 |
| **Rna** | Ribonuclease I | 0.231269 | 0.000024 |
| **Tal** | Transaldolase | 0.231802 | 0.000086 |
| **GlgX** | Glycogen debranching enzyme | 0.232366 | 0.000209 |
| **PuuC** | Aldehyde dehydrogenase PuuC | 0.234382 | 0.000087 |
| **ArsC** | Arsenate reductase | 0.238134 | 0.000639 |
| **PxpA** | 5-oxoprolinase subunit A | 0.238652 | 0.000033 |
| **GJJ01\_27785** | DUF3833 family protein | 0.240155 | 0.041039 |
| **YbhB** | Kinase inhibitor | 0.240365 | 0.00011 |
| **B4U21\_29030** | DUF1454 domain-containing protein | 0.241252 | 0.007096 |
| **YbaY** | Glycoprotein-polysaccharide metabolism | 0.241824 | 0.012013 |
| **LacE\_3** | Glycerol-3-phosphate ABC transporter | 0.24237 | 0.00339 |
| **ElaB\_1** | Bacterial protein of uncharacterized function (DUF883) | 0.242818 | 0.000058 |
| **FcuA** | Putative TonB-dependent receptor | 0.244485 | 0.221708 |
| **KdgR\_2** | Helix-turn-helix domain-containing protein | 0.244708 | 0.000379 |
| **SerA** | 2-oxoglutarate reductase | 0.246688 | 0.000892 |
| **Bcr\_1** | Bcr/CflA family efflux transporter | 0.247259 | 0.000715 |
| **YceF** | 7-methyl-GTP pyrophosphatase | 0.248232 | 0.000314 |
| **YbiO** | Mechanosensitive channel protein | 0.24904 | 0.000071 |
| **RutR\_3** | HTH-type transcriptional repressor NicS | 0.2497 | 0.000307 |
| **SoxB\_1** | D-amino acid dehydrogenase | 0.249719 | 0.000002 |
| **GltP** | Proton/glutamate-aspartate symporter | 0.250951 | 0.000082 |
| **YrdN** | 4-oxalocrotonate tautomerase | 0.251045 | 0.034569 |
| **GldA** | DhaD protein | 0.251065 | 0.00002 |
| **Fbp** | Fructose-1,6-bisphosphatase class 1 | 0.252436 | 0.000001 |
| **ArnT** | Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase | 0.252748 | 0.099169 |
| **GlgC** | Glucose-1-phosphate adenylyltransferase | 0.253095 | 0.000017 |
| **IraP** | Anti-adapter protein IraP | 0.253141 | 0.000119 |
| **LivJ** | Branched chain amino acid ABC transporter substrate-binding protein LivJ | 0.254311 | 0.00041 |
| **GlmS\_3** | Glucosamine--fructose-6-phosphate aminotransferase | 0.25487 | 0.001771 |
| **YaeP** | UPF0253 protein B4U21\_01555 | 0.25525 | 0.000263 |
| **PtrA\_2** | Pitrilysin | 0.255561 | 0.000743 |
| **FeaB** | Aldehyde dehydrogenase family protein | 0.257515 | 0.001038 |
| **YvoA\_1** | HTH-type transcriptional repressor yvoA | 0.258225 | 0.000011 |
| **CdaR** | Carbohydrate diacid regulon transcriptional regulator CdaR | 0.258435 | 0.000001 |
| **GJJ01\_17095** | AsmA family protein | 0.258459 | 0.002568 |
| **YedY** | Protein-methionine-sulfoxide reductase catalytic subunit MsrP | 0.258578 | 0.129441 |
| **G5637\_15640** | Putative lyase | 0.258836 | 0.000089 |
| **GhrB** | Glyoxylate/hydroxypyruvate reductase B | 0.260594 | 0.000021 |
| **B4U21\_14760** | DUF2526 domain-containing protein | 0.260803 | 0.176016 |
| **LeuB** | 3-isopropylmalate dehydrogenase | 0.26201 | 0.000001 |
| **FtsP** | Cell division protein FtsP | 0.262194 | 0.000172 |
| **PoxB** | Pyruvate dehydrogenase | 0.262724 | 0.000058 |
| **LplT** | Lysophospholipid transporter LplT | 0.263778 | 0.000353 |
| **B4U21\_05280** | Zinc ribbon-containing protein | 0.265521 | 0.000006 |
| **MetC** | Cystathionine beta-lyase | 0.265561 | 0.007926 |
| **RocF** | Arginase | 0.265971 | 0.000038 |
| **GcvP** | Glycine dehydrogenase (decarboxylating) | 0.266689 | 0.000001 |
| **PutP** | Sodium/proline symporter | 0.266839 | 0.000161 |
| **GstB\_3** | Glutathione S-transferase | 0.266919 | 0.000235 |
| **Gap** | Glyceraldehyde-3-phosphate dehydrogenase | 0.266993 | 0.000861 |
| **CitE2** | Citrate (pro-3S)-lyase subunit beta | 0.267458 | 0.000106 |
| **GsiA\_7** | Nickel import ATP-binding protein NikE | 0.267986 | 0.130505 |
| **KduD** | 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase | 0.268555 | 0.001168 |
| **AraC\_1** | Arabinose operon regulatory protein | 0.268839 | 0.00185 |
| **CitF** | Citrate lyase alpha chain | 0.269113 | 0.005947 |
| **YgfA** | 5-formyltetrahydrofolate cyclo-ligase | 0.269228 | 0.000751 |
| **BANRA\_02381** | Acetyltransferase | 0.270824 | 0.000139 |
| **GsiC** | Dipeptide transport system permease DppB | 0.272105 | 0.132026 |
| **Rsd** | Regulator of sigma D | 0.275188 | 0.000057 |
| **BANRA\_02298** | Divergent polysaccharide deacetylase family protein | 0.275233 | 0.003629 |
| **B4U21\_29360** | Putative secreted protein | 0.275308 | 0.001217 |
| **B4U21\_30240** | PTS lactose transporter subunit IIB | 0.275412 | 0.015766 |
| **YqeD** | 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase | 0.275506 | 0.001471 |
| **RpoS2** | Regulator of RpoS | 0.275956 | 0.000131 |
| **ArnC** | Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase | 0.276279 | 0.000012 |
| **GabD\_2** | Succinate-semialdehyde dehydrogenase | 0.277082 | 0.000901 |
| **XylC** | 4-aminobutyraldehyde dehydrogenase | 0.2782 | 0.002672 |
| **YfcE** | Phosphoesterase | 0.278763 | 0.000975 |
| **SbmC** | DNA gyrase inhibitor | 0.27888 | 0.000211 |
| **CysZ** | Sulfate transporter CysZ | 0.280306 | 0.000066 |
| **ScrA** | Negative regulator of SacY activity | 0.28035 | 0.017148 |
| **Por\_2** | Fructuronate reductase | 0.280376 | 0.000552 |
| **OmpR** | DNA-binding response regulator | 0.280685 | 0.00008 |
| **RpoS** | RNA polymerase sigma factor RpoS | 0.280963 | 0.000741 |
| **YhaH** | DUF805 domain-containing protein | 0.281069 | 0.009303 |
| **KipI\_2** | 5-oxoprolinase subunit PxpB | 0.281671 | 0.000293 |
| **YdgJ\_3** | Oxidoreductase | 0.282003 | 0.012771 |
| **MmuM** | Homocysteine S-methyltransferase | 0.282291 | 0 |
| **ArnD** | Probable 4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase ArnD | 0.282721 | 0.00029 |
| **DM059\_04510** | Transcriptional repressor | 0.282786 | 0.007416 |
| **ProX** | Glycine betaine/L-proline ABC transporter substrate-binding protein ProX | 0.284443 | 0.029774 |
| **LsrF** | 3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase | 0.284502 | 0.00428 |
| **B4U21\_24985** | 26 kDa periplasmic immunogenic protein | 0.285284 | 0.000003 |
| **NhoA** | N-hydroxyarylamine O-acetyltransferase | 0.285308 | 0.000005 |
| **YciS** | Lipopolysaccharide assembly protein A | 0.285692 | 0.002002 |
| **YgdR\_2** | Lipoprotein ygdR | 0.285809 | 0.000005 |
| **RlmF** | Ribosomal RNA large subunit methyltransferase F | 0.287161 | 0.007093 |
| **IolC\_1** | 2-dehydro-3-deoxygluconokinase | 0.287605 | 0.000103 |
| **ChbA\_2** | PTS lactose/cellobiose transporter subunit IIA | 0.287612 | 0.000023 |
| **CitB2** | Transcriptional regulatory protein | 0.288211 | 0.000071 |
| **PaaX** | Phenylacetic acid degradation operon Negative regulatory protein PaaX | 0.288615 | 0.008184 |
| **UreC** | Urease subunit alpha | 0.289176 | 0.000813 |
| **FadH** | 2,4-dienoyl-CoA reductase | 0.290094 | 0.00001 |
| **CsiE** | CsiE protein | 0.291475 | 0.069399 |
| **Pal** | Peptidoglycan-associated protein | 0.293999 | 0.001322 |
| **GatY** | D-tagatose-1,6-bisphosphate aldolase subunit GatY | 0.295352 | 0.000708 |
| **YmdB** | O-acetyl-ADP-ribose deacetylase | 0.29572 | 0.000001 |
| **BglX** | Beta-D-glucoside glucohydrolase | 0.295869 | 0.000002 |
| **D1220\_26550** | C-lysozyme inhibitor | 0.296016 | 0.000109 |
| **AhpC** | Alkyl hydroperoxide reductase C | 0.297206 | 0.000987 |
| **OpuBC** | ABC transporter substrate-binding protein | 0.298853 | 0.000152 |
| **FepB** | Fe2+-enterobactin ABC transporter substrate-binding protein | 0.300961 | 0.020664 |
| **GdhA\_1** | Glutamate dehydrogenase | 0.301161 | 0.000024 |
| **PtsH** | Phosphocarrier protein HPr | 0.302172 | 0.0198 |
| **YpwA** | Metal-dependent carboxypeptidase | 0.302518 | 0.000008 |
| **YiaD** | Inner membrane lipoprotein YiaD | 0.30515 | 0.000642 |
| **GJJ01\_02240** | Glutathione S-transferase | 0.305434 | 0.010971 |
| **SurA** | Chaperone SurA | 0.306148 | 0.000001 |
| **B4U21\_08235** | DUF1311 domain-containing protein | 0.307647 | 0.002 |
| **YdcF** | Protein ydcF | 0.308248 | 0.000094 |
| **YbdG\_2** | Mechanosensitive ion channel | 0.308515 | 0.006787 |
| **YqjG** | Glutathione S-transferase | 0.308625 | 0.000088 |
| **SucD** | Succinate--CoA ligase [ADP-forming] subunit alpha | 0.310071 | 0.000015 |
| **AttT** | AttT protein | 0.311615 | 0.005462 |
| **EmtA** | Endo-type membrane-bound lytic murein transglycosylase A | 0.31284 | 0.0194 |
| **GJJ01\_02105** | HAD-IC family P-type ATPase | 0.313046 | 0.000014 |
| **DhaK\_2** | Dihydroxyacetone kinase, ATP-dependent | 0.315617 | 0.000037 |
| **PspA** | Phage shock protein A | 0.316038 | 0.001437 |
| **YdgH** | DUF1471 domain-containing protein | 0.316345 | 0.000103 |
| **YtfK** | DUF1107 domain-containing protein | 0.316478 | 0.057832 |
| **RihC** | Non-specific ribonucleoside hydrolase RihC | 0.316494 | 0.006557 |
| **SltY** | Peptidoglycan lytic exotransglycosylase | 0.318498 | 0.000029 |
| **ErfK** | L,D-transpeptidase | 0.318876 | 0.000356 |
| **YncE\_2** | Putative receptor | 0.318995 | 0.000006 |
| **IlvN** | Acetolactate synthase | 0.319224 | 0.00595 |
| **CopA** | Copper-exporting P-type ATPase A | 0.321082 | 0.020756 |
| **PtsP** | Phosphoenolpyruvate--protein phosphotransferase | 0.321585 | 0.020539 |
| **AtpE** | ATP synthase subunit c | 0.322608 | 0.065129 |
| **YcaC\_2** | Amidohydrolase | 0.322634 | 0.190808 |
| **YbdK** | Putative glutamate--cysteine ligase 2 | 0.322726 | 0.004366 |
| **YheI** | ABC transporter ATP-binding protein | 0.325952 | 0.000194 |
| **DmlR\_2** | D-malate degradation protein R | 0.32617 | 0.045564 |
| **B4U21\_31735** | Thiamin phosphate synthase | 0.326684 | 0.016301 |
| **YqcA** | Flavodoxin | 0.326869 | 0.000034 |
| **DmlR\_15** | LysR family transcriptional regulator | 0.327893 | 0.238262 |
| **ETE82\_15245** | SIS domain-containing protein | 0.330463 | 0.007802 |
| **DsbD\_2** | Cytochrome c-type biogenesis protein DsbD | 0.33067 | 0.001358 |
| **TraT** | TraT complement resistance protein | 0.330683 | 0.001957 |
| **PuuE** | 4-aminobutyrate--2-oxoglutarate transaminase | 0.330712 | 0.000672 |
| **YgaD\_1** | C-terminal domain of CinA type S | 0.33137 | 0.004088 |
| **YjjV** | Deoxyribonuclease | 0.331484 | 0.006685 |
| **CydA\_1** | Cytochrome bd-I ubiquinol oxidase subunit 1 | 0.332082 | 0.000497 |
| **UreE** | Urease accessory protein UreE | 0.332851 | 0.000126 |
| **B4U21\_29690** | Outer membrane lipoprotein YidQ | 0.332876 | 0.00309 |
| **B4U21\_15465** | CadC family transcriptional regulator | 0.333616 | 0.000506 |
| **B4U25\_27875** | DUF4440 domain-containing protein | 0.336379 | 0.000375 |
| **NpdA** | NAD-dependent protein deacylase | 0.336451 | 0.000033 |
| **DppA\_5** | ABC transporter substrate-binding protein | 0.33744 | 0.005263 |
| **PpnP** | Pyrimidine/purine nucleoside phosphorylase | 0.337571 | 0.000346 |
| **CfxP** | Phosphoribulokinase | 0.337826 | 0.000384 |
| **Dcp** | Dipeptidyl carboxypeptidase Dcp | 0.338667 | 0.000484 |
| **GmuD\_2** | 6-phospho-beta-glucosidase | 0.339183 | 0.010975 |
| **GsiA\_14** | ABC transporter ATP-binding protein | 0.339885 | 0.087936 |
| **AndAa** | Anthranilate 1,2-dioxygenase system ferredoxin--NAD(+) reductase component | 0.340029 | 0.000697 |
| **GcvT** | Aminomethyltransferase | 0.340591 | 0.000012 |
| **GJJ01\_06285** | GNAT family N-acetyltransferase | 0.340983 | 0.010077 |
| **YnhG** | L,D-transpeptidase YnhG | 0.341107 | 0.000072 |
| **LimB\_2** | LLM class flavin-dependent oxidoreductase | 0.341132 | 0.000273 |
| **FrsA** | Esterase FrsA | 0.341294 | 0.000089 |
| **NfuA** | Fe/S biogenesis protein NfuA | 0.341946 | 0.000078 |
| **TilS** | tRNA(Ile)-lysidine synthase | 0.342665 | 0.000013 |
| **ApbE\_1** | FAD:protein FMN transferase | 0.343985 | 0.004242 |
| **BANRA\_02142** | DUF2756 domain-containing protein | 0.344665 | 0.07231 |
| **PldA** | Phospholipase A1 | 0.345747 | 0.054895 |
| **GltK\_1** | Amino acid ABC transporter permease | 0.346488 | 0.003309 |
| **BANRA\_03358** | Inner membrane protein YqjK | 0.346909 | 0.030048 |
| **yhcB** | Cytochrome d ubiquinol oxidase subunit 3 | 0.348007 | 0.000015 |
| **sodA** | Superoxide dismutase | 0.348201 | 0.002054 |
| **ridA\_2** | Endoribonuclease L-PSP | 0.34847 | 0.002043 |
| **efeO** | Iron uptake system component EfeO | 0.348689 | 0.000253 |
| **YdiB\_1** | Shikimate 5-dehydrogenase | 0.348752 | 0.027415 |
| **HpaG** | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase | 0.349276 | 0.006786 |
| **Aat** | Leucyl/phenylalanyl-tRNA--protein transferase | 0.35105 | 0.001574 |
| **YihX** | Alpha-D-glucose 1-phosphate phosphatase YihX | 0.351938 | 0.000187 |
| **FdhF\_1** | CbbBc protein | 0.35248 | 0.014027 |
| **AcnB** | Aconitate hydratase B | 0.353133 | 0 |
| **YccF** | Inner membrane protein YccF | 0.353139 | 0.002339 |
| **BglG** | Beta-glucoside operon transcriptional antiterminator | 0.353332 | 0.01136 |
| **GJJ01\_00275** | Methyltransferase domain-containing protein | 0.353669 | 0.00749 |
| **MsrB** | Peptide methionine sulfoxide reductase MsrB | 0.353908 | 0.004879 |
| **AcrB\_3** | Efflux pump membrane transporter | 0.355919 | 0.000712 |
| **OsmY\_3** | BON domain-containing protein | 0.356398 | 0.000398 |
| **ApaG** | Protein ApaG | 0.35722 | 0.000157 |
| **YjcE** | Na(+)/H(+) exchanger protein | 0.357545 | 0.000337 |
| **RffM** | UDP-N-acetyl-D-mannosaminuronic acid transferase | 0.358713 | 0.00041 |
| **B4U21\_14460** | TetR family transcriptional regulator | 0.359794 | 0.000999 |
| **SucC** | Succinate--CoA ligase [ADP-forming] subunit beta | 0.360304 | 0.000001 |
| **AceB** | Malate synthase | 0.361172 | 0.021739 |
| **YccU** | CoA-binding protein | 0.361626 | 0.000335 |
| **SlyA\_1** | MarR family transcriptional regulator | 0.361641 | 0.000263 |
| **HemF** | Oxygen-dependent coproporphyrinogen-III oxidase | 0.362165 | 0.179324 |
| **FumC** | Fumarate hydratase class II | 0.362902 | 0.003778 |
| **BglT** | Glycoside hydrolase | 0.36319 | 0.006915 |
| **GloB** | Hydroxyacylglutathione hydrolase | 0.363659 | 0.000657 |
| **BglH\_2** | 6-phospho-beta-glucosidase | 0.363985 | 0.003727 |
| **CpoB** | Cell division coordinator CpoB | 0.364086 | 0.000529 |
| **YciI** | YciI family protein | 0.364341 | 0.009834 |
| **SthA** | Soluble pyridine nucleotide transhydrogenase | 0.366483 | 0.000865 |
| **B4U21\_32950** | Putative cytoplasmic protein | 0.366589 | 0.412813 |
| **RibE** | Riboflavin synthase | 0.366667 | 0.000027 |
| **ArtP** | Arginine ABC transporter ATP-binding protein ArtP | 0.366942 | 0.000278 |
| **PaaF** | Phenylacetate-coenzyme A ligase | 0.368538 | 0.00244 |
| **YxeP\_5** | Amidohydrolase | 0.3687 | 0.022233 |
| **GstB\_3** | Glutathione S-transferase | 0.368712 | 0.000191 |
| **RbnZ** | Ribonuclease BN | 0.368993 | 0.004316 |
| **AcnA** | Aconitate hydratase | 0.369062 | 0.000066 |
| **MprA** | McrB protein | 0.369515 | 0.001124 |
| **YjaB\_1** | Acetyltransferase | 0.369974 | 0.000327 |
| **SppA** | Protease 4 | 0.370199 | 0.000067 |
| **YoaC** | DUF1889 domain-containing protein | 0.371009 | 0.002705 |
| **YfbT** | Putative phosphatase | 0.371048 | 0.00012 |
| **YajI** | DUF3251 domain-containing protein | 0.372091 | 0.000286 |
| **Skp** | Chaperone protein Skp | 0.372362 | 0.000305 |
| **YfbU** | UPF0304 protein B4U21\_20295 | 0.372468 | 0.000023 |
| **FadR\_1** | HTH-type transcriptional regulator BetI | 0.372838 | 0.001507 |
| **RamA\_2** | Amidase | 0.372939 | 0.068495 |
| **YfeY** | Outer membrane lipoprotein YfeY | 0.373437 | 0.000015 |
| **Ggt** | Gamma-glutamyltransferase | 0.37387 | 0.000103 |
| **OdhB** | Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex | 0.374159 | 0.00022 |
| **GlpD** | Glycerol-3-phosphate dehydrogenase | 0.374481 | 0.000018 |
| **FdxH** | Formate dehydrogenase iron-sulfur subunit | 0.374766 | 0.000441 |
| **CutC** | Copper homeostasis protein CutC | 0.374921 | 0.000146 |
| **AsnB** | Asparagine synthase (glutamine-hydrolyzing) | 0.375172 | 0 |
| **DmlA** | D-malate dehydrogenase [decarboxylating] | 0.376004 | 0.000048 |
| **BsaA\_1** | Thioredoxin/glutathione peroxidase BtuE | 0.376591 | 0.000015 |
| **CysQ** | 3'(2'),5'-bisphosphate nucleotidase CysQ | 0.377125 | 0.000193 |
| **RihA** | Pyrimidine-specific ribonucleoside hydrolase RihA | 0.37825 | 0.000002 |
| **LdcC** | Lysine decarboxylase 2, constitutive | 0.379757 | 0.000024 |
| **CodA\_2** | Cytosine deaminase | 0.379798 | 0.125254 |
| **RbsD** | D-ribose pyranase | 0.381135 | 0.13485 |
| **B4U21\_10820** | Uncharacterized protein | 0.381155 | 0.089169 |
| **RdoA** | Stress response kinase A | 0.381546 | 0.000068 |
| **DgkA** | Diacylglycerol kinase | 0.38208 | 0.154268 |
| **B4U21\_33640** | Exported protein | 0.382195 | 0.001469 |
| **CbiH** | Cobalt-precorrin-3B C(17)-methyltransferase | 0.382197 | 0.000294 |
| **ProB** | Glutamate 5-kinase | 0.383234 | 0.165574 |
| **FadI** | 3-ketoacyl-CoA thiolase | 0.38434 | 0.002307 |
| **LspA** | Lipoprotein signal peptidase | 0.384471 | 0.404363 |
| **YnfB** | UPF0482 protein B4U21\_12195 | 0.38559 | 0.00073 |
| **OmpA** | Integral membrane protein YfiB | 0.386246 | 0.005779 |
| **YbbN** | Co-chaperone YbbN | 0.386605 | 0.000192 |
| **AhpF** | Alkyl hydroperoxide reductase subunit F | 0.387389 | 0.00004 |
| **LacI\_2** | Lac operon transcriptional repressor | 0.387681 | 0.000374 |
| **Glk** | Glucokinase | 0.389488 | 0.000062 |
| **YceB** | Lipoprotein | 0.391371 | 0.000121 |
| **GarD\_1** | Altronate dehydratase | 0.392183 | 0.016863 |
| **ETE82\_06505** | Iron-containing alcohol dehydrogenase | 0.393371 | 0.000226 |
| **YtfL** | DUF21 domain-containing protein | 0.393388 | 0.000081 |
| **PhoP** | DNA-binding transcriptional regulator PhoP | 0.394789 | 0.000146 |
| **RseB** | Anti-sigma E factor | 0.394852 | 0.000054 |
| **UshA** | Bifunctional UDP-sugar hydrolase/5'-nucleotidase | 0.396035 | 0.000728 |
| **Rof** | Rho-binding antiterminator | 0.396266 | 0.000763 |
| **Tag** | 3-methyl-adenine DNA glycosylase I | 0.396722 | 0.000785 |
| **NrdF** | Ribonucleoside-diphosphate reductase subunit beta | 0.397475 | 0.073457 |
| **DmlR\_9** | LysR family transcriptional regulator | 0.397901 | 0.023969 |
| **YobH** | Uncharacterized protein YobH | 0.397993 | 0.003101 |
| **PecS** | MarR family transcriptional regulator | 0.398079 | 0.074282 |
| **PcaF** | 3-oxoadipyl-CoA thiolase | 0.398885 | 0.001482 |
| **LuxS** | S-ribosylhomocysteine lyase | 0.398933 | 0.000126 |
| **B4U25\_18720** | DNA-binding response regulator | 0.401896 | 0.000431 |
| **QorA\_1** | Bifunctional zinc-containing alcohol dehydrogenase/quinone oxidoreductase | 0.403854 | 0.001136 |
| **GJJ01\_02085** | MBL fold metallo-hydrolase | 0.404196 | 0.300604 |
| **NfsA** | NADPH-dependent oxidoreductase | 0.405275 | 0.075248 |
| **DkgA** | 2,5-didehydrogluconate reductase DkgA | 0.406031 | 0.021013 |
| **Dxs\_3** | Transketolase | 0.406824 | 0.000362 |
| **CreB** | DNA-binding response regulator | 0.407024 | 0.008601 |
| **Idi** | Isopentenyl-diphosphate Delta-isomerase | 0.407028 | 0.000858 |
| **PdxH** | Pyridoxine/pyridoxamine 5'-phosphate oxidase | 0.407436 | 0.000274 |
| **LeuA\_1** | 2-isopropylmalate synthase | 0.408463 | 0.031444 |
| **CodB\_2** | Cytosine permease | 0.408603 | 0.002934 |
| **GJJ01\_19385** | Dihydrofolate reductase | 0.409227 | 0.009147 |
| **PepQ** | Xaa-Pro dipeptidase | 0.40929 | 0.000004 |
| **DhaK2** | DhaK2 protein | 0.409488 | 0.000071 |
| **CycA2** | CycA2 protein | 0.410425 | 0.003734 |
| **Mqo** | Probable malate:quinone oxidoreductase | 0.41068 | 0.000037 |
| **PuuB** | FAD-binding oxidoreductase | 0.411362 | 0.002167 |
| **RfaG** | Glycosyltransferase | 0.411794 | 0.000217 |
| **SseA** | Sulfurtransferase | 0.412166 | 0.000074 |
| **BANRA\_00128** | E3 ubiquitin--protein ligase | 0.41246 | 0.000169 |
| **B4U21\_02160** | L,D-transpeptidase family protein | 0.412744 | 0.012824 |
| **OppD** | ABC transporter ATP-binding protein | 0.413792 | 0.000661 |
| **PrlC** | Oligopeptidase A | 0.414021 | 0.00001 |
| **KefF** | Glutathione-regulated potassium-efflux system ancillary protein KefF | 0.414126 | 0.008596 |
| **PtsO** | HPr family phosphocarrier protein | 0.415529 | 0.070997 |
| **OprM\_2** | Efflux transporter outer membrane subunit | 0.415795 | 0.210517 |
| **LptA** | Lipopolysaccharide export system protein LptA | 0.416125 | 0.023737 |
| **OsmY\_2** | Divisome-associated lipoprotein YraP | 0.416285 | 0.000543 |
| **IcaR** | TetR family transcriptional regulator | 0.417263 | 0.00001 |
| **bcp** | Thioredoxin peroxidase | 0.417577 | 0.000023 |
| **BVX91\_22805** | ISNCY family transposase | 0.417618 | 0.046062 |
| **AspA** | Aspartate ammonia-lyase | 0.418893 | 0.000018 |
| **Fic\_1** | Cell filamentation protein Fic | 0.420071 | 0.011076 |
| **YgdG** | Flap endonuclease Xni | 0.421141 | 0.404513 |
| **TrpA** | Tryptophan synthase alpha chain | 0.422108 | 0.002934 |
| **YbgI** | GTP cyclohydrolase 1 type 2 | 0.422122 | 0.000285 |
| **MraZ** | Transcriptional regulator MraZ | 0.422278 | 0.000286 |
| **GabD\_1** | NADP-dependent succinate-semialdehyde dehydrogenase | 0.422366 | 0.002067 |
| **PabC** | Aminodeoxychorismate lyase | 0.423101 | 0.004305 |
| **OpgB** | Phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransferase | 0.423354 | 0.000251 |
| **GrxC** | Glutaredoxin | 0.42381 | 0.000198 |
| **TrpC** | Multifunctional fusion protein | 0.423994 | 0.005084 |
| **YeaD** | Putative glucose-6-phosphate 1-epimerase | 0.42557 | 0.000001 |
| **MdtE\_2** | Efflux RND transporter periplasmic adaptor subunit | 0.426114 | 0.077934 |
| **WecF** | TDP-N-acetylfucosamine:lipid II N-acetylfucosaminyltransferase | 0.42623 | 0.000728 |
| **YhjH\_1** | Cyclic di-GMP phosphodiesterase YhjH | 0.426835 | 0.000617 |
| **RppH** | RNA pyrophosphohydrolase | 0.427375 | 0.000228 |
| **UspA\_2** | Universal stress protein | 0.427546 | 0.001298 |
| **YqhD** | Alcohol dehydrogenase | 0.427732 | 0.022365 |
| **DD581\_14885** | Acetyltransferase | 0.427964 | 0.000035 |
| **B4U21\_15085** | RND transporter | 0.428631 | 0.128534 |
| **GcvR** | Glycine cleavage system transcriptional repressor | 0.429137 | 0.019015 |
| **GpmB** | Probable phosphoglycerate mutase GpmB | 0.429946 | 0.000211 |
| **YcgE\_2** | HTH-type transcriptional regulator MlrA | 0.430791 | 0.17532 |
| **BANRA\_02356** | AsmA family protein | 0.430924 | 0.000064 |
| **OsmE** | DNA-binding transcriptional activator OsmE | 0.431205 | 0.002228 |
| **Icd** | Isocitrate dehydrogenase [NADP] | 0.431344 | 0.000005 |
| **PpiB** | Peptidyl-prolyl cis-trans isomerase | 0.431514 | 0.003876 |
| **G7Z27\_14405** | Dimethyl sulfoxide reductase subunit A | 0.432379 | 0.064307 |
| **MlaB** | Lipid asymmetry maintenance protein MlaB | 0.432383 | 0.000792 |
| **KdpE** | DNA-binding response regulator | 0.433096 | 0.000228 |
| **DcuA** | Anaerobic C4-dicarboxylate transporter | 0.435171 | 0.10123 |
| **NuoK** | NADH-quinone oxidoreductase subunit K | 0.435709 | 0.00127 |
| **TatA** | Sec-independent protein translocase protein TatA | 0.438741 | 0.000059 |
| **YecD** | Hydrolase | 0.439175 | 0.000002 |
| **PyrG\_1** | CTP synthase (glutamine hydrolyzing) | 0.439315 | 0.000116 |
| **AraB\_1** | FGGY-family pentulose kinase | 0.439343 | 0.025738 |
| **TktB\_1** | Transketolase | 0.439585 | 0.000066 |
| **SpeG** | SpeG protein | 0.439642 | 0.070322 |
| **DeoC** | Deoxyribose-phosphate aldolase | 0.439704 | 0.041886 |
| **DegP** | Periplasmic serine endoprotease DegP-like | 0.439717 | 0.000021 |
| **YhaK** | Pirin family protein | 0.441034 | 0.008557 |
| **YciO** | Threonylcarbamoyl-AMP synthase | 0.44147 | 0.004299 |
| **MtlD** | Mannitol-1-phosphate 5-dehydrogenase | 0.441816 | 0.034971 |
| **FucA\_3** | Aldolase | 0.442625 | 0.009996 |
| **NhaA** | Na(+)/H(+) antiporter NhaA | 0.442927 | 0.02608 |
| **GJJ01\_01620** | FtsX-like permease family protein | 0.443085 | 0.13899 |
| **Hda** | DnaA regulatory inactivator Hda | 0.443399 | 0.001562 |
| **RlmA** | 23S rRNA (Guanine(745)-N(1))-methyltransferase | 0.443781 | 0.009748 |
| **PhrB** | Deoxyribodipyrimidine photo-lyase | 0.44414 | 0.075023 |
| **AldA** | Aldehyde dehydrogenase | 0.445348 | 0.003547 |
| **GdhA\_1** | Glutamate dehydrogenase | 0.445993 | 0.000367 |
| **B4U21\_29825** | Phosphopantetheinyl transferase | 0.446303 | 0.01156 |
| **GvcA** | Gcv operon activator | 0.446733 | 0.006813 |
| **YfcD** | Uncharacterized Nudix hydrolase YfcD | 0.446895 | 0.000956 |
| **GcvH** | Glycine cleavage system H protein | 0.447315 | 0.003342 |
| **Pat** | GNAT family N-acetyltransferase | 0.447763 | 0.024326 |
| **AscG\_2** | HTH-type transcriptional regulator AscG | 0.449206 | 0.004024 |
| **YybR\_1** | HxlR family transcriptional regulator | 0.449502 | 0.072723 |
| **YajL** | DJ-1 family protein | 0.450154 | 0.000182 |
| **B4U21\_25860** | Siderophore-interacting protein | 0.450312 | 0.00006 |
| **NudL** | Uncharacterized Nudix hydrolase NudL | 0.450464 | 0.001043 |
| **YdiA** | Putative phosphoenolpyruvate synthase regulatory protein | 0.451468 | 0.004276 |
| **UlaD** | 3-keto-L-gulonate-6-phosphate decarboxylase | 0.451543 | 0.024018 |
| **BANRA\_02140** | Ketosteroid isomerase-related protein | 0.4516 | 0.002138 |
| **TrmJ** | tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ | 0.452452 | 0.000466 |
| **IlvA** | L-threonine dehydratase | 0.452619 | 0.003169 |
| **YfbR** | 5'-deoxynucleotidase B6R99\_06510 | 0.455124 | 0.029196 |
| **MmsA** | 3-oxopropanoate dehydrogenase | 0.456801 | 0.008746 |
| **RimJ** | 30S ribosomal protein S5 alanine N-acetyltransferase | 0.457504 | 0.044955 |
| **CysK** | Cysteine synthase | 0.457785 | 0.000083 |
| **CobD** | L-threonine-O-3-phosphate decarboxylase | 0.45802 | 0.00308 |
| **ArcA** | Aerobic respiration control protein arcA | 0.458287 | 0.000196 |
| **HexR\_3** | DNA-binding transcriptional regulator HexR | 0.458367 | 0.025028 |
| **ETE94\_29105** | GTP-binding protein | 0.458556 | 0.001261 |
| **GppA** | Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase | 0.459641 | 0.000368 |
| **YnfD** | DUF1161 domain-containing protein | 0.460565 | 0.06912 |
| **CobA** | Siroheme synthase | 0.460779 | 0.003365 |
| **Amn** | AMP nucleosidase | 0.461368 | 0.000094 |
| **CpdB** | 2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase | 0.461766 | 0.011031 |
| **NamA** | FMN oxidoreductase | 0.462022 | 0.000371 |
| **MtnD** | Acireductone dioxygenase | 0.463043 | 0.0054 |
| **CobO** | Corrinoid adenosyltransferase | 0.464587 | 0.002969 |
| **PbpD** | Biosynthetic peptidoglycan transglycosylase | 0.464771 | 0.001766 |
| **EmrA** | Inner membrane protein yibH | 0.46556 | 0.000282 |
| **PutA** | Bifunctional protein PutA | 0.465794 | 0.00005 |
| **YiiM** | 6-N-hydroxylaminopurine resistance protein | 0.465908 | 0.003479 |
| **DsbC** | Thiol:disulfide interchange protein | 0.466553 | 0.000605 |
| **CreA** | Protein CreA | 0.467089 | 0.004446 |
| **YfiC** | tRNA1(Val) (adenine(37)-N6)-methyltransferase | 0.468219 | 0.040278 |
| **Rnk** | Regulator of nucleoside diphosphate kinase | 0.468673 | 0.000019 |
| **B4U21\_28050** | Phenolic acid decarboxylase | 0.470316 | 0.035181 |
| **B4U21\_13655** | ASCH domain-containing protein | 0.47062 | 0.016167 |
| **GlpQ** | Glycerophosphodiester phosphodiesterase | 0.471464 | 0.000138 |
| **GJJ01\_14605** | 2-dehydropantoate 2-reductase | 0.471567 | 0.030523 |
| **MtnA** | Methylthioribose-1-phosphate isomerase | 0.471777 | 0.009656 |
| **YhcM\_1** | Cell division protein ZapE | 0.472126 | 0.00009 |
| **CysM** | Cysteine synthase | 0.473175 | 0.007024 |
| **YjgR** | DUF853 family protein | 0.47322 | 0.00014 |
| **RhaR** | HTH-type transcriptional activator RhaR | 0.474109 | 0.091166 |
| **HcaR\_2** | LysR family transcriptional regulator | 0.475975 | 0.016147 |
| **NlpD** | Lipoprotein NlpD | 0.476077 | 0.00006 |
| **PepP** | Xaa-Pro aminopeptidase | 0.476365 | 0.009683 |
| **RfbA** | Glucose-1-phosphate thymidylyltransferase | 0.47649 | 0.001009 |
| **IhfB** | Integration host factor subunit beta | 0.478014 | 0.000561 |
| **GsiA\_1** | Dipeptide transport ATP-binding protein DppD | 0.478341 | 0.137526 |
| **SrlE\_2** | PTS glucitol/sorbitol transporter subunit IIB | 0.48015 | 0.000535 |
| **B4U25\_39520** | Transcriptional regulator | 0.481252 | 0.002626 |
| **OxyR\_1** | LysR family transcriptional regulator | 0.481324 | 0.005454 |
| **GalK** | Galactokinase | 0.481765 | 0.000385 |
| **Sdh** | Oxidoreductase | 0.481772 | 0.236396 |
| **RidA\_1** | 2-iminobutanoate/2-iminopropanoate deaminase | 0.482109 | 0.000604 |
| **YqeF** | 3-ketoacyl-CoA thiolase | 0.482941 | 0.021869 |
| **UxaB** | Altronate oxidoreductase | 0.48343 | 0.292845 |
| **PspB** | Envelope stress response membrane protein PspB | 0.483576 | 0.001197 |
| **DcrB** | DUF1795 domain-containing protein | 0.484024 | 0.000924 |
| **ETE82\_15865** | Formate dehydrogenase | 0.484358 | 0.017954 |
| **ManY\_3** | Mannose/fructose/sorbose family PTS transporter subunit IIC | 0.484584 | 0.000144 |
| **NuoN** | NADH-quinone oxidoreductase subunit N | 0.484821 | 0.000949 |
| **YjjA** | DUF2501 domain-containing protein | 0.486374 | 0.000271 |
| **AspC** | Aminotransferase | 0.487582 | 0.000011 |
| **B4U25\_17585** | DUF3313 domain-containing protein | 0.487976 | 0.007484 |
| **PgsA** | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase | 0.488136 | 0.001572 |
| **AsnA** | Aspartate--ammonia ligase | 0.488191 | 0.000178 |
| **AaeR** | D-malate degradation protein R | 0.488227 | 0.010231 |
| **SucA** | Oxoglutarate dehydrogenase (succinyl-transferring) | 0.490007 | 0.000001 |
| **YggN** | DUF2884 domain-containing protein | 0.490266 | 0.000418 |
| **SinR\_2** | Cupin domain-containing protein | 0.490389 | 0.002384 |
| **YdjH\_2** | 2-dehydro-3-deoxygluconokinase | 0.49041 | 0.000453 |
| **GlpR\_1** | DeoR family transcriptional regulator | 0.490536 | 0.00113 |
| **PepN** | Aminopeptidase N | 0.491031 | 0.000024 |
| **SmpA** | Outer membrane protein assembly factor BamE | 0.491761 | 0.000513 |
| **HupB** | DNA-binding protein HU-beta | 0.492573 | 0.000128 |
| **LldD** | L-lactate dehydrogenase | 0.492861 | 0.000047 |
| **RutR** | HTH-type transcriptional regulator RutR | 0.493647 | 0.003806 |
| **YcgF\_1** | BLUF domain/cyclic diguanylate phosphodiesterase (EAL) domain protein | 0.49367 | 0.0001 |
| **MoeB** | Molybdopterin biosynthesis protein MoeB | 0.49378 | 0.144415 |
| **CvpA** | Colicin V production protein | 0.494108 | 0.001948 |
| **YecE** | DUF72 domain-containing protein | 0.494663 | 0.000379 |
| **Dld** | Quinone-dependent D-lactate dehydrogenase | 0.495997 | 0.000134 |
| **B4U21\_09230** | DUF488 domain-containing protein | 0.496924 | 0.000469 |
| **YafJ** | Class II glutamine amidotransferase | 0.497255 | 0.000068 |
| **RaiA** | Ribosomal subunit interface protein | 0.498398 | 0.000128 |
| **TreB** | EIIBC-Tre | 0.500172 | 0.003413 |
| **CytR** | DNA-binding transcriptional regulator CytR | 0.500292 | 0.000318 |
| **TpiA** | Triosephosphate isomerase | 0.50058 | 0.003283 |
| **UspE** | Universal stress protein E | 0.50187 | 0.000011 |
| **B4U21\_07625** | DNA-binding protein | 0.501997 | 0.00126 |
| **YbiC\_2** | Ldh family oxidoreductase | 0.502363 | 0.022313 |
| **UreG** | Urease accessory protein UreG | 0.503105 | 0.003728 |
| **LysA** | Diaminopimelate decarboxylase | 0.504599 | 0.00429 |
| **YggG\_2** | M48 family metalloprotease | 0.504867 | 0.000467 |
| **GarR** | 2-hydroxy-3-oxopropionate reductase | 0.505423 | 0.000298 |
| **B4U25\_41320** | DUF2164 domain-containing protein | 0.506877 | 0.232528 |
| **AldB\_2** | Aldehyde dehydrogenase | 0.507283 | 0.00514 |
| **TorZ** | Biotin sulfoxide reductase | 0.50833 | 0.041373 |
| **GshA** | Glutamate--cysteine ligase | 0.508631 | 0.00017 |
| **HisJ** | Histidine ABC transporter | 0.509931 | 0.000169 |
| **TopA\_1** | DNA topoisomerase 1 | 0.512242 | 0.01655 |
| **B4U21\_05600** | DUF2517 domain-containing protein | 0.512443 | 0.041222 |
| **YgdH** | AMP nucleosidase | 0.512544 | 0.000128 |
| **C2U49\_27415** | DNA-binding transcriptional regulator | 0.512934 | 0.005892 |
| **YgeA** | Aspartate racemase | 0.512938 | 0.000957 |
| **ElbB** | Glyoxalase | 0.51423 | 0.000071 |
| **GalR** | Galactose operon repressor | 0.514414 | 0.001641 |
| **ThrA** | Bifunctional aspartokinase/homoserine dehydrogenase | 0.514435 | 0.00025 |
| **YgjG** | Putrescine aminotransferase | 0.514599 | 0.126611 |
| **IlvN** | Acetolactate synthase | 0.516071 | 0.003768 |
| **PdxY** | Pyridoxal kinase PdxY | 0.516967 | 0.023053 |
| **FolA** | Dihydrofolate reductase | 0.517338 | 0.000648 |
| **DacC** | Serine-type D-Ala-D-Ala carboxypeptidase | 0.518416 | 0.000027 |
| **HspQ** | Heat shock protein HspQ | 0.518507 | 0.07358 |
| **GlpG** | Rhomboid protease GlpG | 0.518593 | 0.005168 |
| **RbsK** | Ribokinase | 0.519304 | 0.028088 |
| **Rpe** | Ribulose-phosphate 3-epimerase | 0.520248 | 0.001153 |
| **YciH** | Stress response translation initiation inhibitor YciH | 0.520398 | 0.018969 |
| **WecB** | UDP-N-acetylglucosamine 2-epimerase | 0.520454 | 0.002019 |
| **SelD** | Selenide, water dikinase | 0.520473 | 0.000225 |
| **B4U21\_11670** | DUF945 domain-containing protein | 0.52056 | 0.001312 |
| **YhbS** | Acetyltransferase | 0.521188 | 0.004165 |
| **B4U21\_08460** | Lipoprotein | 0.522452 | 0.012866 |
| **YaiW** | DUF1615 domain-containing protein | 0.522457 | 0.000139 |
| **MsrA** | Peptide methionine sulfoxide reductase MsrA | 0.523262 | 0.008547 |
| **PheA** | Bifunctional chorismate mutase/prephenate dehydratase | 0.523497 | 0.000389 |
| **ClpA** | ATP-dependent Clp protease ATP-binding subunit | 0.524047 | 0.000056 |
| **HemE** | Uroporphyrinogen decarboxylase | 0.524128 | 0.000337 |
| **MviM** | Gfo/Idh/MocA family oxidoreductase | 0.524483 | 0.00169 |
| **TyrB\_2** | Aminotransferase | 0.52449 | 0.000066 |
| **FxsA** | Membrane protein FxsA | 0.524561 | 0.018865 |
| **OppF** | ABC transporter ATP-binding protein | 0.524854 | 0.000583 |
| **NagK** | N-acetyl-D-glucosamine kinase | 0.525002 | 0.000091 |
| **ClsB** | Cardiolipin synthase B | 0.525196 | 0.004142 |
| **ThiL** | Thiamine-monophosphate kinase | 0.527696 | 0.026257 |
| **AzoR** | FMN-dependent NADH-azoreductase | 0.529252 | 0.000027 |
| **PqiC** | ABC-type uncharacterized transport system, auxiliary component | 0.529851 | 0.007976 |
| **YajO** | Aldo/keto reductase | 0.531068 | 0.002125 |
| **YihD** | DUF1040 family protein | 0.531233 | 0.007527 |
| **EmrB** | Multidrug efflux MFS transporter permease subunit EmrB | 0.53141 | 0.098909 |
| **WabN** | Deacetylase | 0.531626 | 0.104787 |
| **LsrF\_2** | Phospho-2-dehydro-3-deoxyheptonate aldolase | 0.532613 | 0.050423 |
| **UbiF\_2** | 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase | 0.533257 | 0.000947 |
| **UbiG** | Ubiquinone biosynthesis O-methyltransferase | 0.533464 | 0.000005 |
| **AroA** | 3-phosphoshikimate 1-carboxyvinyltransferase | 0.533807 | 0.000027 |
| **DedA** | DedA family protein | 0.535015 | 0.020086 |
| **SdhA** | Succinate dehydrogenase flavoprotein subunit | 0.536324 | 0.00023 |
| **MutM** | Formamidopyrimidine-DNA glycosylase | 0.536793 | 0.020209 |
| **YgfZ** | tRNA-modifying protein YgfZ | 0.537841 | 0.000227 |
| **BlaSHV-28** | Beta-lactamase | 0.537883 | 0.004009 |
| **RraA** | Regulator of ribonuclease activity A | 0.53806 | 0.001715 |
| **MdoD** | Glucans biosynthesis protein D | 0.538484 | 0.000023 |
| **MutY** | Adenine DNA glycosylase | 0.538591 | 0.005141 |
| **B4U21\_32340** | DUF4156 domain-containing protein | 0.539291 | 0.013035 |
| **ManZ\_2** | PTS mannose transporter subunit IID | 0.539988 | 0.000852 |
| **Flk** | Flagella biosynthesis regulator | 0.540052 | 0.078276 |
| **KdpB** | Potassium-transporting ATPase ATP-binding subunit | 0.540115 | 0.002606 |
| **DgoD** | D-galactonate dehydratase | 0.540268 | 0.030455 |
| **LsrG** | (4S)-4-hydroxy-5-phosphonooxypentane-2,3-dione isomerase | 0.541379 | 0.09699 |
| **BglY** | Beta-galactosidase | 0.542491 | 0.001568 |
| **ArtJ\_2** | ABC transporter arginine-binding protein 1 | 0.543276 | 0.007396 |
| **ETE60\_06755** | Sucrose-6-phosphate hydrolase | 0.544196 | 0.113206 |
| **Bfr** | Bacterioferritin | 0.544679 | 0.004195 |
| **FliY\_4** | Cystine ABC transporter | 0.545161 | 0.014481 |
| **RssA** | NTE family protein rssA | 0.545258 | 0.067925 |
| **FumA** | Fumarate hydratase class I | 0.545395 | 0.000031 |
| **LolB** | Outer-membrane lipoprotein LolB | 0.545671 | 0.009518 |
| **AcrB** | Efflux pump membrane transporter | 0.54577 | 0.000277 |
| **RimL** | 50S ribosomal protein L7/L12-serine acetyltransferase | 0.545833 | 0.012083 |
| **AmpD** | 1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD | 0.547369 | 0.005986 |
| **BglA\_1** | 6-phospho-beta-glucosidase | 0.547497 | 0.067984 |
| **B4U21\_19045** | Helix-turn-helix domain-containing protein | 0.547689 | 0.185092 |
| **FadL** | Long-chain fatty acid transport protein | 0.547855 | 0.028102 |
| **PdxB** | Erythronate-4-phosphate dehydrogenase | 0.54811 | 0.000059 |
| **YmjA** | DUF2543 domain-containing protein | 0.548124 | 0.000313 |
| **B4U25\_31190** | B3/4 domain | 0.548206 | 0.005581 |
| **YhfA** | OsmC family protein | 0.548583 | 0.0003 |
| **SodA** | Superoxide dismutase | 0.548836 | 0.000235 |
| **RpiA** | Ribose-5-phosphate isomerase A | 0.549087 | 0.000399 |
| **Dgt** | Deoxyguanosinetriphosphate triphosphohydrolase | 0.549788 | 0.068795 |
| **BANRA\_02439** | DUF3748 domain-containing protein | 0.549815 | 0.000971 |
| **YjgM** | GNAT family N-acetyltransferase | 0.550193 | 0.012717 |
| **GJJ01\_09305** | Lipoate--protein ligase family protein | 0.550362 | 0.070877 |
| **Pgl** | 6-phosphogluconolactonase | 0.550533 | 0.000945 |
| **MsrC** | Free methionine-R-sulfoxide reductase | 0.550999 | 0.000016 |
| **YdfG** | Bifunctional NADP-dependent 3-hydroxy acid dehydrogenase/3-hydroxypropionate dehydrogenase YdfG | 0.551126 | 0.000828 |
| **NadE** | NH(3)-dependent NAD(+) synthetase | 0.551189 | 0.000086 |
| **MalH** | 6-phospho-alpha-glucosidase | 0.552394 | 0.08025 |
| **NadD** | Probable nicotinate-nucleotide adenylyltransferase | 0.552882 | 0.00141 |
| **GalP** | Arabinose-proton symporter | 0.553717 | 0.001057 |
| **NudE** | ADP compounds hydrolase nudE | 0.554819 | 0.000604 |
| **YciC** | UPF0259 membrane protein B4U25\_11700 | 0.554878 | 0.01396 |
| **Cho** | Cho protein | 0.555708 | 0.044944 |
| **FldC** | (R)-phenyllactyl-CoA dehydratase beta subunit | 0.555771 | 0.001297 |
| **Pgk** | Phosphoglycerate kinase | 0.557159 | 0.000393 |
| **YihI** | Der GTPase-activating protein YihI | 0.558135 | 0.009929 |
| **YegS** | Probable lipid kinase YegS-like | 0.558705 | 0.000142 |
| **FabY** | Acetyltransferase | 0.558731 | 0.027416 |
| **MsyB** | Acidic protein msyB | 0.558794 | 0.036122 |
| **B4U21\_24615** | GNAT family N-acetyltransferase | 0.55893 | 0.360454 |
| **HisJ\_2** | ABC transporter substrate-binding protein | 0.55905 | 0.0556 |
| **AcrA** | AcrA protein | 0.559624 | 0.000066 |
| **ClpB** | Chaperone protein ClpB | 0.55971 | 0.001193 |
| **GarD\_1** | Galactarate dehydratase (L-threo-forming) | 0.560294 | 0.000241 |
| **GlpT** | Glycerol-3-phosphate transporter | 0.561066 | 0.000037 |
| **LysS** | Lysine--tRNA ligase | 0.561127 | 0.000371 |
| **IbpB** | Small heat shock protein IbpB | 0.561348 | 0.023591 |
| **GalS** | DNA-binding transcriptional regulator GalS | 0.56149 | 0.077216 |
| **RlmB** | 23S rRNA (guanosine-2'-O-)-methyltransferase RlmB | 0.561612 | 0.027005 |
| **BANRA\_01590** | Uncharacterized protein | 0.561859 | 0.040583 |
| **FusA** | Elongation factor G | 0.561948 | 0.017042 |
| **Dtd** | D-aminoacyl-tRNA deacylase | 0.562907 | 0.00268 |
| **RecD** | RecBCD enzyme subunit RecD | 0.564394 | 0.002161 |
| **GuaC** | GMP reductase | 0.565816 | 0.000058 |
| **ThiQ** | Thiamine import ATP-binding protein ThiQ | 0.565843 | 0.002023 |
| **AscG\_1** | AscBF operon repressor | 0.565877 | 0.000313 |
| **LpoB** | Penicillin-binding protein activator LpoB | 0.565912 | 0.0013 |
| **BglH\_2** | 6-phospho-beta-glucosidase | 0.565996 | 0.013539 |
| **IspA** | (2E,6E)-farnesyl diphosphate synthase | 0.566413 | 0.03759 |
| **YedJ** | Metal-dependent phosphohydrolase | 0.566555 | 0.000497 |
| **FdhE** | Protein FdhE homolog | 0.566806 | 0.000051 |
| **LacI\_1** | Lac operon transcriptional repressor | 0.567017 | 0.000791 |
| **IolE\_1** | Putative epimerase/isomerase | 0.567592 | 0.184929 |
| **CpxA** | Histidine kinase | 0.567714 | 0.007175 |
| **SecG** | Protein-export membrane protein SecG | 0.567778 | 0.006381 |
| **ArgH** | Argininosuccinate lyase | 0.567942 | 0.000188 |
| **Fmt** | Methionyl-tRNA formyltransferase | 0.568726 | 0.000158 |
| **Slp** | Outer membrane protein Slp | 0.570591 | 0.002457 |
| **HisP** | Histidine ABC transporter | 0.570651 | 0.005668 |
| **Smg** | Protein Smg | 0.571719 | 0.208561 |
| **YcgE\_1** | HTH-type transcriptional regulator ycgE | 0.57264 | 0.000819 |
| **YcjF** | UPF0283 membrane protein F1D54\_16305 | 0.572945 | 0.02134 |
| **DapA\_2** | Dihydrodipicolinate synthase | 0.573186 | 0.208343 |
| **KdsB** | 3-deoxy-manno-octulosonate cytidylyltransferase | 0.573991 | 0.003589 |
| **YybR\_2** | Putative transcriptional regulator | 0.574858 | 0.102618 |
| **YcgM** | 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (Catechol pathway) | 0.575152 | 0.009536 |
| **GreB** | Transcription elongation factor GreB | 0.575808 | 0.034874 |
| **RsmS** | DUF2496 domain-containing protein | 0.575894 | 0.000602 |
| **YegH** | CBS domain-containing protein | 0.576688 | 0.039982 |
| **KsgA** | Ribosomal RNA small subunit methyltransferase A | 0.576895 | 0.000065 |
| **ZipA** | Cell division protein ZipA | 0.577124 | 0.07657 |
| **CorC** | CNNM family magnesium/cobalt transport protein CorC | 0.577482 | 0.000299 |
| **RecF** | DNA replication and repair protein RecF | 0.580158 | 0.08501 |
| **PtsN** | Nitrogen regulatory protein | 0.581031 | 0.015967 |
| **Lon\_1** | Lon protease | 0.581933 | 0.00123 |
| **CelA\_3** | PTS sugar transporter subunit IIB | 0.583246 | 0.005509 |
| **HemH** | Ferrochelatase | 0.583473 | 0.000817 |
| **PhoB** | Phosphate regulon transcriptional regulatory protein PhoB | 0.584781 | 0.000901 |
| **AroG** | Phospho-2-dehydro-3-deoxyheptonate aldolase | 0.584888 | 0.001342 |
| **RlmC** | 23S rRNA (uracil(747)-C(5))-methyltransferase RlmC | 0.585504 | 0.005732 |
| **YjeR** | Oligoribonuclease | 0.585605 | 0.00058 |
| **MacB** | Macrolide export ATP-binding/permease protein MacB | 0.58588 | 0.082188 |
| **QorB** | NAD(P)H-binding protein | 0.586202 | 0.002041 |
| **GalM** | Aldose 1-epimerase | 0.586714 | 0.000402 |
| **MurQ\_1** | Glucokinase regulatory protein | 0.587449 | 0.077392 |
| **UxaC** | Uronate isomerase | 0.588217 | 0.037991 |
| **BANRA\_01598** | dTDP-glucose pyrophosphorylase | 0.588386 | 0.210569 |
| **XylB** | Xylulose kinase | 0.589398 | 0.016798 |
| **RffG\_1** | SDR family NAD(P)-dependent oxidoreductase | 0.589682 | 0.000215 |
| **Nfi** | Endonuclease V | 0.589939 | 0.006887 |
| **SbcD** | Nuclease SbcCD subunit D | 0.591355 | 0.001138 |
| **FrlB\_3** | Phosphosugar isomerase | 0.59219 | 0.361035 |
| **DjlA** | Co-chaperone protein DjlA | 0.592708 | 0.002051 |
| **Crp** | Catabolite activator protein | 0.592766 | 0.000029 |
| **B4U21\_12410** | DUF4177 domain-containing protein | 0.592876 | 0.105051 |
| **B4U21\_18205** | 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase | 0.592981 | 0.007877 |
| **AroF** | Phospho-2-dehydro-3-deoxyheptonate aldolase | 0.593884 | 0.137242 |
| **GshB** | Glutathione synthetase | 0.59389 | 0.000252 |
| **Afr\_3** | 1,5-anhydro-D-fructose reductase | 0.593942 | 0.000745 |
| **MgsA** | Methylglyoxal synthase | 0.594737 | 0.130287 |
| **YajR\_2** | MFS transporter | 0.594828 | 0.017926 |
| **SlyB** | Outer membrane lipoprotein SlyB | 0.594912 | 0.0168 |
| **MltC** | Membrane-bound lytic murein transglycosylase C | 0.594951 | 0.019518 |
| **Tdk** | Thymidine kinase | 0.595621 | 0.000054 |
| **Tpx** | Thiol peroxidase | 0.596161 | 0.000468 |
| **YbeY** | Endoribonuclease YbeY | 0.597466 | 0.003081 |
| **CcpA\_1** | LacI family transcriptional regulator | 0.597667 | 0.227506 |
| **RodA** | Peptidoglycan glycosyltransferase MrdB | 0.598022 | 0.05463 |
| **KstR2\_2** | TetR family transcriptional regulator | 0.598234 | 0.270964 |
| **YhdN** | Aldo/keto reductase | 0.598388 | 0.010236 |
| **GlcR\_3** | DeoR family transcriptional regulator | 0.599379 | 0.072523 |
| **DegQ** | Periplasmic serine endoprotease DegP-like | 0.599574 | 0.014661 |
| **GJJ01\_04245** | Cupin domain-containing protein | 0.600198 | 0.006671 |
| **HtrB** | Lipid A biosynthesis lauroyltransferase | 0.601248 | 0.296474 |
| **AmiC\_2** | N-acetylmuramoyl-L-alanine amidase | 0.602247 | 0.000057 |
| **SapB** | Antimicrobial peptide ABC transporter permease SapB | 0.602346 | 0.148184 |
| **YetF\_1** | DUF421 domain-containing protein | 0.603087 | 0.104955 |
| **LexA** | LexA repressor | 0.604717 | 0.000435 |
| **NorG** | Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme | 0.605219 | 0.250245 |
| **YggX** | Probable Fe(2+)-trafficking protein | 0.605267 | 0.000559 |
| **SeqA** | Negative modulator of initiation of replication | 0.605332 | 0.000518 |
| **PyrC** | Dihydroorotase | 0.606231 | 0.000566 |
| **GJJ01\_10080** | MCE family protein | 0.606783 | 0.087057 |
| **RnhA** | Ribonuclease H | 0.607945 | 0.033548 |
| **Pyk** | Pyruvate kinase | 0.607971 | 0.000145 |
| **YdfH** | FCD domain-containing protein | 0.608033 | 0.001398 |
| **YggL** | DUF469 domain-containing protein | 0.608553 | 0.461795 |
| **YfgF\_2** | Diguanylate cyclase/cyclic diguanylate phosphodiesterase | 0.609337 | 0.014707 |
| **YgiN** | Antibiotic biosynthesis monooxygenase | 0.609551 | 0.000399 |
| **SlyD** | Peptidyl-prolyl cis-trans isomerase | 0.609817 | 0.000066 |
| **GJJ01\_09125** | AsmA2 domain-containing protein | 0.610238 | 0.001622 |
| **UvrB** | UvrABC system protein B | 0.610878 | 0.029962 |
| **GalE** | UDP-glucose 4-epimerase | 0.61094 | 0.000027 |
| **NagZ** | Beta-hexosaminidase | 0.611967 | 0.013219 |
| **YhhX** | Oxidoreductase | 0.612311 | 0.015955 |
| **ExoX** | Exodeoxyribonuclease X | 0.613286 | 0.224197 |
| **CyaY** | Iron-sulfur cluster assembly protein CyaY | 0.61455 | 0.000791 |
| **RbsR\_5** | Ribose operon repressor | 0.615348 | 0.052782 |
| **ArgG** | Argininosuccinate synthase | 0.616029 | 0.008471 |
| **GlnP** | GlnP protein | 0.616238 | 0.007726 |
| **YjiA\_1** | CobW/P47K family protein | 0.617514 | 0.004895 |
| **QorA\_3** | NADPH:quinone reductase | 0.617672 | 0.001729 |
| **AstE\_2** | Succinylglutamate desuccinylase | 0.617712 | 0.424883 |
| **PncA** | Bifunctional nicotinamidase/pyrazinamidase | 0.619391 | 0.014007 |
| **CbpA** | Curved DNA-binding protein | 0.620005 | 0.000522 |
| **ETE82\_03295** | Succinate-semialdehyde dehydrogenase | 0.620504 | 0.000983 |
| **Psd** | Phosphatidylserine decarboxylase proenzyme | 0.620709 | 0.000016 |
| **ZapD** | Cell division protein ZapD | 0.621235 | 0.002438 |
| **LolA** | Outer-membrane lipoprotein carrier protein | 0.62255 | 0.019763 |
| **MetA** | Homoserine O-succinyltransferase | 0.622705 | 0.267653 |
| **LysC** | Aspartokinase | 0.62318 | 0.000746 |
| **BL124\_00032005** | UPF0294 protein BL124\_00032005 | 0.623218 | 0.052542 |
| **MzrA** | Modulator protein MzrA | 0.623646 | 0.149938 |
| **NuoG** | NADH-quinone oxidoreductase | 0.623672 | 0.000161 |
| **YcgJ** | Methyltransferase domain-containing protein | 0.624628 | 0.030267 |
| **HslV** | ATP-dependent protease subunit HslV | 0.625358 | 0.043566 |
| **YggS** | Pyridoxal phosphate homeostasis protein | 0.626256 | 0.000033 |
| **GmhA** | Phosphoheptose isomerase | 0.626371 | 0.000486 |
| **PnbA** | Carboxylic ester hydrolase | 0.627262 | 0.003358 |
| **PanE** | 2-dehydropantoate 2-reductase | 0.627458 | 0.08054 |
| **HdfR** | HTH-type transcriptional regulator HdfR | 0.627515 | 0.000132 |
| **HemA** | Glutamyl-tRNA reductase | 0.628165 | 0.071839 |
| **HemD** | Uroporphyrinogen-III synthase | 0.629074 | 0.034272 |
| **RseC** | RseC protein | 0.629462 | 0.497569 |
| **GJJ01\_03680** | Putative transport protein F1D54\_09695 | 0.629556 | 0.003605 |
| **BL124\_00002440** | NAD(P)-dependent oxidoreductase | 0.630724 | 0.000849 |
| **MetH** | Methionine synthase | 0.631718 | 0.000424 |
| **Ugd** | UDP-glucose 6-dehydrogenase | 0.632404 | 0.000225 |
| **SgrR\_2** | HTH-type transcriptional regulator SgrR | 0.632959 | 0.002325 |
| **PurM** | Phosphoribosylformylglycinamidine cyclo-ligase | 0.633613 | 0.011224 |
| **YcdY** | Chaperone protein YcdY | 0.634091 | 0.004585 |
| **B4U21\_01020** | UPF0231 protein B4U21\_01020 | 0.634245 | 0.009683 |
| **SlyA** | Transcriptional regulator SlyA | 0.63637 | 0.00014 |
| **AroC** | Chorismate synthase | 0.636597 | 0.004254 |
| **Mlc\_2** | Making large colonies protein | 0.636617 | 0.006356 |
| **SdhB** | Succinate dehydrogenase iron-sulfur subunit | 0.637567 | 0.01227 |
| **UxuA\_2** | Mannonate dehydratase | 0.637668 | 0.033028 |
| **MurD** | UDP-N-acetylmuramoylalanine--D-glutamate ligase | 0.638661 | 0.007566 |
| **FeoC** | Probable [Fe-S]-dependent transcriptional repressor | 0.638871 | 0.538889 |
| **BamD** | Outer membrane protein assembly factor BamD | 0.639001 | 0.000656 |
| **LeuC** | 3-isopropylmalate dehydratase large subunit | 0.639186 | 0.001159 |
| **XeaX** | Carnitine monooxygenase reductase subunit | 0.639207 | 0.038872 |
| **Dcm** | Cytosine-specific methyltransferase | 0.639361 | 0.00708 |
| **LeuD** | 3-isopropylmalate dehydratase small subunit | 0.639412 | 0.353398 |
| **LsrR\_1** | Cytochrome C biogenesis protein CcdA | 0.639774 | 0.067117 |
| **FbaA** | Fructose-bisphosphate aldolase | 0.640102 | 0.000511 |
| **NarI** | NarI protein | 0.641082 | 0.013131 |
| **B4U21\_32995** | 2-dehydro-3-deoxyphosphooctonate aldolase | 0.641134 | 0.022775 |
| **YejG** | YejG protein | 0.641245 | 0.084871 |
| **GltB** | GltB protein | 0.641932 | 0.0002 |
| **RlmJ** | Ribosomal RNA large subunit methyltransferase J | 0.642894 | 0.004239 |
| **TusA\_2** | Putative sulfurtransferase YedF | 0.642908 | 0.301132 |
| **EnvZ** | Histidine kinase | 0.642918 | 0.130216 |
| **YhjJ** | Insulinase family protein | 0.643129 | 0.007104 |
| **AnmK** | Anhydro-N-acetylmuramic acid kinase | 0.643563 | 0.015834 |
| **Prc** | Carboxy terminal-processing peptidase | 0.644445 | 0.003052 |
| **NhaR** | LysR family transcriptional regulator | 0.645126 | 0.007844 |
| **PssA** | CDP-diacylglycerol--serine O-phosphatidyltransferase | 0.645386 | 0.005127 |
| **PlsX** | Phosphate acyltransferase | 0.645883 | 0.004909 |
| **YqiB** | DUF1249 domain-containing protein | 0.64689 | 0.091344 |
| **NlhH** | Alpha/beta hydrolase fold domain-containing protein | 0.647776 | 0.107439 |
| **DkgB** | 2,5-didehydrogluconate reductase DkgB | 0.647874 | 0.000052 |
| **RspB** | Putative dehydrogenase, NAD(P)-binding, starvation-sensing protein | 0.64824 | 0.052191 |
| **YicI** | Alpha-xylosidase | 0.648432 | 0.415002 |
| **OsmC** | OsmC family peroxiredoxin | 0.648959 | 0.031352 |
| **PflA** | Pyruvate formate-lyase-activating enzyme | 0.649481 | 0.000192 |
| **MutT** | 7,8-dihydro-8-oxoguanine-triphosphatase | 0.649784 | 0.001404 |
| **GarL** | 5-keto-4-deoxy-D-glucarate aldolase | 0.650062 | 0.043057 |
| **YheO** | Putative regulator | 0.650391 | 0.000217 |
| **CitD2** | Citrate lyase acyl carrier protein | 0.650605 | 0.002643 |
| **XthA** | Exodeoxyribonuclease III | 0.65063 | 0.000024 |
| **FhlA** | FhlA protein | 0.650855 | 0.01793 |
| **ClpP** | ATP-dependent Clp protease proteolytic subunit | 0.65093 | 0.001992 |
| **GbpR** | Galactose-binding protein regulator | 0.652251 | 0.026579 |
| **MgtA** | Magnesium-transporting ATPase, P-type 1 | 0.652333 | 0.079714 |
| **PptA** | Tautomerase PptA | 0.653026 | 0.010977 |
| **Crr** | Crr protein | 0.654351 | 0.000194 |
| **DmlR\_21** | HTH-type transcriptional regulator PgrR | 0.654513 | 0.41976 |
| **YcaR** | UPF0434 protein B4U21\_07450 | 0.655417 | 0.00117 |
| **YacG** | DNA gyrase inhibitor YacG | 0.655483 | 0.001602 |
| **HosA** | HosA protein | 0.65587 | 0.003668 |
| **Ddl** | D-alanine--D-alanine ligase | 0.656016 | 0.002042 |
| **RsmJ** | Ribosomal RNA small subunit methyltransferase J | 0.656728 | 0.000848 |
| **IlvE** | Branched-chain-amino-acid aminotransferase | 0.657054 | 0.000055 |
| **SerC** | Phosphoserine aminotransferase | 0.658004 | 0.00002 |
| **DeoC2** | Deoxyribose-phosphate aldolase | 0.658344 | 0.0007 |
| **SerB** | O-phosphoserine phosphohydrolase | 0.658465 | 0.000147 |
| **BL124\_00018790** | UPF0257 lipoprotein BL124\_00018790 | 0.659107 | 0.005342 |
| **DapL\_1** | Alanine transaminase | 0.659523 | 0.000405 |
| **DiaA** | DnaA initiator-associating protein DiaA | 0.660135 | 0.001883 |
| **PhnA** | Alkylphosphonate utilization operon protein PhnA | 0.660437 | 0.024225 |
| **FtsE** | Cell division ATP-binding protein FtsE | 0.660547 | 0.000466 |
| **PurN** | Phosphoribosylglycinamide formyltransferase | 0.660806 | 0.001701 |
| **PriC** | Primosomal replication protein N | 0.661614 | 0.334078 |
| **YiiS\_1** | DUF406 domain-containing protein | 0.662084 | 0.004106 |
| **Hpt** | Hypoxanthine phosphoribosyltransferase | 0.66211 | 0.043424 |
| **MtfA** | Protein MtfA | 0.662979 | 0.100317 |
| **TldD** | Metalloprotease TldD | 0.663418 | 0.000219 |
| **Kbl** | 2-amino-3-ketobutyrate coenzyme A ligase | 0.663552 | 0.008756 |
| **YhhW\_2** | Cupin domain-containing protein | 0.664076 | 0.030313 |
| **YhgF** | 30S ribosomal protein S1 | 0.664182 | 0.000072 |
| **NuoI** | NADH-quinone oxidoreductase subunit I | 0.664355 | 0.050477 |
| **HflC** | Protein HflC | 0.664498 | 0.001525 |
| **YgbJ** | 2-(Hydroxymethyl)glutarate dehydrogenase | 0.665096 | 0.002976 |
| **BANRA\_02075** | UPF0270 protein BANRA\_02075 | 0.666269 | 0.164532 |
| **NlpE** | Copper homeostasis protein CutF / Lipoprotein NlpE | 0.666657 | 0.002369 |
| **TsaA** | Alkyl hydroperoxide reductase C | 0.667659 | 0.00119 |
| **YrbK** | Lipopolysaccharide export system protein LptC | 0.667695 | 0.221464 |
| **ApbE2** | FAD:protein FMN transferase | 0.668435 | 0.000633 |
| **BssS** | Biofilm formation regulator BssS | 0.668513 | 0.148881 |
| **KefC** | Glutathione-regulated potassium-efflux system protein KefC | 0.668898 | 0.073421 |
| **Cdd** | Cytidine deaminase | 0.669119 | 0.048629 |
| **RibA** | GTP cyclohydrolase-2 | 0.669776 | 0.001038 |
| **MsgA** | DNA damage-inducible protein I | 0.670073 | 0.002002 |
| **PepD** | Aminoacyl-histidine dipeptidase | 0.671253 | 0.003916 |
| **TopB** | DNA topoisomerase 3 | 0.671776 | 0.005772 |
| **FolX** | D-erythro-7,8-dihydroneopterin triphosphate epimerase | 0.672994 | 0.011724 |
| **YceH** | UPF0502 protein B6R99\_10675 | 0.673899 | 0.005465 |
| **Lyx\_1** | Carbohydrate kinase | 0.674398 | 0.043128 |
| **RuvB** | Holliday junction ATP-dependent DNA helicase RuvB | 0.674493 | 0.00184 |
| **HtpG** | Chaperone protein HtpG | 0.674651 | 0.002636 |
| **DmlR\_10** | HTH-type transcriptional regulator DmlR | 0.674993 | 0.001943 |
| **TrpB** | Tryptophan synthase beta chain | 0.676309 | 0.006133 |
| **YdhF** | Aldo/keto reductase | 0.676684 | 0.01879 |
| **FtsI** | Peptidoglycan D,D-transpeptidase FtsI | 0.676707 | 0.01972 |
| **YbfF** | Acyl-CoA esterase | 0.677197 | 0.024813 |
| **BirA** | Bifunctional ligase/repressor BirA | 0.677321 | 0.037165 |
| **YbiP** | Phosphoethanolamine transferase | 0.678067 | 0.187966 |
| **TrxA** | Thioredoxin | 0.678918 | 0.003097 |
| **PurD** | Phosphoribosylamine--glycine ligase | 0.679038 | 0.270438 |
| **GlyA** | Serine hydroxymethyltransferase | 0.67937 | 0.00214 |
| **AcpP** | Acyl carrier protein | 0.679733 | 0.002115 |
| **CpdA\_1** | 3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA | 0.680367 | 0.001705 |
| **SbmA** | Microcin B17 transporter | 0.682244 | 0.213543 |
| **YcfH** | Deoxyribonuclease | 0.682274 | 0.001408 |
| **YbdG** | Mechanosensitive ion channel | 0.682371 | 0.01462 |
| **Can** | Carbonic anhydrase | 0.684318 | 0.243035 |
| **GrxA** | GlrX1 protein | 0.684753 | 0.015302 |
| **AcrA\_1** | Efflux RND transporter periplasmic adaptor subunit | 0.686601 | 0.025946 |
| **YrbF** | ABC transporter ATP-binding protein | 0.687568 | 0.002289 |
| **YajQ** | UPF0234 protein B4U25\_03790 | 0.68845 | 0.001071 |
| **DeoB** | Phosphopentomutase | 0.688474 | 0.000679 |
| **McbR** | GntR family transcriptional regulator | 0.688519 | 0.113116 |
| **GrpE** | Protein GrpE | 0.689116 | 0.001888 |
| **PurC** | Phosphoribosylaminoimidazole-succinocarboxamide synthase | 0.690437 | 0.001081 |
| **AsnC** | AsnC protein | 0.690591 | 0.083056 |
| **SupH** | Cof-type HAD-IIB family hydrolase | 0.690665 | 0.01252 |
| **HisF** | Imidazole glycerol phosphate synthase subunit HisF | 0.690748 | 0.013802 |
| **PtsG\_1** | EIICBA-Glc | 0.69104 | 0.00174 |
| **YbiB** | DNA-binding protein YbiB | 0.692072 | 0.002046 |
| **YfhA** | Quorum-sensing regulator protein F | 0.692125 | 0.039229 |
| **GroES** | 10 kDa chaperonin | 0.6927 | 0.001306 |
| **YdaM\_2** | Diguanylate cyclase | 0.693322 | 0.210271 |
| **DnaK** | Chaperone protein DnaK | 0.694007 | 0.000817 |
| **YajR\_1** | MFS transporter | 0.694201 | 0.003754 |
| **FabR** | HTH-type transcriptional repressor FabR | 0.694733 | 0.075562 |
| **FruR\_2** | Catabolite repressor/activator | 0.694927 | 0.001028 |
| **LrpC** | AsnC family transcriptional regulator | 0.695518 | 0.576131 |
| **TrpS** | Tryptophan--tRNA ligase | 0.695673 | 0.000525 |
| **MetQ\_1** | Lipoprotein | 0.695726 | 0.009653 |
| **YibT** | YibT protein | 0.695957 | 0.297642 |
| **MurQ** | N-acetylmuramic acid 6-phosphate etherase | 0.696253 | 0.017299 |
| **AroB** | 3-dehydroquinate synthase | 0.696464 | 0.000073 |
| **NuoA** | NADH-quinone oxidoreductase subunit A | 0.69737 | 0.000857 |
| **NuoC** | NADH-quinone oxidoreductase subunit C/D | 0.698144 | 0.000102 |
| **MalG** | MalG protein | 0.698934 | 0.084247 |
| **TehB** | Tellurite resistance methyltransferase TehB | 0.698983 | 0.002932 |
| **YaeQ** | YaeQ family protein | 0.699537 | 0.005129 |
| **GpmA** | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase | 0.700032 | 0.005497 |
| **Asd** | Aspartate-semialdehyde dehydrogenase | 0.700639 | 0.004262 |
| **FolM** | Dihydromonapterin reductase | 0.700783 | 0.001545 |
| **GlcR\_4** | DeoR family transcriptional regulator | 0.701045 | 0.031928 |
| **Mpl** | UDP-N-acetylmuramate--L-alanyl-gamma-D-glutamyl-meso-2,6-diaminoheptandioate ligase | 0.701473 | 0.001119 |
| **FtsW** | Probable peptidoglycan glycosyltransferase FtsW | 0.701721 | 0.008462 |
| **ArgD** | Acetylornithine/succinyldiaminopimelate aminotransferase | 0.703042 | 0.013006 |
| **BaiA1** | Bile acid 7-dehydroxylase 1/3 | 0.703323 | 0.238363 |
| **IolS\_3** | Aldo-keto reductase | 0.704229 | 0.121753 |
| **BN49\_2482** | Bacterial regulatory proteins, tetR family | 0.704566 | 0.327506 |
| **BepA\_1** | Beta-barrel assembly-enhancing protease | 0.704886 | 0.120124 |
| **RamA\_2** | (R)-stereoselective amidase | 0.705498 | 0.055366 |
| **ManX** | EIIAB-Man | 0.706511 | 0.001258 |
| **HolB** | DNA polymerase III subunit delta' | 0.707066 | 0.012276 |
| **B4U21\_24675** | YCII-related domain | 0.707509 | 0.41737 |
| **Tal** | Transaldolase | 0.708712 | 0.001292 |
| **BglA\_1** | 6-phospho-beta-glucosidase | 0.70902 | 0.001372 |
| **YdiI** | 1,4-dihydroxy-2-naphthoyl-CoA hydrolase | 0.709339 | 0.010784 |
| **TrpD** | Anthranilate phosphoribosyltransferase | 0.709682 | 0.027867 |
| **EntA** | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase | 0.70997 | 0.010789 |
| **YqjI** | PadR family transcriptional regulator | 0.710328 | 0.028444 |
| **PhoU** | Phosphate-specific transport system accessory protein PhoU | 0.710507 | 0.009319 |
| **Gor** | Glutathione reductase | 0.712191 | 0.000107 |
| **SpeE** | Polyamine aminopropyltransferase | 0.712233 | 0.000493 |
| **Map** | Methionine aminopeptidase | 0.713082 | 0.023949 |
| **HisE** | Histidine biosynthesis bifunctional protein HisIE | 0.71373 | 0.131135 |
| **ModC** | Molybdenum import ATP-binding protein ModC | 0.716724 | 0.131279 |
| **LpxK** | Tetraacyldisaccharide 4'-kinase | 0.716951 | 0.003664 |
| **PrfB** | Peptide chain release factor 2 | 0.717278 | 0.000049 |
| **GreA** | Transcription elongation factor GreA | 0.717773 | 0.000228 |
| **Pad1\_2** | Flavin prenyltransferase UbiX | 0.717992 | 0.014497 |
| **GlxK\_1** | Glycerate 2-kinase | 0.718002 | 0.103053 |
| **Mfd** | Transcription-repair-coupling factor | 0.718038 | 0.101966 |
| **NadC** | Quinolinate phosphoribosyltransferase [decarboxylating] | 0.720032 | 0.008745 |
| **MltA** | Membrane-bound lytic murein transglycosylase A | 0.720044 | 0.016736 |
| **Pgi** | Glucose-6-phosphate isomerase | 0.720483 | 0.000316 |
| **RsxC** | Ion-translocating oxidoreductase complex subunit C | 0.720643 | 0.024685 |
| **HemC** | Porphobilinogen deaminase | 0.721509 | 0.003307 |
| **YtfP** | AIG2 family protein | 0.722444 | 0.00439 |
| **YjbR\_2** | MmcQ/YjbR family DNA-binding protein | 0.725575 | 0.039409 |
| **AcrR\_1** | AcrR (Fragment) | 0.726798 | 0.232874 |
| **ZntB** | Zinc transport protein ZntB | 0.728662 | 0.228869 |
| **MoaE2** | MPT synthase subunit 2 | 0.728706 | 0.474336 |
| **MinE** | Cell division topological specificity factor | 0.729472 | 0.00841 |
| **Agp** | 3-phytase | 0.729786 | 0.315437 |
| **B4U21\_28540** | DUF3053 domain-containing protein | 0.730128 | 0.012525 |
| **YghU** | Disulfide-bond oxidoreductase YghU | 0.730164 | 0.004852 |
| **AbgR\_1** | DNA-binding transcriptional regulator | 0.731393 | 0.450897 |
| **YciA** | Acyl-CoA thioester hydrolase YciA | 0.731895 | 0.089714 |
| **FumB2** | Fumarate hydratase class I | 0.732764 | 0.000449 |
| **DdlA** | D-alanine--D-alanine ligase | 0.733201 | 0.009044 |
| **YrdB** | DUF1488 domain-containing protein | 0.734226 | 0.382832 |
| **GltA\_1** | Citrate synthase | 0.734316 | 0.282388 |
| **GlpR\_4** | FucR protein | 0.734431 | 0.360858 |
| **C2U49\_04825** | GNAT family N-acetyltransferase | 0.735067 | 0.582758 |
| **MurC** | UDP-N-acetylmuramate--L-alanine ligase | 0.735846 | 0.001817 |
| **IhfA** | Integration host factor subunit alpha | 0.736194 | 0.015486 |
| **TruD** | tRNA pseudouridine synthase D | 0.736439 | 0.011727 |
| **GJJ01\_23945** | 4-carboxymuconolactone decarboxylase | 0.737159 | 0.037432 |
| **PntB** | NAD(P) transhydrogenase subunit beta | 0.737397 | 0.002834 |
| **HslU** | ATP-dependent protease ATPase subunit HslU | 0.737466 | 0.000314 |
| **Dxr** | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | 0.737906 | 0.009336 |
| **GJJ01\_26265** | YbaK/prolyl-tRNA synthetase associated domain-containing protein | 0.737928 | 0.085792 |
| **AlaA** | Alanine transaminase AlaA | 0.737941 | 0.003622 |
| **Tkt** | Transketolase (Fragment) | 0.738128 | 0.001153 |
| **YeiP** | Elongation factor P-like protein | 0.738378 | 0.016085 |
| **QseD** | Cell density-dependent motility repressor | 0.738783 | 0.186817 |
| **WalR\_2** | DNA-binding response regulator | 0.739503 | 0.084991 |
| **CitG2** | Probable 2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase | 0.739816 | 0.292909 |
| **GJJ01\_08160** | Adenylate cyclase | 0.740263 | 0.004172 |
| **PstA** | Phosphate transport system permease protein PstA | 0.741171 | 0.022171 |
| **SpeD** | S-adenosylmethionine decarboxylase proenzyme | 0.741403 | 0.123162 |
| **GJJ01\_03295** | MBL fold metallo-hydrolase | 0.741863 | 0.010052 |
| **Epd** | D-erythrose-4-phosphate dehydrogenase | 0.74288 | 0.00239 |
| **Dcd** | dCTP deaminase | 0.74311 | 0.000696 |
| **YfjD** | DUF21 domain-containing protein | 0.743965 | 0.013056 |
| **BamA** | Outer membrane protein assembly factor BamA | 0.744185 | 0.020226 |
| **Tdh** | L-threonine 3-dehydrogenase | 0.744205 | 0.030511 |
| **RpmG** | 50S ribosomal protein L33 | 0.744227 | 0.419425 |
| **GJJ01\_11005** | GNAT family N-acetyltransferase | 0.744428 | 0.129095 |
| **AmiA** | N-acetylmuramoyl-L-alanine amidase | 0.7448 | 0.193419 |
| **GlnD** | Bifunctional uridylyltransferase/uridylyl-removing enzyme | 0.745396 | 0.016313 |
| **DnaN** | Beta sliding clamp | 0.746454 | 0.000406 |
| **YhjD** | inner membrane protein YhjD | 0.746457 | 0.011358 |
| **FdnG** | Formate dehydrogenase-N subunit alpha | 0.746838 | 0.184027 |
| **Cof\_2** | Cof protein | 0.747001 | 0.001275 |
| **FtsB** | Cell division protein FtsB | 0.747045 | 0.006551 |
| **Ung** | Uracil-DNA glycosylase | 0.747133 | 0.035625 |
| **NarX** | Sensor protein | 0.748243 | 0.450299 |
| **RnpA** | Ribonuclease P protein component | 0.749787 | 0.000071 |
| **YihG** | Acyltransferase | 0.749819 | 0.743978 |
| **KdsA** | 2-dehydro-3-deoxyphosphooctonate aldolase | 0.749845 | 0.000227 |
| **ApaH** | Bis(5'-nucleosyl)-tetraphosphatase, symmetrical | 0.749989 | 0.194878 |
| **LpoA** | Penicillin-binding protein activator LpoA | 0.750683 | 0.001616 |
| **TonB** | Protein TonB | 0.750912 | 0.114462 |
| **PdxK** | Pyridoxal kinase | 0.75343 | 0.357221 |
| **GlpR\_8** | DEOR protein | 0.754321 | 0.04263 |
| **C3F39\_01005** | Diguanylate cyclase | 0.754445 | 0.140544 |
| **GlpR\_6** | DNA-binding transcriptional repressor | 0.754519 | 0.007741 |
| **PlsY** | Glycerol-3-phosphate acyltransferase | 0.75464 | 0.018073 |
| **UvrD** | DNA helicase | 0.754693 | 0.001651 |
| **YhjQ** | Cell division protein | 0.754844 | 0.523655 |
| **MobA** | Molybdenum cofactor guanylyltransferase | 0.755209 | 0.528929 |
| **Mdh** | L-lactate dehydrogenase | 0.755243 | 0.001112 |
| **PanC** | Pantothenate synthetase | 0.755296 | 0.010651 |
| **IlvI\_1** | Acetolactate synthase | 0.75608 | 0.066924 |
| **YbgC** | 4-hydroxybenzoyl-CoA thioesterase | 0.756566 | 0.017178 |
| **PdxA** | 4-hydroxythreonine-4-phosphate dehydrogenase | 0.757322 | 0.072454 |
| **DmlR\_5** | HTH-type transcriptional regulator DmlR | 0.758087 | 0.000347 |
| **SdiA** | Regulatory activator SdiA | 0.759715 | 0.079871 |
| **LutR\_2** | D-Galactonate repressor DgoR | 0.760421 | 0.024617 |
| **icaB** | Polysaccharide deacetylase | 0.760462 | 0.059351 |
| **GJJ01\_13115** | CinA-like protein | 0.761322 | 0.065556 |
| **PhoR** | Phosphate regulon sensor protein PhoR | 0.762596 | 0.483451 |
| **YbjS** | 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase | 0.762976 | 0.02448 |
| **Ttr** | Acetyltransferase | 0.763011 | 0.030543 |
| **DapA** | 4-hydroxy-tetrahydrodipicolinate synthase | 0.763305 | 0.000058 |
| **RluB** | Pseudouridine synthase | 0.763393 | 0.002921 |
| **NuoB** | NADH-quinone oxidoreductase subunit B | 0.763495 | 0.010136 |
| **YqfB** | N(4)-acetylcytidine amidohydrolase | 0.763994 | 0.000142 |
| **SpoT** | Bifunctional (P)ppGpp synthase/hydrolase SpoT | 0.764195 | 0.036983 |
| **RbsA\_5** | Ribose import ATP-binding protein RbsA | 0.764657 | 0.010433 |
| **IspD** | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | 0.764716 | 0.112867 |
| **HpcB** | 3,4-dihydroxyphenylacetate 2,3-dioxygenase | 0.764918 | 0.265907 |
| **RpmE** | 50S ribosomal protein L31 | 0.766174 | 0.084615 |
| **PanB** | 3-methyl-2-oxobutanoate hydroxymethyltransferase | 0.766338 | 0.040197 |
| **GalF** | Alpha-D-glucosyl-1-phosphate uridylyltransferase | 0.767302 | 0.00003 |
| **SpeA** | Biosynthetic arginine decarboxylase | 0.767575 | 0.006459 |
| **WecC** | UDP-N-acetyl-D-mannosamine dehydrogenase | 0.769496 | 0.00272 |
| **PncB** | Nicotinate phosphoribosyltransferase | 0.770924 | 0.060468 |
| **YbhK** | Putative gluconeogenesis factor | 0.771209 | 0.003001 |
| **MiaA** | tRNA dimethylallyltransferase | 0.771585 | 0.002737 |
| **YfeX** | Dyp-type peroxidase | 0.771979 | 0.006521 |
| **MarR** | DNA-binding transcriptional repressor MarR | 0.77333 | 0.178755 |
| **FumD** | Fumarase D | 0.773775 | 0.069168 |
| **TusA** | Sulfur carrier protein TusA | 0.774166 | 0.06528 |
| **BL124\_00024950** | O-antigen ligase domain-containing protein | 0.774608 | 0.179691 |
| **BANRA\_00238** | Family 10 glycosylhydrolase | 0.775044 | 0.514487 |
| **GluQRS** | Glutamyl-Q tRNA(Asp) synthetase | 0.776534 | 0.098001 |
| **ZapB** | Cell division protein ZapB | 0.777636 | 0.508017 |
| **TesB** | Acyl-CoA thioesterase 2 | 0.778559 | 0.042113 |
| **MipA** | MipA/OmpV family protein | 0.778954 | 0.13795 |
| **TrxB** | Thioredoxin reductase | 0.779701 | 0.02974 |
| **GmhB** | D,D-heptose 1,7-bisphosphate phosphatase | 0.780051 | 0.123251 |
| **SopA** | Plasmid-partitioning protein SopA | 0.780484 | 0.009127 |
| **SuhB\_2** | Inositol-1-monophosphatase | 0.780495 | 0.644144 |
| **B4U25\_10275** | UPF0227 protein B4U25\_10275 | 0.780636 | 0.018654 |
| **Mug** | G/U mismatch-specific DNA glycosylase | 0.780673 | 0.034992 |
| **SspA** | SspA protein | 0.780935 | 0.002413 |
| **YniC\_2** | 2-deoxyglucose-6-phosphatase | 0.781755 | 0.002418 |
| **YgfF** | 1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase | 0.782016 | 0.032346 |
| **HinT** | HIT-like protein hinT | 0.782645 | 0.046668 |
| **Nfo** | Probable endonuclease 4 | 0.785163 | 0.02429 |
| **RarA** | Replication-associated recombination protein A | 0.785238 | 0.059791 |
| **CysH** | Phosphoadenosine phosphosulfate reductase | 0.785599 | 0.115672 |
| **Fur** | Ferric uptake regulation protein | 0.786091 | 0.009922 |
| **ManA** | Mannose-6-phosphate isomerase | 0.7861 | 0.001895 |
| **Tmk** | Thymidylate kinase | 0.786623 | 0.001397 |
| **FabF\_1** | 3-oxoacyl-[acyl-carrier-protein] synthase 2 | 0.787907 | 0.034893 |
| **RibD** | Riboflavin biosynthesis protein RibD | 0.788444 | 0.031353 |
| **NrdA** | Ribonucleoside-diphosphate reductase | 0.789055 | 0.005326 |
| **RadA** | DNA repair protein RadA | 0.789537 | 0.041541 |
| **Era** | GTPase Era | 0.790491 | 0.005781 |
| **RelB** | RelB/StbD replicon stabilization protein (Antitoxin to RelE/StbE) | 0.791988 | 0.56305 |
| **RsxG** | Ion-translocating oxidoreductase complex subunit G | 0.79266 | 0.15816 |
| **NarJ** | NarJ protein | 0.793236 | 0.003859 |
| **QuiA** | Glucose dehydrogenase | 0.794529 | 0.000714 |
| **HemX** | HemX protein | 0.794619 | 0.016893 |
| **UgpQ** | Glycerophosphodiester phosphodiesterase | 0.795707 | 0.092197 |
| **DtpA** | Dipeptide and tripeptide permease A | 0.796017 | 0.045749 |
| **B4U21\_32230** | Plasmid stability protein | 0.796221 | 0.097399 |
| **AvtA** | Aspartate aminotransferase | 0.796362 | 0.01786 |
| **GlnB** | GlnB protein | 0.796492 | 0.003847 |
| **DhaM** | Phosphoenolpyruvate--glycerone phosphotransferase | 0.796903 | 0.02632 |
| **BioB** | Biotin synthase | 0.796943 | 0.613207 |
| **Gsp\_2** | Glutathionylspermidine synthase | 0.797259 | 0.044536 |
| **MdoH** | Glucans biosynthesis glucosyltransferase H | 0.797372 | 0.000939 |
| **GapA** | Glyceraldehyde-3-phosphate dehydrogenase | 0.797501 | 0.034769 |
| **YxeP\_1** | Amidohydrolase | 0.798856 | 0.627459 |
| **YcdX** | Probable phosphatase B6R99\_10555 | 0.799091 | 0.042393 |
| **FrdC** | Fumarate reductase subunit C | 0.799617 | 0.082947 |
| **OtsB** | Trehalose 6-phosphate phosphatase | 0.799815 | 0.074191 |
| **MdtP\_2** | MdtP family multidrug efflux transporter outer membrane subunit | 0.801013 | 0.463254 |
| **GJJ01\_17595** | Glycosyltransferase | 0.801209 | 0.087292 |
| **HflX** | GTPase HflX | 0.801338 | 0.002255 |
| **ProP** | Glycine betaine/L-proline transporter ProP | 0.801917 | 0.016579 |
| **PcaB** | 3-carboxy-cis,cis-muconate cycloisomerase | 0.802354 | 0.516687 |
| **WecD** | dTDP-fucosamine acetyltransferase | 0.80283 | 0.38074 |
| **YcgL** | YcgL domain-containing protein B4U21\_17620 | 0.803169 | 0.081855 |
| **YifE** | UPF0438 protein YifE | 0.803246 | 0.010649 |
| **AmpG** | AmpG permease | 0.804541 | 0.323351 |
| **MalP\_1** | Alpha-1,4 glucan phosphorylase | 0.806204 | 0.062276 |
| **SfsA** | Sugar fermentation stimulation protein homolog | 0.806342 | 0.099976 |
| **Uup** | ATP-binding protein Uup | 0.806531 | 0.094772 |
| **MtlK\_2** | D-arabinitol 4-dehydrogenase | 0.80692 | 0.192311 |
| **Zwf** | Glucose-6-phosphate 1-dehydrogenase | 0.810102 | 0.006132 |
| **CsiR** | CsiR, transcriptional repressor of CsiD | 0.810445 | 0.394461 |
| **B4U21\_28315** | Protein of uncharacterized function (DUF2629) | 0.811559 | 0.492748 |
| **Fes** | Enterobactin esterase | 0.812108 | 0.130508 |
| **MdtN** | Multidrug transporter subunit MdtN | 0.812326 | 0.05429 |
| **GlmM** | Phosphoglucosamine mutase | 0.812463 | 0.002564 |
| **EmrK\_1** | HlyD family efflux transporter periplasmic adaptor subunit | 0.813858 | 0.145274 |
| **NtrC** | DNA-binding transcriptional regulator NtrC | 0.813884 | 0.035081 |
| **NsrR\_2** | HTH-type transcriptional repressor NsrR | 0.817223 | 0.008489 |
| **DnaT\_1** | Primosomal protein 1 | 0.817558 | 0.282902 |
| **PcaI** | 3-oxoacid CoA-transferase subunit A | 0.818076 | 0.677658 |
| **PpiC\_1** | Peptidylprolyl isomerase | 0.818293 | 0.095865 |
| **RecA** | Protein RecA | 0.818753 | 0.040177 |
| **DnaX** | DNA polymerase III subunit gamma/tau | 0.819687 | 0.043463 |
| **AbgR\_1** | HTH-type transcriptional regulator AbgR | 0.820723 | 0.014082 |
| **PdhR\_1** | DNA-binding transcriptional repressor LldR | 0.821288 | 0.006377 |
| **RsmF** | Ribosomal RNA small subunit methyltransferase F | 0.821296 | 0.003073 |
| **B4U25\_30705** | Arylsulfatase | 0.823022 | 0.030593 |
| **DapD** | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase | 0.824566 | 0.001021 |
| **IspF** | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase | 0.825455 | 0.110162 |
| **YdgJ\_2** | Gfo/Idh/MocA family oxidoreductase | 0.825655 | 0.507597 |
| **GloA** | Lactoylglutathione lyase | 0.826548 | 0.000737 |
| **ChbF\_1** | 6-phospho-beta-glucosidase | 0.826667 | 0.128775 |
| **ZntR** | HTH-type transcriptional regulator ZntR | 0.826748 | 0.70312 |
| **ElyC** | Envelope biogenesis factor ElyC | 0.828425 | 0.077686 |
| **PepB** | Peptidase B | 0.829102 | 0.1547 |
| **IspB** | Octaprenyl diphosphate synthase | 0.83 | 0.021676 |
| **SanA** | Outer membrane permeability protein SanA | 0.830757 | 0.561472 |
| **RamR** | HTH-type transcriptional repressor Bm3R1 | 0.83143 | 0.41059 |
| **ArgA** | Amino-acid acetyltransferase | 0.831498 | 0.747223 |
| **ThrC** | Threonine synthase | 0.833085 | 0.077157 |
| **TyrA** | T-protein | 0.833572 | 0.002555 |
| **Ppa\_2** | Inorganic pyrophosphatase | 0.833984 | 0.013993 |
| **MinD\_2** | Iron-sulfur cluster carrier protein | 0.834466 | 0.010707 |
| **CsrA** | Translational regulator CsrA | 0.834532 | 0.487834 |
| **RpmA** | 50S ribosomal protein L27 | 0.835349 | 0.08297 |
| **HemN** | Coproporphyrinogen-III oxidase | 0.835794 | 0.097353 |
| **Hmp** | Flavohemoprotein | 0.835839 | 0.371677 |
| **Rnr** | Ribonuclease R | 0.836009 | 0.004947 |
| **GJJ01\_27790** | DUF1722 domain-containing protein | 0.83703 | 0.242057 |
| **InfA** | Translation initiation factor IF-1 | 0.837444 | 0.287856 |
| **PqiB** | Intermembrane transport protein PqiB | 0.837759 | 0.07475 |
| **ThiF\_1** | HesA/MoeB/ThiF family protein | 0.837888 | 0.205551 |
| **GlpR\_1** | DeoR/GlpR family transcriptional regulator | 0.837953 | 0.004391 |
| **Fdx** | 2Fe-2S ferredoxin | 0.838645 | 0.164538 |
| **LtaE** | Low specificity L-threonine aldolase | 0.838967 | 0.070015 |
| **MaeA** | NAD-dependent malic enzyme | 0.838982 | 0.199489 |
| **DmlR\_16** | D-malate degradation protein R | 0.839166 | 0.385344 |
| **PstB** | Phosphate import ATP-binding protein PstB | 0.839707 | 0.076703 |
| **GJJ01\_02200** | GNAT family N-acetyltransferase | 0.840651 | 0.653801 |
| **Fre** | Fre protein | 0.84069 | 0.004784 |
| **NadR** | Multifunctional transcriptional regulator/nicotinamide-nucleotide adenylyltransferase/ribosylnicotinamide kinase NadR | 0.841386 | 0.309216 |
| **Rnb** | Exoribonuclease 2 | 0.841697 | 0.037821 |
| **Ppk1** | Polyphosphate kinase | 0.841765 | 0.016681 |
| **ZntA** | Lead, cadmium, zinc and mercury-transporting ATPase | 0.841771 | 0.052523 |
| **Adk** | Adenylate kinase | 0.841949 | 0.016648 |
| **AroH** | Phospho-2-dehydro-3-deoxyheptonate aldolase | 0.842564 | 0.009543 |
| **DmlR\_8** | LysR family transcriptional regulator | 0.8429 | 0.699216 |
| **AroE** | Shikimate dehydrogenase (NADP(+)) | 0.84299 | 0.077933 |
| **Udp** | Uridine phosphorylase | 0.843208 | 0.155855 |
| **NudF\_1** | ADP-ribose diphosphatase | 0.843931 | 0.03622 |
| **RhmD** | L-rhamnonate dehydratase | 0.844105 | 0.549246 |
| **RimP** | Ribosome maturation factor RimP | 0.844151 | 0.021361 |
| **AdaA\_2** | AraC family transcriptional regulator | 0.844309 | 0.144271 |
| **LptE** | LPS-assembly lipoprotein LptE | 0.844422 | 0.106359 |
| **RlmD** | 23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD | 0.844475 | 0.022854 |
| **SufA** | Fe-S cluster assembly scaffold SufA | 0.846215 | 0.385455 |
| **YghZ** | Ion-channel protein | 0.84659 | 0.061845 |
| **Ppx** | Exopolyphosphatase | 0.847378 | 0.051225 |
| **SohB** | Protease SohB | 0.847577 | 0.061613 |
| **FepC** | FepC protein | 0.847794 | 0.387007 |
| **MacA** | MacA protein | 0.847982 | 0.014428 |
| **RsmG** | Ribosomal RNA small subunit methyltransferase G | 0.848331 | 0.082439 |
| **Efp** | Elongation factor P | 0.848362 | 0.010414 |
| **B4U21\_26100** | Lipoprotein | 0.849213 | 0.107752 |
| **IolI** | Inosose isomerase | 0.850459 | 0.141233 |
| **YejK** | Nucleoid-associated protein B6R99\_06920 | 0.850592 | 0.001906 |
| **MsbB** | Lipid A biosynthesis myristoyltransferase | 0.850656 | 0.04965 |
| **YtfQ** | ABC transporter periplasmic-binding protein YtfQ | 0.850892 | 0.330827 |
| **CyaA** | Adenylate cyclase | 0.851295 | 0.465825 |
| **XerD\_1** | Tyrosine recombinase XerD | 0.851556 | 0.270855 |
| **FabH** | 3-oxoacyl-[acyl-carrier-protein] synthase 3 | 0.851638 | 0.111659 |
| **Lnt** | Apolipoprotein N-acyltransferase | 0.85174 | 0.119588 |
| **MalY** | Cystathionine beta-lyase | 0.851936 | 0.12051 |
| **YdfZ** | Putative selenium delivery protein YdfZ | 0.852356 | 0.18859 |
| **TolR** | Tol-Pal system protein TolR | 0.852724 | 0.005859 |
| **TrmJ** | tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ | 0.853077 | 0.188869 |
| **MoaA** | GTP 3',8-cyclase | 0.853263 | 0.215064 |
| **GJJ01\_14630** | Dicarboxylate transport | 0.853361 | 0.295177 |
| **CmoM** | tRNA 5-carboxymethoxyuridine methyltransferase | 0.85424 | 0.082154 |
| **YrbA** | Acid stress protein IbaG | 0.85471 | 0.126033 |
| **FtsZ** | Cell division protein FtsZ | 0.854991 | 0.023329 |
| **SorC\_2** | Helix-turn-helix domain-containing protein | 0.855309 | 0.028112 |
| **IleS** | Isoleucine--tRNA ligase | 0.857596 | 0.056256 |
| **MazG** | Nucleoside triphosphate pyrophosphohydrolase | 0.858044 | 0.105 |
| **B4U21\_18600** | Molybdopterin-dependent oxidoreductase | 0.858192 | 0.07147 |
| **RcsD** | Phosphotransferase RcsD | 0.85954 | 0.363008 |
| **PtsJ** | Transcriptional regulator PtsJ | 0.859869 | 0.339193 |
| **FhuA\_2** | Ferrioxamine receptor | 0.859877 | 0.455476 |
| **NrdB** | Ribonucleoside-diphosphate reductase | 0.860201 | 0.014005 |
| **TyrS** | Tyrosine--tRNA ligase | 0.860614 | 0.047839 |
| **CspC** | Cold shock protein CspC | 0.860659 | 0.00343 |
| **B4U21\_27925** | DUF2500 domain-containing protein | 0.860974 | 0.512755 |
| **RluD** | Pseudouridine synthase | 0.861564 | 0.005986 |
| **MoeA** | Molybdopterin molybdenumtransferase | 0.862213 | 0.069048 |
| **GumN** | Conjugal transfer protein TraB | 0.862332 | 0.65004 |
| **CycB** | Maltodextrin-binding protein | 0.863602 | 0.605739 |
| **FolC** | Dihydrofolate synthase/folylpolyglutamate synthase | 0.863635 | 0.062733 |
| **Add** | Adenosine deaminase | 0.863847 | 0.165691 |
| **IspU** | Ditrans,polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific) | 0.864627 | 0.144851 |
| **LpxC** | UDP-3-O-acyl-N-acetylglucosamine deacetylase | 0.864885 | 0.176307 |
| **YciU** | UPF0263 protein B4U21\_16780 | 0.865172 | 0.27711 |
| **Lpp** | Major outer membrane lipoprotein Lpp | 0.865933 | 0.273537 |
| **FhuC\_4** | Manganese ABC transporter, ATP-binding protein SitB | 0.866308 | 0.27009 |
| **GldA\_2** | Glycerol dehydrogenase | 0.866316 | 0.019903 |
| **YbhC** | Pectinesterase | 0.866318 | 0.201333 |
| **SpeC** | Ornithine decarboxylase | 0.866566 | 0.491164 |
| **UvrA** | UvrABC system protein A | 0.868664 | 0.006128 |
| **ChbG** | Chitooligosaccharide deacetylase | 0.869148 | 0.158703 |
| **FdoG** | FdoG protein | 0.869393 | 0.001575 |
| **YcjX** | Predicted ATPase | 0.869473 | 0.00849 |
| **PrtB** | Oligopeptidase B | 0.87054 | 0.252586 |
| **YvdD** | Cytokinin riboside 5'-monophosphate phosphoribohydrolase | 0.871784 | 0.090413 |
| **B4U21\_26220** | UPF0306 protein B4U21\_26220 | 0.871806 | 0.211655 |
| **FtsX** | Cell division protein FtsX | 0.872939 | 0.101308 |
| **SerS** | Serine--tRNA ligase | 0.873281 | 0.0004 |
| **RlpA** | Endolytic peptidoglycan transglycosylase RlpA | 0.873595 | 0.053794 |
| **PyrI** | Aspartate carbamoyltransferase regulatory chain | 0.874113 | 0.140875 |
| **BamC** | Outer membrane protein assembly factor BamC | 0.874449 | 0.200109 |
| **YhbJ** | RNase adapter protein RapZ | 0.874774 | 0.323131 |
| **DppB\_1** | Dipeptide ABC transporter permease DppB | 0.875181 | 0.304745 |
| **FabD** | Malonyl CoA-acyl carrier protein transacylase | 0.876226 | 0.003478 |
| **TolQ** | Tol-Pal system protein TolQ | 0.876299 | 0.146148 |
| **TreR** | HTH-type transcriptional regulator TreR | 0.876551 | 0.361695 |
| **OprM\_1** | Multidrug resistance outer membrane protein MdtP | 0.877158 | 0.458039 |
| **RraB** | Regulator of ribonuclease activity B | 0.87723 | 0.113558 |
| **RuvX** | Putative pre-16S rRNA nuclease | 0.877545 | 0.22393 |
| **YecJ** | DUF2766 domain-containing protein | 0.878582 | 0.290299 |
| **YwaD** | Aminopeptidase | 0.878693 | 0.546953 |
| **SelU** | tRNA 2-selenouridine synthase | 0.878835 | 0.118728 |
| **UppP** | Undecaprenyl-diphosphatase | 0.87935 | 0.484249 |
| **ProA** | Gamma-glutamyl phosphate reductase | 0.88037 | 0.030185 |
| **TamA** | Autotransporter assembly factor TamA | 0.882719 | 0.374361 |
| **YcdB** | Deferrochelatase/peroxidase | 0.882764 | 0.32121 |
| **LplA** | Lipoate-protein ligase A | 0.883216 | 0.386835 |
| **PyrE** | Orotate phosphoribosyltransferase | 0.88327 | 0.159404 |
| **AroP** | AroP protein | 0.883296 | 0.184847 |
| **FabF** | 3-oxoacyl-[acyl-carrier-protein] synthase 2 | 0.883524 | 0.082695 |
| **RoxA\_1** | 50S ribosomal protein L16 3-hydroxylase | 0.883662 | 0.325186 |
| **OmpA** | Outer membrane protein A | 0.884621 | 0.218399 |
| **LptG** | LPS export ABC transporter permease LptG | 0.884716 | 0.134777 |
| **Lrp** | Leucine-responsive regulatory protein | 0.885052 | 0.11856 |
| **LysN\_1** | 2-aminoadipate transaminase | 0.885143 | 0.328001 |
| **YecC** | Arginine transport ATP-binding protein ArtM | 0.88519 | 0.009314 |
| **MnmA** | tRNA-specific 2-thiouridylase MnmA | 0.885826 | 0.058029 |
| **SdaA** | L-serine dehydratase | 0.886156 | 0.038613 |
| **Cmk** | Cytidylate kinase | 0.887148 | 0.043045 |
| **UbiA** | 4-hydroxybenzoate octaprenyltransferase | 0.887582 | 0.817755 |
| **MutH** | DNA mismatch repair protein MutH | 0.888736 | 0.440005 |
| **PckA** | Phosphoenolpyruvate carboxykinase (ATP) | 0.88945 | 0.090097 |
| **CysS** | Cysteine--tRNA ligase | 0.889528 | 0.228995 |
| **UbiB** | Probable protein kinase UbiB | 0.890081 | 0.480488 |
| **DapE** | Succinyl-diaminopimelate desuccinylase | 0.890094 | 0.141573 |
| **HslR** | Heat shock protein 15 | 0.89054 | 0.755427 |
| **SbcB** | Exodeoxyribonuclease I | 0.892048 | 0.011649 |
| **EngB** | Probable GTP-binding protein EngB | 0.892656 | 0.271239 |
| **LepB** | Signal peptidase I | 0.893099 | 0.160027 |
| **QueF** | NADPH-dependent 7-cyano-7-deazaguanine reductase | 0.8933 | 0.213613 |
| **FolP\_2** | Dihydropteroate synthase | 0.894911 | 0.150641 |
| **BANRA\_02412** | DUF1198 family protein | 0.895162 | 0.673767 |
| **KatG** | Catalase-peroxidase | 0.895286 | 0.118619 |
| **YeeZ** | NAD(P)-dependent oxidoreductase | 0.895683 | 0.381177 |
| **Pgm** | Alpha-D-glucose phosphate-specific phosphoglucomutase | 0.896014 | 0.754065 |
| **NnrD** | Bifunctional NAD(P)H-hydrate repair enzyme | 0.897061 | 0.618545 |
| **HldD** | ADP-L-glycero-D-manno-heptose-6-epimerase | 0.897455 | 0.011926 |
| **HflK** | Protein HflK | 0.897829 | 0.182253 |
| **KdsD** | Arabinose 5-phosphate isomerase | 0.898566 | 0.114666 |
| **BdhA\_2** | D-beta-hydroxybutyrate dehydrogenase | 0.898679 | 0.108049 |
| **DgoA\_1** | 2-dehydro-3-deoxy-6-phosphogalactonate aldolase | 0.899006 | 0.811534 |
| **NuoF** | NADH-quinone oxidoreductase subunit F | 0.899105 | 0.109433 |
| **YvoA\_2** | 2-aminoethylphosphonate uptake and metabolism regulator | 0.8994 | 0.004831 |
| **UbiD** | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase | 0.899496 | 0.108681 |
| **YtfB** | OapA protein | 0.899617 | 0.638768 |
| **IspH** | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | 0.900386 | 0.123484 |
| **PucG** | Alanine--glyoxylate aminotransferase family protein | 0.900544 | 0.294395 |
| **B4U21\_16400** | Signal peptide protein | 0.900588 | 0.646133 |
| **CarA** | Carbamoyl-phosphate synthase small chain | 0.900612 | 0.065803 |
| **B4U25\_40120** | Peptidyl-prolyl cis-trans isomerase | 0.900643 | 0.360738 |
| **RimN** | Threonylcarbamoyl-AMP synthase | 0.900807 | 0.062345 |
| **FbaA\_2** | Class II fructose-bisphosphate aldolase | 0.901111 | 0.308233 |
| **SecF** | Protein-export membrane protein SecF | 0.901739 | 0.177434 |
| **SelO** | Protein adenylyltransferase SelO | 0.90188 | 0.524535 |
| **MtlA** | EIICBA-Mtl | 0.9021 | 0.146598 |
| **GJJ01\_24345** | MBL fold metallo-hydrolase | 0.90236 | 0.519904 |
| **PdhR\_4** | FCD domain-containing protein | 0.902997 | 0.017654 |
| **RpsF** | 30S ribosomal protein S6 | 0.903364 | 0.443161 |
| **BANRA\_01257** | 6-deoxy-6-sulfogluconolactonase | 0.903798 | 0.097655 |
| **HldE** | Bifunctional protein HldE | 0.904203 | 0.039912 |
| **PurF** | Amidophosphoribosyltransferase | 0.905136 | 0.135675 |
| **MurE** | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase | 0.906102 | 0.054595 |
| **CvrA** | K(+)/H(+) antiporter NhaP2 | 0.907314 | 0.703819 |
| **B4U21\_21150** | Neutral zinc metallopeptidase | 0.907621 | 0.667224 |
| **RcnR** | Metal-sensing transcriptional repressor | 0.907779 | 0.533436 |
| **SorC** | DNA-binding transcriptional regulator | 0.907796 | 0.445352 |
| **DusC** | tRNA-dihydrouridine(16) synthase | 0.907924 | 0.729508 |
| **YidA** | Cof-type HAD-IIB family hydrolase | 0.908563 | 0.241113 |
| **ProC** | Pyrroline-5-carboxylate reductase | 0.909113 | 0.086949 |
| **DamX** | Cell division protein DamX | 0.909156 | 0.387598 |
| **GlpX** | Fructose-1,6-bisphosphatase | 0.910047 | 0.097206 |
| **CbiL** | Cobalt-factor II C(20)-methyltransferase | 0.910376 | 0.58255 |
| **PpnK** | NAD kinase | 0.910851 | 0.367323 |
| **ETE82\_00890** | Gluconate 2-dehydrogenase subunit 3 family protein | 0.911111 | 0.54773 |
| **TopA\_1** | DNA topoisomerase 1 | 0.912408 | 0.039748 |
| **UreA** | Urease subunit gamma | 0.912674 | 0.732596 |
| **SspB** | ClpXP protease specificity-enhancing factor | 0.912964 | 0.344414 |
| **FadR** | Fatty acid metabolism regulator protein | 0.913039 | 0.001138 |
| **C2U49\_03050** | YciK family oxidoreductase | 0.913586 | 0.443567 |
| **BN49\_pII0099** | Alpha/beta fold hydrolase | 0.913907 | 0.268855 |
| **MetF** | Methylenetetrahydrofolate reductase | 0.914804 | 0.691882 |
| **Rnc** | Ribonuclease 3 | 0.915568 | 0.270833 |
| **MdlB** | MdlB protein | 0.917437 | 0.366338 |
| **GlnQ** | GlnQ protein | 0.91813 | 0.038223 |
| **RsmD** | Ribosomal RNA small subunit methyltransferase D | 0.918315 | 0.653891 |
| **TolA** | Cell envelope integrity inner membrane protein TolA | 0.918851 | 0.065376 |
| **PtsI** | Phosphoenolpyruvate-protein phosphotransferase | 0.919516 | 0.005903 |
| **HtrB2** | Lipid A biosynthesis lauroyltransferase | 0.919981 | 0.324856 |
| **Cfa\_2** | Methyltransferase domain-containing protein | 0.920199 | 0.784922 |
| **BANRA\_02721** | DUF1481 domain-containing protein | 0.92027 | 0.855198 |
| **Ssb** | Single-stranded DNA-binding protein | 0.920459 | 0.40037 |
| **B4U25\_39220** | Nucleotidyl transferase AbiEii/AbiGii toxin family protein | 0.921355 | 0.779551 |
| **ProY** | ProY protein | 0.921423 | 0.896595 |
| **YbbK** | Protein QmcA | 0.922761 | 0.39807 |
| **AtpF** | ATP synthase subunit b | 0.922904 | 0.07422 |
| **PurT** | Formate-dependent phosphoribosylglycinamide formyltransferase | 0.924146 | 0.124918 |
| **GalU** | UTP--glucose-1-phosphate uridylyltransferase | 0.925453 | 0.023376 |
| **AceA** | Isocitrase | 0.925737 | 0.249629 |
| **CbiC** | CbiC protein | 0.927744 | 0.416942 |
| **GntT** | Gluconate transporter | 0.927799 | 0.677502 |
| **QseG** | Two-component system QseEF-associated lipoprotein QseG | 0.928849 | 0.453859 |
| **HslO** | 33 kDa chaperonin | 0.929831 | 0.01535 |
| **XseA** | Exodeoxyribonuclease 7 large subunit | 0.930421 | 0.569262 |
| **RsgA** | Small ribosomal subunit biogenesis GTPase RsgA | 0.931705 | 0.053384 |
| **TrmA** | tRNA/tmRNA (uracil-C(5))-methyltransferase | 0.931844 | 0.558974 |
| **FtsY** | Signal recognition particle receptor FtsY | 0.932065 | 0.038618 |
| **DnaJ** | Chaperone protein DnaJ | 0.93284 | 0.342553 |
| **DinI\_2** | DNA damage-inducible protein I | 0.93284 | 0.914311 |
| **GJJ01\_12190** | C-type cytochrome | 0.932965 | 0.623258 |
| **PcaR** | Helix-turn-helix domain-containing protein | 0.933261 | 0.258874 |
| **TsaA** | Putative methyltransferase, YaeB/AF\_0241 family | 0.933476 | 0.49491 |
| **SapA** | Antimicrobial peptide ABC transporter substrate-binding protein SapA | 0.933957 | 0.615219 |
| **C3F39\_26570** | FAD-binding oxidoreductase | 0.934133 | 0.686346 |
| **Rob** | MDR efflux pump AcrAB transcriptional activator RobA | 0.934398 | 0.013058 |
| **YddE** | Phenazine biosynthesis protein PhzF | 0.934451 | 0.720494 |
| **PdxA2** | 4-hydroxythreonine-4-phosphate dehydrogenase | 0.934632 | 0.106425 |
| **ZapA** | Cell division protein ZapA | 0.934796 | 0.226868 |
| **FadD** | Long-chain-fatty-acid--CoA ligase FadD | 0.935378 | 0.039274 |
| **HrpB** | ATP-dependent helicase HrpB | 0.935861 | 0.294198 |
| **SufC** | ABC transporter ATP-binding protein | 0.937756 | 0.185635 |
| **Tus** | DNA replication terminus site-binding protein | 0.938286 | 0.171576 |
| **Eno** | Enolase | 0.938688 | 0.068138 |
| **AtpB** | ATP synthase subunit a | 0.939939 | 0.722337 |
| **DapF** | Diaminopimelate epimerase | 0.940056 | 0.394481 |
| **B4U25\_25590** | DUF2633 domain-containing protein | 0.940164 | 0.708975 |
| **YusV\_2** | ATP-binding cassette domain-containing protein | 0.940677 | 0.607974 |
| **MinD** | Cell division inhibitor MinD | 0.9408 | 0.254366 |
| **PlsC** | 1-acyl-sn-glycerol-3-phosphate acyltransferase | 0.941339 | 0.260496 |
| **TrmL** | tRNA (cytidine(34)-2'-O)-methyltransferase | 0.941554 | 0.22626 |
| **PurK** | N5-carboxyaminoimidazole ribonucleotide synthase | 0.943679 | 0.126371 |
| **Map** | Methionine aminopeptidase | 0.944727 | 0.487829 |
| **PpiC\_2** | Peptidylprolyl isomerase | 0.944772 | 0.461038 |
| **YdiK** | AI-2E family transporter | 0.944919 | 0.648892 |
| **BhsA\_2** | DUF1471 domain-containing protein | 0.945018 | 0.835991 |
| **DkgB\_1** | 2,5-diketo-D-gluconic acid reductase B | 0.946549 | 0.28005 |
| **ParE** | DNA topoisomerase 4 subunit B | 0.946589 | 0.213057 |
| **SpeB** | Agmatinase | 0.947423 | 0.270722 |
| **TatB** | Sec-independent protein translocase protein TatB | 0.947866 | 0.785965 |
| **MdoG** | Glucans biosynthesis protein G | 0.949094 | 0.060561 |
| **Ndk** | Nucleoside diphosphate kinase | 0.949095 | 0.235047 |
| **BamB** | Outer membrane protein assembly factor BamB | 0.949741 | 0.581846 |
| **MioC\_2** | FMN-binding protein MioC | 0.949911 | 0.515927 |
| **CynR\_7** | HTH-type transcriptional regulator CynR | 0.950168 | 0.672324 |
| **FldA** | Flavodoxin | 0.950442 | 0.549968 |
| **FtsL** | Cell division protein FtsL | 0.951897 | 0.307 |
| **HisB** | Histidine biosynthesis bifunctional protein HisB | 0.95243 | 0.157968 |
| **B4U21\_09235** | DUF333 domain-containing protein | 0.95285 | 0.654905 |
| **FolE** | GTP cyclohydrolase 1 | 0.953105 | 0.289049 |
| **HolD** | DNA polymerase III subunit psi | 0.95312 | 0.727365 |
| **Pcp** | Pyrrolidone-carboxylate peptidase | 0.953903 | 0.544808 |
| **Por\_1** | D-mannonate oxidoreductase | 0.956457 | 0.555015 |
| **ModE** | Molybdenum-dependent transcriptional regulator | 0.957028 | 0.632244 |
| **YbdF** | MmcQ/YjbR family DNA-binding protein | 0.95757 | 0.724293 |
| **CoaE** | Dephospho-CoA kinase | 0.957848 | 0.394989 |
| **RutB\_3** | Isochorismatase | 0.958174 | 0.87048 |
| **DcyD** | D-cysteine desulfhydrase | 0.95872 | 0.264433 |
| **UspG\_1** | Universal stress protein | 0.96006 | 0.315215 |
| **G5637\_19290** | DUF2594 family protein | 0.960086 | 0.725832 |
| **BcsE** | Cellulose biosynthesis protein BcsE | 0.960347 | 0.729081 |
| **MetG** | Methionine--tRNA ligase | 0.960723 | 0.354654 |
| **DapB** | 4-hydroxy-tetrahydrodipicolinate reductase | 0.960755 | 0.653148 |
| **MgtE** | Magnesium transporter MgtE | 0.960869 | 0.834753 |
| **PabB** | Aminodeoxychorismate synthase | 0.961044 | 0.845142 |
| **AtpC** | ATP synthase epsilon chain | 0.96268 | 0.926005 |
| **RluF** | Pseudouridine synthase | 0.962825 | 0.564906 |
| **XylE\_1** | 3-methylcatechol 2,3-dioxygenase | 0.963671 | 0.912845 |
| **SrlQ** | Arabinose 5-phosphate isomerase | 0.96478 | 0.10499 |
| **LeuS** | Leucine--tRNA ligase | 0.965014 | 0.269597 |
| **Gsk** | Inosine-guanosine kinase | 0.965526 | 0.818427 |
| **CydD** | Cysteine/glutathione ABC transporter permease/ATP-binding protein CydD | 0.965695 | 0.790154 |
| **HsdS** | Type I restriction endonuclease | 0.966275 | 0.749374 |
| **PanM** | PanD regulatory factor | 0.966453 | 0.711743 |
| **YobD** | UPF0266 membrane protein GJJ01\_10160 | 0.966991 | 0.932705 |
| **GspA** | DUF4422 domain-containing protein | 0.967577 | 0.716292 |
| **DsbB** | Disulfide bond formation protein B | 0.967646 | 0.338026 |
| **NifU** | Iron-sulfur cluster assembly scaffold protein IscU | 0.968284 | 0.475041 |
| **YajG** | Lipoprotein | 0.968949 | 0.837219 |
| **YpeA** | Acetyltransferase B4U21\_20885 | 0.970215 | 0.693891 |
| **Tal** | Transaldolase | 0.970906 | 0.910798 |
| **PurE** | N5-carboxyaminoimidazole ribonucleotide mutase | 0.972784 | 0.307484 |
| **SutR\_4** | Anaerobic benzoate catabolism transcriptional regulator | 0.973374 | 0.577459 |
| **YbeZ** | AAA family ATPase | 0.973421 | 0.497375 |
| **LdhA** | 2-hydroxyacid dehydrogenase | 0.974445 | 0.587979 |
| **RuvA** | Holliday junction ATP-dependent DNA helicase RuvA | 0.974613 | 0.887075 |
| **YneJ** | HTH-type transcriptional regulator gltR | 0.974838 | 0.934197 |
| **LgrD** | NAD-dependent epimerase/dehydratase family protein | 0.975472 | 0.797672 |
| **HscA** | Chaperone protein HscA | 0.976495 | 0.522998 |
| **DinG** | ATP-dependent DNA helicase DinG | 0.976603 | 0.876141 |
| **BetB\_2** | NAD/NADP-dependent betaine aldehyde dehydrogenase | 0.978228 | 0.390112 |
| **ThrB** | Homoserine kinase | 0.979279 | 0.923743 |
| **YqaB** | Fructose-1-phosphate phosphatase YqaB | 0.979452 | 0.71242 |
| **PldB** | Lysophospholipase | 0.979559 | 0.932909 |
| **CitX** | Apo-citrate lyase phosphoribosyl-dephospho-CoA transferase | 0.980003 | 0.853595 |
| **PcaD** | 3-oxoadipate enol-lactonase | 0.982071 | 0.597866 |
| **RcsB** | Transcriptional regulatory protein RcsB | 0.98257 | 0.836874 |
| **GroL** | 60 kDa chaperonin | 0.983643 | 0.738075 |
| **HadI** | (R)-2-hydroxyglutaryl-CoA dehydratase activator | 0.983646 | 0.954342 |
| **TreA\_2** | Alpha,alpha-phosphotrehalase | 0.984095 | 0.771865 |
| **XylA** | Xylose isomerase | 0.984313 | 0.967302 |
| **GJJ01\_13875** | AAA family ATPase | 0.984418 | 0.981306 |
| **YpdB** | DNA-binding response regulator | 0.984426 | 0.826603 |
| **LptB\_1** | Lipopolysaccharide export system ATP-binding protein LptB | 0.984768 | 0.788258 |
| **DeoR** | DNA-binding transcriptional repressor DeoR | 0.986585 | 0.853357 |
| **ValS** | Valine--tRNA ligase | 0.988281 | 0.797196 |
| **HolC** | DNA polymerase III subunit chi | 0.988867 | 0.887396 |
| **YhiN** | Aminoacetone oxidase family FAD-binding enzyme | 0.989119 | 0.889801 |
| **UbiF\_1** | 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase | 0.990803 | 0.93965 |
| **RbfA** | Ribosome-binding factor A | 0.991377 | 0.732375 |
| **DeoA** | Thymidine phosphorylase | 0.991545 | 0.901432 |
| **GlyQ** | Glycine--tRNA ligase alpha subunit | 0.991714 | 0.937178 |
| **YejL** | UPF0352 protein B4U21\_19870 | 0.992076 | 0.94105 |
| **YlaC** | Inner membrane protein | 0.99214 | 0.967821 |
| **RpoA** | DNA-directed RNA polymerase subunit alpha | 0.992489 | 0.91345 |
| **Gsp** | Bifunctional glutathionylspermidine amidase/glutathionylspermidine synthase | 0.992867 | 0.872513 |
| **DD581\_08425** | Elongation factor Tu (Fragment) | 0.994998 | 0.927011 |
| **GltX** | Glutamate--tRNA ligase | 0.995073 | 0.849114 |
| **YqjE** | Membrane protein | 0.995233 | 0.861094 |
| **TusD** | Sulfurtransferase TusD | 0.995687 | 0.977198 |
| **PyrD** | Dihydroorotate dehydrogenase (quinone) | 0.996327 | 0.744355 |
| **GlmS** | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] | 0.99695 | 0.948601 |
| **NagA** | N-acetylglucosamine-6-phosphate deacetylase | 0.998492 | 0.979278 |
| **CoaD** | Phosphopantetheine adenylyltransferase | 0.998898 | 0.992513 |
| **Dat** | Dat protein | 1.000074 | 0.997577 |
| **BANRA\_04491** | DUF523 domain-containing protein | 1.000937 | 0.995429 |
| **YqgE** | UPF0301 protein B4U21\_25090 | 1.001024 | 0.984568 |
| **MukE** | Chromosome partition protein MukE | 1.003108 | 0.90506 |
| **AscG\_2** | HTH-type transcriptional regulator AscG | 1.003109 | 0.963685 |
| **NagD** | HAD-IIA family hydrolase | 1.003328 | 0.956825 |
| **FabA** | 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase | 1.003551 | 0.931208 |
| **HemL** | Glutamate-1-semialdehyde 2,1-aminomutase | 1.004455 | 0.879261 |
| **GJJ01\_01625** | Outer membrane protein | 1.004736 | 0.981786 |
| **IciA** | HTH-type transcriptional regulator ArgP | 1.005172 | 0.936304 |
| **HupA** | DNA-binding protein | 1.005559 | 0.936133 |
| **IgaA** | IgaA | 1.005804 | 0.976884 |
| **ThyA** | Thymidylate synthase | 1.006222 | 0.956513 |
| **B4U25\_10290** | Glycine zipper 2TM domain-containing protein | 1.006626 | 0.986458 |
| **LolE** | Lipoprotein transporter subunit LolE | 1.007705 | 0.949982 |
| **YecM** | Protein yecM | 1.008032 | 0.959978 |
| **KdbD** | Histidine kinase | 1.008459 | 0.983589 |
| **YrbD** | ABC transporter periplasmic substrate-binding protein | 1.008937 | 0.868881 |
| **AidB** | Isovaleryl-CoA dehydrogenase | 1.010774 | 0.921045 |
| **Cls** | Cardiolipin synthase A | 1.011139 | 0.921998 |
| **RibF** | Riboflavin biosynthesis protein | 1.01139 | 0.899148 |
| **Rep** | ATP-dependent DNA helicase Rep | 1.012693 | 0.858535 |
| **Ompk17** | Outer membrane protein X | 1.013876 | 0.971424 |
| **AglB** | 6-phospho-alpha-glucosidase | 1.013954 | 0.911158 |
| **UbiE** | Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE | 1.014827 | 0.749703 |
| **DeoD** | Purine nucleoside phosphorylase DeoD-type | 1.015467 | 0.904124 |
| **AmpE** | AmpE protein | 1.01552 | 0.953103 |
| **YbiS** | L,D-transpeptidase | 1.015992 | 0.905813 |
| **YebO** | Uncharacterized protein YebO | 1.016838 | 0.86731 |
| **ProS\_2** | Cys-tRNA(Pro)/cys-tRNA(Cys) deacylase | 1.016968 | 0.922435 |
| **Rng** | Ribonuclease G | 1.017356 | 0.751211 |
| **Fnr** | FNR family transcription factor | 1.017791 | 0.835577 |
| **CsdA** | Cysteine desulfurase CsdA | 1.017971 | 0.787392 |
| **MviM\_1** | Oxidoreductase | 1.018545 | 0.877577 |
| **YgfX** | Inner membrane protein | 1.018647 | 0.985262 |
| **Ppc** | Phosphoenolpyruvate carboxylase | 1.018687 | 0.554418 |
| **CueR** | Copper efflux regulator | 1.021377 | 0.748638 |
| **IlvY** | DNA-binding transcriptional regulator IlvY | 1.021432 | 0.854339 |
| **TruA** | tRNA pseudouridine synthase A | 1.02272 | 0.154706 |
| **Asd2** | Aspartate-semialdehyde dehydrogenase | 1.024934 | 0.890874 |
| **ArgB** | Acetylglutamate kinase | 1.025753 | 0.420817 |
| **Rne** | Ribonuclease E | 1.026359 | 0.59786 |
| **CorA** | Magnesium transport protein CorA | 1.026532 | 0.299934 |
| **Hha\_1** | Haemolysin expression modulating protein | 1.027439 | 0.909142 |
| **CspA** | Cold shock protein CspA | 1.027777 | 0.537736 |
| **FabG\_9** | 3-oxoacyl-[acyl-carrier-protein] reductase | 1.028045 | 0.790572 |
| **Lrp\_4** | AsnC family transcriptional regulator | 1.028616 | 0.905892 |
| **PpiD** | Peptidylprolyl isomerase | 1.028824 | 0.518625 |
| **B4U25\_24840** | Putative DNA-binding transcriptional regulator | 1.029093 | 0.918521 |
| **HflB\_1** | ATP-dependent zinc metalloprotease FtsH | 1.029796 | 0.508839 |
| **RhlB** | ATP-dependent RNA helicase RhlB | 1.030685 | 0.471986 |
| **MukB** | Chromosome partition protein MukB | 1.030741 | 0.544787 |
| **ThiE** | Thiamine-phosphate synthase | 1.031218 | 0.952659 |
| **RsmH** | Ribosomal RNA small subunit methyltransferase H | 1.031377 | 0.476863 |
| **AllS\_5** | HTH-type transcriptional activator AllS | 1.031914 | 0.6988 |
| **OxaA** | Membrane protein insertase YidC | 1.031935 | 0.530368 |
| **IspG** | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) | 1.032001 | 0.437736 |
| **ClpX** | ATP-dependent Clp protease ATP-binding subunit ClpX | 1.034008 | 0.503244 |
| **MetB** | Cystathionine gamma-synthase | 1.034097 | 0.681996 |
| **PurA** | Adenylosuccinate synthetase | 1.034131 | 0.601473 |
| **FhuD** | Fe(3+)-hydroxamate ABC transporter substrate-binding protein FhuD | 1.034153 | 0.842701 |
| **MinC** | Probable septum site-determining protein MinC | 1.03461 | 0.702525 |
| **GrxD** | Glutaredoxin | 1.035166 | 0.42676 |
| **RpoD** | RNA polymerase sigma factor RpoD | 1.036189 | 0.450324 |
| **B4U21\_18290** | Lipoprotein | 1.036624 | 0.79274 |
| **AlaS** | Alanine--tRNA ligase | 1.037522 | 0.076603 |
| **PyrF** | Orotidine 5'-phosphate decarboxylase | 1.037577 | 0.649227 |
| **Hns\_1** | DNA-binding protein | 1.037718 | 0.483508 |
| **DmlR\_10** | LysR family transcriptional regulator | 1.038082 | 0.738829 |
| **MsbA\_1** | ATP-dependent lipid A-core flippase | 1.038121 | 0.429955 |
| **YhdH** | Acryloyl-CoA reductase | 1.038166 | 0.927461 |
| **YtfJ** | Protein ytfJ | 1.038412 | 0.628598 |
| **DcuR** | Transcriptional regulatory protein | 1.03901 | 0.584747 |
| **RdgB** | dITP/XTP pyrophosphatase | 1.039513 | 0.630769 |
| **PurB** | Adenylosuccinate lyase | 1.039942 | 0.029148 |
| **MalQ** | 4-alpha-glucanotransferase | 1.041192 | 0.917268 |
| **GanB** | Arabinogalactan endo-beta-1,4-galactanase | 1.041697 | 0.916666 |
| **YbaL** | Kef family K(+) transporter | 1.041855 | 0.746978 |
| **RplY** | 50S ribosomal protein L25 | 1.043398 | 0.026802 |
| **Apt** | Adenine phosphoribosyltransferase | 1.043649 | 0.25547 |
| **BetU** | BCCT family transporter | 1.044978 | 0.584952 |
| **LolC** | Lipoprotein-releasing ABC transporter permease subunit LolC | 1.045048 | 0.529403 |
| **BANRA\_01242** | tRNA-uridine aminocarboxypropyltransferase | 1.045085 | 0.529079 |
| **PurR** | HTH-type transcriptional repressor PurR | 1.045786 | 0.315524 |
| **LysS** | Lysine--tRNA ligase | 1.046575 | 0.265145 |
| **PrfA** | Peptide chain release factor 1 | 1.047578 | 0.618429 |
| **OmpK36** | OmpK36 | 1.04767 | 0.723667 |
| **TypA** | GTP-binding protein | 1.048588 | 0.456188 |
| **DadB** | Alanine racemase | 1.049057 | 0.694668 |
| **YcfL** | DUF1425 domain-containing protein | 1.04909 | 0.873473 |
| **CysB** | Cys regulon transcriptional activator | 1.049522 | 0.204885 |
| **MtnN** | 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase | 1.04955 | 0.318904 |
| **MutS** | DNA mismatch repair protein MutS | 1.049695 | 0.708291 |
| **DrrA** | ABC transporter ATP-binding protein | 1.049996 | 0.423172 |
| **AnsP** | AnsP protein | 1.051191 | 0.758546 |
| **GlnS** | Glutamine--tRNA ligase | 1.05242 | 0.133784 |
| **Gph** | Phosphoglycolate phosphatase | 1.052642 | 0.714657 |
| **YghB** | DedA family inner membrane protein YghB | 1.052829 | 0.661823 |
| **LigA** | DNA ligase | 1.055265 | 0.340233 |
| **MdeA** | DgaE family pyridoxal phosphate-dependent ammonia lyase | 1.055293 | 0.54234 |
| **B4U21\_01060** | YacC family pilotin-like protein | 1.055728 | 0.743371 |
| **MltB** | Lytic murein transglycosylase B | 1.056343 | 0.610324 |
| **YceG** | Endolytic murein transglycosylase | 1.058448 | 0.628242 |
| **UspG2** | Universal stress protein | 1.058644 | 0.936107 |
| **Dut** | Deoxyuridine 5'-triphosphate nucleotidohydrolase | 1.059653 | 0.270332 |
| **HisS** | Histidine--tRNA ligase | 1.060088 | 0.254485 |
| **YpdA** | Histidine kinase | 1.060162 | 0.928667 |
| **YhbV** | Ubiquinone biosynthesis protein UbiV | 1.06017 | 0.848307 |
| **BetA** | Oxygen-dependent choline dehydrogenase | 1.061452 | 0.439902 |
| **RlmI** | Ribosomal RNA large subunit methyltransferase I | 1.061823 | 0.564691 |
| **Alr** | Alanine racemase | 1.062269 | 0.672449 |
| **YhdE** | dTTP/UTP pyrophosphatase | 1.062796 | 0.52096 |
| **Frr** | Ribosome-recycling factor | 1.062798 | 0.070814 |
| **YigA** | DUF484 domain-containing protein | 1.063806 | 0.610872 |
| **PanD** | Aspartate 1-decarboxylase | 1.063813 | 0.610292 |
| **LolD\_2** | Lipoprotein-releasing system ATP-binding protein LolD | 1.064184 | 0.494087 |
| **Gnd** | 6-phosphogluconate dehydrogenase, decarboxylating | 1.064479 | 0.207432 |
| **UvrC** | UvrABC system protein C | 1.065285 | 0.278983 |
| **FolD** | Bifunctional protein FolD | 1.065526 | 0.078703 |
| **GntK** | Gluconokinase | 1.065649 | 0.09714 |
| **MutL** | DNA mismatch repair protein MutL | 1.066164 | 0.535958 |
| **RlmE** | Ribosomal RNA large subunit methyltransferase E | 1.067344 | 0.197368 |
| **RodZ** | Cytoskeleton protein RodZ | 1.067827 | 0.507974 |
| **BioH** | Pimeloyl-[acyl-carrier protein] methyl ester esterase | 1.068873 | 0.344488 |
| **YjiY** | Carbon starvation protein | 1.068948 | 0.624211 |
| **LapB** | Lipopolysaccharide assembly protein B | 1.069769 | 0.733924 |
| **YajC** | Sec translocon accessory complex subunit YajC | 1.07067 | 0.398926 |
| **FruB\_2** | EIII-Fru | 1.070756 | 0.811003 |
| **YpfH** | Esterase | 1.071301 | 0.4503 |
| **ArgS** | Arginine--tRNA ligase | 1.071471 | 0.329511 |
| **SlpA** | Peptidyl-prolyl cis-trans isomerase | 1.071742 | 0.755255 |
| **LacZ** | Beta-galactosidase | 1.071786 | 0.36277 |
| **HemB** | Delta-aminolevulinic acid dehydratase | 1.072493 | 0.184344 |
| **YjiA\_2** | GTP-binding protein | 1.072511 | 0.250946 |
| **AcpH** | Acyl carrier protein phosphodiesterase | 1.072841 | 0.642645 |
| **RluE** | Pseudouridine synthase | 1.073259 | 0.763359 |
| **FabG\_2** | 3-oxoacyl-ACP reductase | 1.073487 | 0.783984 |
| **SapC** | Antimicrobial peptide ABC transporter permease SapC | 1.073727 | 0.794347 |
| **SpeG\_1** | GNAT family N-acetyltransferase | 1.073951 | 0.863559 |
| **RpsU** | 30S ribosomal protein S21 | 1.074627 | 0.478481 |
| **B4U25\_14410** | ROK family protein | 1.075314 | 0.754124 |
| **GlpE** | Thiosulfate sulfurtransferase GlpE | 1.076485 | 0.359306 |
| **DegS** | Peptidase Do | 1.077558 | 0.614999 |
| **GutB\_1** | Galactitol-1-phosphate 5-dehydrogenase | 1.078171 | 0.808588 |
| **FabG** | 3-oxoacyl-[acyl-carrier-protein] reductase | 1.07831 | 0.046953 |
| **RibB** | 3,4-dihydroxy-2-butanone 4-phosphate synthase | 1.078519 | 0.355811 |
| **SlmA** | Nucleoid occlusion factor SlmA | 1.078636 | 0.434366 |
| **FruA** | PTS fructose transporter subunit IIBC | 1.08044 | 0.586224 |
| **MetJ** | Met repressor | 1.080579 | 0.306542 |
| **NadA** | Quinolinate synthase A | 1.08171 | 0.673578 |
| **MalI** | Degradation activator | 1.082763 | 0.588994 |
| **HflD** | High frequency lysogenization protein HflD homolog | 1.083077 | 0.469118 |
| **NqrF** | Na(+)-translocating NADH-quinone reductase subunit F | 1.083114 | 0.524252 |
| **SopB** | ParB/RepB/Spo0J family plasmid partition protein | 1.083128 | 0.457689 |
| **ParM** | PRTRC system protein D | 1.083327 | 0.085251 |
| **YjjK** | Energy-dependent translational throttle protein EttA | 1.08355 | 0.010773 |
| **AccC1** | Biotin carboxylase | 1.083883 | 0.087562 |
| **QueC** | 7-cyano-7-deazaguanine synthase | 1.084023 | 0.204066 |
| **PurH** | Bifunctional purine biosynthesis protein PurH | 1.084115 | 0.124542 |
| **PorA** | Pyruvate-flavodoxin oxidoreductase | 1.084993 | 0.344318 |
| **Ddc** | Aspartate aminotransferase family protein | 1.085225 | 0.092028 |
| **AhcY** | Adenosylhomocysteinase | 1.085326 | 0.321855 |
| **Gmk** | Guanylate kinase | 1.086492 | 0.048731 |
| **YdgJ\_1** | Oxidoreductase | 1.086958 | 0.205253 |
| **GlgB** | 1,4-alpha-glucan branching enzyme GlgB | 1.086996 | 0.392979 |
| **RecG** | ATP-dependent DNA helicase RecG | 1.087438 | 0.530453 |
| **DD581\_13285** | UPF0597 protein C7V41\_21510 | 1.087555 | 0.411522 |
| **KdgR\_1** | DNA-binding transcriptional regulator KdgR | 1.08785 | 0.070769 |
| **ThiM** | Hydroxyethylthiazole kinase | 1.088026 | 0.602276 |
| **RcsF** | Outer membrane lipoprotein RcsF | 1.089697 | 0.491416 |
| **CspE** | Cold shock-like protein CspE | 1.089827 | 0.426391 |
| **CysN** | Sulfate adenylyltransferase subunit 1 | 1.090885 | 0.541192 |
| **YedI** | DUF808 domain-containing protein | 1.090959 | 0.438948 |
| **IlvD** | Dihydroxy-acid dehydratase | 1.092952 | 0.068121 |
| **Wzc** | Inner membrane tyrosine autokinase | 1.094217 | 0.448594 |
| **PriB** | Primosomal replication protein N | 1.096478 | 0.723719 |
| **BANRA\_03325** | Permease | 1.096614 | 0.767976 |
| **MdcR** | HTH-type transcriptional regulator gltC | 1.097433 | 0.219979 |
| **PntA** | NAD(P) transhydrogenase subunit alpha | 1.098288 | 0.069221 |
| **AroK\_1** | Adenylate kinase | 1.098864 | 0.641008 |
| **FrdA** | Fumarate reductase flavoprotein subunit | 1.099041 | 0.136797 |
| **SuhB\_1** | Inositol-1-monophosphatase | 1.101024 | 0.080117 |
| **VapC** | Ribonuclease VapC | 1.1013 | 0.260171 |
| **CobT** | Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase | 1.102418 | 0.208108 |
| **GltD** | FAD-dependent oxidoreductase | 1.104349 | 0.244673 |
| **EntF** | Enterobactin non-ribosomal peptide synthetase EntF | 1.104544 | 0.184336 |
| **B4U21\_09740** | YfeABCD regulator yfeE | 1.105073 | 0.742417 |
| **LepA** | Elongation factor 4 | 1.105663 | 0.049112 |
| **Pcm** | Protein-L-isoaspartate O-methyltransferase | 1.107979 | 0.534196 |
| **RdgC** | Recombination-associated protein RdgC | 1.1081 | 0.044017 |
| **GJJ01\_15935** | tRNA/rRNA methyltransferase | 1.108309 | 0.210958 |
| **YbbH\_1** | (Fe-S)-cluster assembly protein | 1.108445 | 0.269703 |
| **IscX** | Protein IscX | 1.108596 | 0.149665 |
| **NrdR** | Transcriptional repressor NrdR | 1.108613 | 0.158449 |
| **SurE** | 5'/3'-nucleotidase SurE | 1.109161 | 0.28253 |
| **PgeF** | Purine nucleoside phosphorylase | 1.111135 | 0.247441 |
| **Tsf** | Elongation factor Ts | 1.111858 | 0.000189 |
| **B4U21\_26905** | GNAT family N-acetyltransferase | 1.113562 | 0.641389 |
| **MdaB** | Flavodoxin family protein | 1.114776 | 0.179915 |
| **SecB** | Protein-export protein SecB | 1.115008 | 0.024778 |
| **YebC** | Probable transcriptional regulatory protein B6R99\_02425 | 1.115304 | 0.052479 |
| **NrdE** | Ribonucleoside-diphosphate reductase | 1.115553 | 0.206138 |
| **CysI** | Sulfite reductase [NADPH] hemoprotein beta-component | 1.115929 | 0.133819 |
| **ZapC** | Cell division protein ZapC | 1.117731 | 0.195142 |
| **MreC** | Cell shape-determining protein MreC | 1.121599 | 0.039393 |
| **MetK** | S-adenosylmethionine synthase | 1.122629 | 0.032434 |
| **TyrB\_1** | Aminotransferase | 1.123046 | 0.737981 |
| **PheS** | Phenylalanine--tRNA ligase alpha subunit | 1.124915 | 0.018348 |
| **YaeL** | Zinc metalloprotease | 1.126747 | 0.179941 |
| **AsmA** | AsmA protein | 1.127766 | 0.182405 |
| **FolK** | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase | 1.12797 | 0.374579 |
| **RbsR\_2** | 2-ketogluconate utilization repressor PtxS | 1.129003 | 0.836735 |
| **RadD\_2** | ATP-dependent helicase | 1.129902 | 0.035432 |
| **YhbY** | RNA-binding protein | 1.131469 | 0.247084 |
| **SixA** | Phosphohistidine phosphatase SixA | 1.13213 | 0.107005 |
| **GlpQ\_1** | Glycerophosphodiester phosphodiesterase | 1.132337 | 0.674298 |
| **LpxA** | Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase | 1.132538 | 0.168241 |
| **DnaA** | Chromosomal replication initiator protein DnaA | 1.134441 | 0.146958 |
| **EngA** | GTPase Der | 1.136653 | 0.043357 |
| **SmpB** | SsrA-binding protein | 1.136777 | 0.028827 |
| **DnaQ** | DNA polymerase III subunit epsilon | 1.137451 | 0.59213 |
| **MurG** | UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase | 1.137639 | 0.10761 |
| **PaaZ** | Bifunctional aldehyde dehydrogenase/enoyl-CoA hydratase | 1.137847 | 0.652733 |
| **GpsA** | Glycerol-3-phosphate dehydrogenase [NAD(P)+] | 1.141356 | 0.059832 |
| **NqrA** | Na(+)-translocating NADH-quinone reductase subunit A | 1.142389 | 0.303321 |
| **YfaU** | 2-keto-3-deoxy-L-rhamnonate aldolase | 1.143936 | 0.760564 |
| **SufB** | Fe-S cluster assembly protein SufB | 1.144371 | 0.131538 |
| **PmbA** | Metalloprotease PmbA | 1.145321 | 0.015005 |
| **Tig** | Trigger factor | 1.145954 | 0.003604 |
| **RpsM** | 30S ribosomal protein S13 | 1.146519 | 0.107291 |
| **OxyR\_1** | LysR family regulatory protein CidR | 1.149208 | 0.517411 |
| **YheS\_2** | ABC transporter ATP-binding protein | 1.1512 | 0.025708 |
| **RpoC** | DNA-directed RNA polymerase subunit beta' | 1.15187 | 0.000283 |
| **YcjG** | Dipeptide epimerase | 1.153984 | 0.380301 |
| **Aas** | Bifunctional protein Aas | 1.154408 | 0.414412 |
| **GalT** | Galactose-1-phosphate uridylyltransferase | 1.15467 | 0.762777 |
| **BtuD** | Vitamin B12 import ATP-binding protein BtuD | 1.155622 | 0.179063 |
| **BglA\_3** | Family 1 glycosylhydrolase | 1.158003 | 0.260668 |
| **GlmU** | Bifunctional protein GlmU | 1.158685 | 0.162062 |
| **YiiS\_1** | DUF406 domain-containing protein | 1.159498 | 0.019697 |
| **Usg** | Aspartate-semialdehyde dehydrogenase | 1.161828 | 0.010608 |
| **SbcC** | Nuclease SbcCD subunit C | 1.161943 | 0.060641 |
| **MurB** | UDP-N-acetylenolpyruvoylglucosamine reductase | 1.163038 | 0.119829 |
| **HisD** | Histidinol dehydrogenase | 1.163183 | 0.756102 |
| **GyrA** | DNA gyrase subunit A | 1.163223 | 0.02926 |
| **B4U21\_17610** | UPF0260 protein B4U21\_17610 | 1.163397 | 0.221793 |
| **RpoN** | RNA polymerase sigma-54 factor | 1.163839 | 0.067996 |
| **Eda** | 2-dehydro-3-deoxy-phosphogluconate aldolase | 1.164128 | 0.068381 |
| **AllS\_4** | LysR family transcriptional regulator | 1.16429 | 0.509296 |
| **Ndh** | FAD-dependent oxidoreductase | 1.16448 | 0.02447 |
| **Mog** | Mog protein | 1.168419 | 0.054948 |
| **YibL** | Protein of uncharacterized function (DUF2810) | 1.169793 | 0.254175 |
| **NudK** | GDP-mannose pyrophosphatase nudK | 1.169979 | 0.090577 |
| **YeaP** | Diguanylate cyclase | 1.170278 | 0.189411 |
| **PatD** | Gamma-aminobutyraldehyde dehydrogenase | 1.171313 | 0.314445 |
| **FrmR** | Metal-sensing transcriptional repressor | 1.17448 | 0.048401 |
| **YehT** | DNA-binding response regulator | 1.176325 | 0.15637 |
| **CatB** | CatB protein | 1.176616 | 0.558168 |
| **IclR** | Acetate operon repressor | 1.177976 | 0.038287 |
| **UvrY** | BarA-associated response regulator UvrY (GacA, SirA) | 1.178653 | 0.466322 |
| **CbiK** | Sirohydrochlorin cobaltochelatase | 1.178913 | 0.043595 |
| **PtsG\_5** | EIICB-Glc | 1.179156 | 0.079818 |
| **IscS** | Cysteine desulfurase IscS | 1.179315 | 0.019469 |
| **LutR\_1** | FCD domain-containing protein | 1.180032 | 0.271564 |
| **Tgt** | Queuine tRNA-ribosyltransferase | 1.180084 | 0.01689 |
| **KstR2\_1** | HTH-type transcriptional repressor KstR2 | 1.180483 | 0.329925 |
| **DnaB** | Replicative DNA helicase | 1.180661 | 0.001611 |
| **PriM** | DNA primase | 1.181016 | 0.108671 |
| **Mtr\_1** | Tryptophan permease | 1.182914 | 0.447293 |
| **YeaZ** | t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaB | 1.1846 | 0.121196 |
| **AspS** | Aspartate--tRNA ligase | 1.184824 | 0.007991 |
| **CysE** | Serine acetyltransferase | 1.188078 | 0.215249 |
| **NusG** | Transcription termination/antitermination protein NusG | 1.188211 | 0.081404 |
| **AroK** | Shikimate kinase 1 | 1.188289 | 0.000877 |
| **B4U21\_25325** | UPF0114 protein B4U21\_25325 | 1.189064 | 0.664558 |
| **PurL** | Phosphoribosylformylglycinamidine synthase | 1.189083 | 0.002039 |
| **RibE** | 6,7-dimethyl-8-ribityllumazine synthase | 1.189534 | 0.010633 |
| **CitA** | Histidine kinase | 1.189615 | 0.30865 |
| **HisA** | 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase | 1.189782 | 0.018447 |
| **RplL** | 50S ribosomal protein L7/L12 | 1.191476 | 0.025149 |
| **DusA** | tRNA-dihydrouridine(20/20a) synthase | 1.191985 | 0.051155 |
| **FusA** | Elongation factor G | 1.19293 | 0.001509 |
| **Lon\_2** | Endopeptidase La | 1.19438 | 0.037376 |
| **YibN** | Molybdopterin biosynthesis protein MoeB | 1.194422 | 0.000109 |
| **MlaA** | Lipoprotein | 1.194495 | 0.206304 |
| **MurA** | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | 1.194816 | 0.006437 |
| **GJJ01\_15355** | GNAT family N-acetyltransferase | 1.19545 | 0.657853 |
| **BANRA\_02224** | tRNA-(Ms[2]io[6]A)-hydroxylase | 1.195745 | 0.233154 |
| **RmuC** | DNA recombination protein RmuC | 1.197085 | 0.027789 |
| **LigT** | RNA 2',3'-cyclic phosphodiesterase | 1.197318 | 0.730728 |
| **CbiF** | Cobalt-precorrin-4 C(11)-methyltransferase | 1.199362 | 0.114049 |
| **YbjD** | ATP-dependent endonuclease | 1.200175 | 0.031649 |
| **Tuf** | Elongation factor Tu (Fragment) | 1.200275 | 0.004909 |
| **PepA** | Probable cytosol aminopeptidase | 1.200333 | 0.001304 |
| **TrmD** | tRNA (guanine-N(1)-)-methyltransferase | 1.20146 | 0.151202 |
| **YhbU\_3** | Peptidase | 1.201787 | 0.046173 |
| **NagB\_2** | Glucosamine-6-phosphate deaminase | 1.202789 | 0.009452 |
| **CarB** | Carbamoyl-phosphate synthase large chain | 1.206254 | 0.000082 |
| **IlvC** | Ketol-acid reductoisomerase (NADP(+)) | 1.207428 | 0.320052 |
| **NarG** | Nitrate reductase (quinone) | 1.208227 | 0.004959 |
| **Dxs\_1** | 1-deoxy-D-xylulose-5-phosphate synthase | 1.208979 | 0.007162 |
| **GatB** | Galactitol-specific phosphotransferase enzyme IIB component | 1.209703 | 0.21656 |
| **RelA** | GTP diphosphokinase | 1.20979 | 0.002588 |
| **TatD** | 3'-5' ssDNA/RNA exonuclease TatD | 1.213218 | 0.014924 |
| **SecD** | Protein translocase subunit SecD | 1.213629 | 0.003022 |
| **AtpA** | ATP synthase subunit alpha | 1.214085 | 0.000135 |
| **LsrK\_1** | Pentose kinase | 1.214515 | 0.76289 |
| **BANRA\_02252** | Amidohydrolase/deacetylase family metallohydrolase | 1.21489 | 0.265984 |
| **BANRA\_00692** | ArsR family transcriptional regulator | 1.215541 | 0.077291 |
| **PspF** | Phage shock protein operon transcriptional activator | 1.216952 | 0.047168 |
| **RsmI** | Ribosomal RNA small subunit methyltransferase I | 1.218387 | 0.069904 |
| **YceD** | 23S rRNA accumulation protein YceD | 1.219086 | 0.005219 |
| **Cnu** | Cnu protein | 1.219689 | 0.007293 |
| **QueA** | S-adenosylmethionine:tRNA ribosyltransferase-isomerase | 1.220429 | 0.007646 |
| **NsrR** | HTH-type transcriptional repressor NsrR | 1.220831 | 0.209114 |
| **PotC** | Spermidine/putrescine ABC transporter membrane protein | 1.221296 | 0.240872 |
| **YojI** | ABC transporter ATP-binding protein | 1.224696 | 0.007243 |
| **PulS** | Lipoprotein, PulS/OutS family | 1.224732 | 0.191795 |
| **AcpS** | Holo-[acyl-carrier-protein] synthase | 1.225452 | 0.212583 |
| **Pth** | Peptidyl-tRNA hydrolase | 1.227105 | 0.258538 |
| **QueE** | 7-carboxy-7-deazaguanine synthase | 1.229032 | 0.032651 |
| **BolA** | BolA family transcriptional regulator | 1.229629 | 0.010307 |
| **PotA\_2** | Spermidine/putrescine import ATP-binding protein PotA | 1.23018 | 0.237261 |
| **MurI** | Glutamate racemase | 1.23122 | 0.109105 |
| **YqiC** | Ubiquinone biosynthesis accessory factor UbiK | 1.231911 | 0.004347 |
| **TrmH** | tRNA (guanosine(18)-2'-O)-methyltransferase | 1.232857 | 0.224227 |
| **FtnA\_2** | Ferritin | 1.233723 | 0.059027 |
| **PyrH** | Uridylate kinase | 1.233845 | 0.007387 |
| **EpmC** | Elongation factor P hydroxylase | 1.235964 | 0.606775 |
| **FtsQ** | Cell division protein FtsQ | 1.236342 | 0.308311 |
| **Cra\_1** | Catabolite repressor/activator | 1.237463 | 0.207749 |
| **PcnB** | Poly(A) polymerase I | 1.238291 | 0.037925 |
| **PrfC** | Peptide chain release factor 3 | 1.241849 | 0.001449 |
| **LpxD** | UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase | 1.241902 | 0.003972 |
| **HmsP** | Biofilm formation regulator HmsP | 1.242169 | 0.029537 |
| **DD581\_07015** | Acetyltransferase | 1.244018 | 0.00292 |
| **GlgA** | Glycogen synthase | 1.244503 | 0.065069 |
| **NusB** | Transcription antitermination protein NusB | 1.246152 | 0.00774 |
| **FabB** | 3-oxoacyl-ACP synthase | 1.249433 | 0.020448 |
| **GsiA\_7** | ABC transporter ATP-binding protein | 1.249707 | 0.017029 |
| **RplS** | 50S ribosomal protein L19 | 1.249735 | 0.011282 |
| **YheS\_2** | ABC transporter ATP-binding protein | 1.25302 | 0.013536 |
| **YjaG** | DUF416 domain-containing protein | 1.253348 | 0.015695 |
| **RffG** | dTDP-glucose 4,6-dehydratase | 1.253942 | 0.00757 |
| **SseB** | Enhanced serine sensitivity protein SseB | 1.254067 | 0.108178 |
| **Smp2** | Membrane protein | 1.254667 | 0.283781 |
| **CmoB** | tRNA U34 carboxymethyltransferase | 1.256083 | 0.438871 |
| **TusE** | Sulfurtransferase | 1.256874 | 0.103351 |
| **B4U25\_14985** | DUF4186 domain-containing protein | 1.257286 | 0.028016 |
| **YaaA** | UPF0246 protein B4U21\_00050 | 1.259645 | 0.042964 |
| **RpsB** | 30S ribosomal protein S2 | 1.260786 | 0.032025 |
| **RimI** | [Ribosomal protein S18]-alanine N-acetyltransferase | 1.26102 | 0.044734 |
| **YjgA** | UPF0307 protein B4U21\_32930 | 1.262582 | 0.065504 |
| **Ffh** | Signal recognition particle protein | 1.263105 | 0.001068 |
| **SdaB** | L-serine dehydratase | 1.263123 | 0.002245 |
| **MrcA** | DD-transpeptidase | 1.266848 | 0.014722 |
| **FrdB** | Fumarate reductase iron-sulfur subunit | 1.268394 | 0.214415 |
| **FabI** | Enoyl-[acyl-carrier-protein] reductase [NADH] | 1.269689 | 0.003173 |
| **CobT** | Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase | 1.269696 | 0.690337 |
| **HisG** | ATP phosphoribosyltransferase | 1.271821 | 0.088378 |
| **MurR** | HTH-type transcriptional regulator MurR | 1.273896 | 0.071289 |
| **C2U49\_13320** | Carboxymuconolactone decarboxylase family protein | 1.273973 | 0.068092 |
| **YieH** | 6-phosphogluconate phosphatase | 1.275444 | 0.208581 |
| **WaaA** | 3-deoxy-D-manno-octulosonic acid transferase | 1.277088 | 0.143985 |
| **ObgE** | GTPase Obg | 1.278428 | 0.126647 |
| **ThrS** | Threonine--tRNA ligase | 1.278472 | 0.000916 |
| **MntR** | Manganese transport regulator | 1.279653 | 0.022208 |
| **PepT** | Peptidase T | 1.282532 | 0.019235 |
| **YjaB\_2** | Acetyltransferase | 1.28452 | 0.001094 |
| **YqeG** | Inner membrane transport protein YqeG | 1.286612 | 0.007491 |
| **MenB** | 1,4-dihydroxy-2-naphthoyl-CoA synthase | 1.287293 | 0.041417 |
| **AccA** | Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | 1.291831 | 0.001312 |
| **RpmD** | 50S ribosomal protein L30 | 1.293471 | 0.049954 |
| **NarL** | DNA-binding response regulator | 1.293493 | 0.005544 |
| **GJJ01\_27690** | Cupin domain-containing protein | 1.294004 | 0.005341 |
| **MalE** | Maltodextrin-binding protein | 1.294961 | 0.004695 |
| **NusA** | Transcription termination/antitermination protein NusA | 1.295202 | 0.001659 |
| **AtpH** | ATP synthase subunit delta | 1.296673 | 0.004893 |
| **GlyS** | Glycine--tRNA ligase beta subunit | 1.29694 | 0.000006 |
| **ParC** | DNA topoisomerase 4 subunit A | 1.29723 | 0.004265 |
| **DedD** | Cell division protein DedD | 1.297624 | 0.005312 |
| **RpoE** | ECF RNA polymerase sigma-E factor | 1.298086 | 0.004248 |
| **YgeR** | LysM peptidoglycan-binding domain-containing protein | 1.298181 | 0.06794 |
| **PdxJ** | Pyridoxine 5'-phosphate synthase | 1.298524 | 0.576105 |
| **PyrB** | Aspartate carbamoyltransferase | 1.298741 | 0.008489 |
| **DnaC** | DNA replication protein DnaC | 1.299365 | 0.001821 |
| **IaaA** | Beta-aspartyl-peptidase | 1.299986 | 0.000854 |
| **Rnd** | Ribonuclease D | 1.302966 | 0.012996 |
| **TamB** | Autotransporter assembly complex protein TamB | 1.303598 | 0.000448 |
| **IlvG** | Acetolactate synthase | 1.305824 | 0.410042 |
| **RpoB** | DNA-directed RNA polymerase subunit beta | 1.306092 | 0.000175 |
| **RnfE** | Ion-translocating oxidoreductase complex subunit E | 1.30683 | 0.337475 |
| **ExbD** | Biopolymer transport protein ExbD | 1.308009 | 0.00098 |
| **EntB** | Isochorismatase | 1.309511 | 0.00322 |
| **SmrA\_1** | UPF0115 protein B6R99\_06315 | 1.3101 | 0.294825 |
| **NarY** | NarY protein | 1.311187 | 0.611162 |
| **NemR** | HTH-type transcriptional repressor NemR | 1.313273 | 0.001899 |
| **FbaB** | Class I fructose-bisphosphate aldolase | 1.313461 | 0.002695 |
| **ThiI** | tRNA sulfurtransferase | 1.317497 | 0.001971 |
| **YeeX** | UPF0265 protein B4U21\_18700 | 1.318191 | 0.010061 |
| **PitA** | Phosphate transporter | 1.318497 | 0.000207 |
| **RpoZ** | DNA-directed RNA polymerase subunit omega | 1.318551 | 0.01878 |
| **PgpB** | PgpB protein | 1.319239 | 0.100214 |
| **Imp** | LPS-assembly protein LptD | 1.319941 | 0.194527 |
| **YrfG** | (S)-2-haloacid dehalogenase | 1.320839 | 0.104594 |
| **RfaC** | ADP-heptose--LPS heptosyltransferase | 1.321432 | 0.000889 |
| **YggT** | Integral membrane protein YggT | 1.321571 | 0.168448 |
| **LpdA** | Dihydrolipoyl dehydrogenase | 1.322143 | 0.000425 |
| **MatP** | Macrodomain Ter protein | 1.322908 | 0.046725 |
| **SrlD** | Sorbitol-6-phosphate 2-dehydrogenase | 1.323504 | 0.003545 |
| **AsnS** | Asparagine--tRNA ligase | 1.323555 | 0.000158 |
| **ProQ** | RNA chaperone ProQ | 1.323628 | 0.000505 |
| **SufD** | Fe-S cluster assembly protein SufD | 1.323649 | 0.004703 |
| **NlpI** | Lipoprotein NlpI | 1.324385 | 0.039793 |
| **PfkA** | ATP-dependent 6-phosphofructokinase | 1.325738 | 0.000017 |
| **PheT** | Phenylalanine--tRNA ligase beta subunit | 1.326629 | 0.000152 |
| **BtuB** | Vitamin B12 transporter BtuB | 1.328196 | 0.052848 |
| **NuoL** | NADH-quinone oxidoreductase subunit L | 1.330935 | 0.011787 |
| **SdhD** | Succinate dehydrogenase hydrophobic membrane anchor subunit | 1.331288 | 0.043225 |
| **NhaB** | Na(+)/H(+) antiporter NhaB | 1.331555 | 0.15113 |
| **SrlB** | PTS glucitol/sorbitol transporter subunit IIA | 1.334021 | 0.005333 |
| **YjiR** | Aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme | 1.334046 | 0.378205 |
| **InfC** | Translation initiation factor IF-3 | 1.334548 | 0.007611 |
| **RsuA** | Pseudouridine synthase | 1.334819 | 0.001974 |
| **YdiK\_2** | AI-2E family transporter | 1.335151 | 0.275936 |
| **Wzi** | Capsule assembly Wzi family protein | 1.336714 | 0.267081 |
| **RsxB** | Ion-translocating oxidoreductase complex subunit B | 1.336741 | 0.507147 |
| **MurF** | UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase | 1.337275 | 0.003696 |
| **GltR\_2** | LysR family transcriptional regulator | 1.338732 | 0.437268 |
| **TsaE** | t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaE | 1.338812 | 0.000141 |
| **UbiH** | 2-octaprenyl-6-methoxyphenol hydroxylase | 1.340079 | 0.040897 |
| **OmpR\_1** | DNA-binding response regulator | 1.34034 | 0.609797 |
| **TrmB** | tRNA (guanine-N(7)-)-methyltransferase | 1.34036 | 0.050813 |
| **GyrB** | DNA gyrase subunit B | 1.343482 | 0.000089 |
| **GuaA** | GMP synthase [glutamine-hydrolyzing] | 1.344057 | 0.000138 |
| **DacA** | Serine-type D-Ala-D-Ala carboxypeptidase | 1.344863 | 0.000565 |
| **IolC\_3** | 5-dehydro-2-deoxygluconokinase | 1.345389 | 0.071485 |
| **HrpA** | ATP-dependent RNA helicase HrpA | 1.346606 | 0.009088 |
| **YcbX\_2** | 2Fe-2S ferredoxin YfaE | 1.351057 | 0.01944 |
| **MscS** | Mechanosensitive channel MscS | 1.351109 | 0.013973 |
| **ArgR** | Arginine repressor | 1.351614 | 0.03005 |
| **SecA** | Protein translocase subunit SecA | 1.351642 | 0.000117 |
| **YdjN** | Cation:dicarboxylase symporter family transporter | 1.351707 | 0.091255 |
| **PrmC** | Release factor glutamine methyltransferase | 1.355895 | 0.112387 |
| **CytR\_2** | LacI family DNA-binding transcriptional regulator | 1.356505 | 0.511782 |
| **B4U21\_06905** | Bacterial sensory transduction regulator | 1.356968 | 0.016321 |
| **HxlR** | HTH-type transcriptional activator HxlR | 1.357434 | 0.020918 |
| **Upp** | Uracil phosphoribosyltransferase | 1.357719 | 0.001085 |
| **NtrB** | Histidine kinase | 1.359173 | 0.018127 |
| **CadC** | CadC family transcriptional regulator | 1.359303 | 0.039882 |
| **CyoA** | Ubiquinol oxidase subunit 2 | 1.360455 | 0.00192 |
| **EntS** | Enterobactin exporter EntS | 1.361101 | 0.564459 |
| **SelB** | SelB translation factor | 1.362775 | 0.095451 |
| **YabJ\_1** | 2-iminobutanoate/2-iminopropanoate deaminase | 1.362939 | 0.013611 |
| **PotF\_1** | ABC transporter substrate-binding protein | 1.364482 | 0.001276 |
| **YffB** | A glutathione-dependent thiol reductase | 1.366367 | 0.032526 |
| **MscS** | Mechanosensitive channel MscK | 1.366798 | 0.009703 |
| **GJJ01\_16205** | Alpha-2-macroglobulin | 1.372783 | 0.011805 |
| **GJJ01\_21115** | 5'-3' exoribonuclease | 1.373192 | 0.030285 |
| **ProS** | Proline--tRNA ligase | 1.374282 | 0.002709 |
| **CysK\_2** | Cysteine synthase | 1.374643 | 0.00958 |
| **HemG** | HemG protein | 1.376598 | 0.005188 |
| **FtsK** | DNA translocase FtsK | 1.381396 | 0.018795 |
| **ZraR\_2** | Response regulator of zinc sigma-54-dependent two-component system | 1.38249 | 0.559007 |
| **RpsP** | 30S ribosomal protein S16 | 1.385687 | 0.03662 |
| **Spr** | Bifunctional murein DD-endopeptidase/murein LD-carboxypeptidase | 1.387354 | 0.000649 |
| **YhaX** | Cof-type HAD-IIB family hydrolase | 1.38746 | 0.326284 |
| **GlnA** | Glutamine synthetase | 1.391089 | 0.003379 |
| **CmpR\_1** | HTH-type transcriptional activator CmpR | 1.392076 | 0.406915 |
| **RplA** | 50S ribosomal protein L1 | 1.392317 | 0.000298 |
| **RsmB** | Ribosomal RNA small subunit methyltransferase B | 1.392724 | 0.007926 |
| **HisH** | Imidazole glycerol phosphate synthase subunit HisH | 1.393164 | 0.008527 |
| **RluC** | Pseudouridine synthase | 1.393716 | 0.001096 |
| **RplF** | 50S ribosomal protein L6 | 1.395529 | 0.001114 |
| **KamA** | EF-P post-translational modification enzyme B | 1.397112 | 0.013432 |
| **PurP** | NCS2 family permease | 1.398496 | 0.278903 |
| **PurU** | Formyltetrahydrofolate deformylase | 1.398591 | 0.019984 |
| **RplB** | 50S ribosomal protein L2 | 1.399344 | 0.003854 |
| **YaiI** | UPF0178 protein B6R99\_07575 | 1.401203 | 0.004247 |
| **Pnp** | Polyribonucleotide nucleotidyltransferase | 1.402937 | 0.000142 |
| **CstA** | Carbon starvation protein A | 1.403166 | 0.276155 |
| **OxyR** | DNA-binding transcriptional regulator OxyR | 1.403453 | 0.00275 |
| **B4U21\_27805** | Death on curing protein, Doc toxin | 1.406071 | 0.184131 |
| **BL124\_00003435** | DUF4056 domain-containing protein | 1.406176 | 0.011912 |
| **MalK\_3** | Maltose/maltodextrin import ATP-binding protein MalK | 1.407634 | 0.00285 |
| **CmpR\_4** | HTH-type transcriptional activator CmpR | 1.40813 | 0.541004 |
| **WzzE** | ECA polysaccharide chain length modulation protein | 1.411079 | 0.007502 |
| **Syd** | Protein Syd | 1.411882 | 0.088758 |
| **NupC** | Nucleoside permease | 1.412843 | 0.007257 |
| **YcaO** | 30S ribosomal protein S12 methylthiotransferase accessory protein YcaO | 1.412914 | 0.018603 |
| **RpsJ** | 30S ribosomal protein S10 | 1.414062 | 0.009449 |
| **NadB** | L-aspartate oxidase | 1.415903 | 0.045411 |
| **RplM** | 50S ribosomal protein L13 | 1.415911 | 0.000318 |
| **WaaF** | ADP-heptose--LPS heptosyltransferase RfaF | 1.416297 | 0.314012 |
| **ProV** | Glycine betaine/L-proline ABC transporter ATP-binding protein | 1.416302 | 0.011618 |
| **FtsA** | Cell division protein FtsA | 1.41861 | 0.000403 |
| **YbjI** | 5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YbjI | 1.418691 | 0.026248 |
| **MalM** | MalM protein | 1.42017 | 0.002051 |
| **Pta** | Phosphate acetyltransferase | 1.421944 | 0.000052 |
| **RpmJ** | 50S ribosomal protein L36 | 1.423953 | 0.000253 |
| **BltD** | GNAT family N-acetyltransferase | 1.425123 | 0.060584 |
| **CadA** | Inducible lysine decarboxylase | 1.427832 | 0.003016 |
| **AnsA** | Asparaginase | 1.429003 | 0.005443 |
| **IbpA** | Small heat shock protein IbpA | 1.43157 | 0.141849 |
| **AcrD** | Efflux pump membrane transporter | 1.432324 | 0.031482 |
| **CoaBC** | Coenzyme A biosynthesis bifunctional protein CoaBC | 1.433119 | 0.011336 |
| **GlsB** | Glutaminase | 1.434235 | 0.00215 |
| **RpmB** | 50S ribosomal protein L28 | 1.435173 | 0.000668 |
| **Lrp\_1** | DNA-binding transcriptional activator DecR | 1.435612 | 0.635013 |
| **RplD** | 50S ribosomal protein L4 | 1.437004 | 0.000222 |
| **KdsC** | 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase KdsC | 1.43864 | 0.12365 |
| **PrmA** | Ribosomal protein L11 methyltransferase | 1.439768 | 0.000279 |
| **AmyA** | Alpha-amylase | 1.441676 | 0.058429 |
| **RecB** | RecBCD enzyme subunit RecB | 1.442279 | 0.007369 |
| **MoaC** | Cyclic pyranopterin monophosphate synthase | 1.445486 | 0.078711 |
| **YbiU** | DUF1479 family protein | 1.445894 | 0.024263 |
| **RecX** | Regulatory protein RecX | 1.446395 | 0.056074 |
| **SecA** | UPF0149 family protein | 1.447456 | 0.002158 |
| **MetN\_3** | Methionine import ATP-binding protein MetN | 1.448147 | 0.093356 |
| **GJJ01\_05905** | Iron-regulated membrane protein | 1.448577 | 0.008065 |
| **YjjG** | 5'-nucleotidase | 1.448899 | 0.062984 |
| **YeaC** | DUF1315 domain-containing protein | 1.45091 | 0.007522 |
| **RpsN** | 30S ribosomal protein S14 | 1.452361 | 0.012083 |
| **RecC** | RecBCD enzyme subunit RecC | 1.45628 | 0.018465 |
| **IutA** | Putative TonB-dependent receptor | 1.45638 | 0.143578 |
| **FdoI** | FdoI protein | 1.456463 | 0.240275 |
| **B4U21\_12950** | ParD-like family protein | 1.457548 | 0.114459 |
| **LptF** | Lipopolysaccharide export system permease protein LptF | 1.457591 | 0.114564 |
| **FepA\_3** | TonB-dependent receptor | 1.459386 | 0.079889 |
| **RimO** | Ribosomal protein S12 methylthiotransferase RimO | 1.460788 | 0.000007 |
| **WaaE** | Glucosyltransferase WaaE | 1.461384 | 0.004706 |
| **PykF** | Pyruvate kinase | 1.462592 | 0.000022 |
| **B4U21\_20510** | YfcL family protein | 1.46316 | 0.019899 |
| **DbpA** | ATP-dependent RNA helicase DbpA | 1.463878 | 0.042951 |
| **RplI** | 50S ribosomal protein L9 | 1.463905 | 0.001638 |
| **RpsT** | 30S ribosomal protein S20 | 1.464476 | 0.000555 |
| **MalF** | Maltose/maltodextrin transport system permease protein | 1.465901 | 0.00272 |
| **RstA** | DNA-binding response regulator | 1.468658 | 0.024551 |
| **B4U25\_19730** | RidA family protein | 1.469687 | 0.452946 |
| **LacC** | Phosphofructokinase | 1.469877 | 0.015807 |
| **RluA** | Pseudouridine synthase | 1.470306 | 0.001135 |
| **YebE** | DUF533 domain-containing protein | 1.471611 | 0.192923 |
| **ZnuA** | High-affinity zinc uptake system protein ZnuA | 1.472306 | 0.002446 |
| **Pat** | Protein acetyltransferase | 1.474413 | 0.341721 |
| **QueG** | Epoxyqueuosine reductase | 1.476724 | 0.190245 |
| **AgaR** | DeoR family transcriptional regulator | 1.477665 | 0.005018 |
| **XerC** | Tyrosine recombinase XerC | 1.480109 | 0.22592 |
| **FecD** | ABC transporter permease | 1.480111 | 0.232536 |
| **ClcA** | H(+)/Cl(-) exchange transporter ClcA | 1.480442 | 0.61721 |
| **YicC** | Protein YicC | 1.483441 | 0.002089 |
| **RatB** | UPF0125 protein B6R99\_20980 | 1.485244 | 0.010855 |
| **RcsC** | Sensor histidine kinase RcsC | 1.485304 | 0.003751 |
| **InfB** | Translation initiation factor IF-2 | 1.489782 | 0.000061 |
| **TsaD** | tRNA N6-adenosine threonylcarbamoyltransferase | 1.490594 | 0.004293 |
| **Spr\_3** | Endopeptidase | 1.490838 | 0.000196 |
| **RpsL** | 30S ribosomal protein S12 | 1.490864 | 0.000257 |
| **AckA\_2** | Acetate kinase | 1.490913 | 0.000992 |
| **RfaQ** | Lipopolysaccharide heptosyltransferase III | 1.493555 | 0.259745 |
| **SecY** | Protein translocase subunit SecY | 1.494446 | 0.058272 |
| **BN49\_1157** | Ribosome association toxin RatA | 1.495869 | 0.028786 |
| **Edd** | Phosphogluconate dehydratase | 1.497894 | 0.000031 |
| **MtnC** | Enolase-phosphatase E1 | 1.498966 | 0.022104 |
| **RlmH** | Ribosomal RNA large subunit methyltransferase H | 1.504129 | 0.193694 |
| **PyrG** | CTP synthase | 1.506807 | 0.00005 |
| **PrsA** | Ribose-phosphate pyrophosphokinase | 1.508749 | 0.000149 |
| **GuaB** | Inosine-5'-monophosphate dehydrogenase | 1.509187 | 0.000868 |
| **NlpA** | Lipoprotein | 1.509647 | 0.01764 |
| **EngD** | Ribosome-binding ATPase YchF | 1.510441 | 0.000242 |
| **ErpA** | Iron-sulfur cluster insertion protein ErpA | 1.511557 | 0.00173 |
| **RpmH** | 50S ribosomal protein L34 | 1.512243 | 0.055832 |
| **YccS** | Efflux (PET) family inner membrane protein YccS | 1.513499 | 0.012529 |
| **CysJ** | Sulfite reductase [NADPH] flavoprotein alpha-component | 1.514644 | 0.000125 |
| **Cfa** | Cfa protein | 1.515064 | 0.000217 |
| **RpsC** | 30S ribosomal protein S3 | 1.515727 | 0.000059 |
| **Udk** | Uridine kinase | 1.517024 | 0.011017 |
| **MnmE** | tRNA modification GTPase MnmE | 1.52177 | 0.000103 |
| **HyaD** | Glycosyltransferase | 1.524658 | 0.069464 |
| **Rho** | Transcription termination factor Rho | 1.526347 | 0.00018 |
| **TruB** | tRNA pseudouridine synthase B | 1.527455 | 0.001426 |
| **C2U49\_08720** | LexA family transcriptional regulator | 1.530287 | 0.275521 |
| **RplT** | 50S ribosomal protein L20 | 1.532011 | 0.00455 |
| **MlaE** | Intermembrane phospholipid transport system permease protein MlaE | 1.53212 | 0.021663 |
| **NhaK\_2** | Na+/H+ antiporter | 1.540953 | 0.083356 |
| **YoaE\_2** | CNNM family cation transport protein YoaE | 1.541997 | 0.00184 |
| **Dam\_2** | Site-specific DNA-methyltransferase (adenine-specific) | 1.542424 | 0.002301 |
| **LldD\_1** | Alpha-hydroxy-acid oxidizing protein | 1.54245 | 0.001011 |
| **YbbL** | Iron ABC transporter ATP-binding protein FetA | 1.543723 | 0.000029 |
| **MurJ** | Probable lipid II flippase MurJ | 1.545587 | 0.021341 |
| **GntR\_2** | Gluconate operon transcriptional repressor GntR | 1.546397 | 0.088851 |
| **GsiA\_11** | ABC transporter ATP-binding protein | 1.54646 | 0.002738 |
| **GntU** | Gluconate transporter | 1.547927 | 0.050046 |
| **HisC** | Histidinol-phosphate aminotransferase | 1.548501 | 0.001741 |
| **XseB** | Exodeoxyribonuclease 7 small subunit | 1.551076 | 0.003941 |
| **SrlR\_3** | DeoR family transcriptional regulator | 1.555636 | 0.084182 |
| **RplR** | 50S ribosomal protein L18 | 1.556776 | 0.000019 |
| **GlpA** | Glycerol-3-phosphate dehydrogenase | 1.557426 | 0.009403 |
| **C2U49\_00080** | 5-oxoprolinase/urea amidolyase family protein | 1.557428 | 0.00201 |
| **RlmG** | Ribosomal RNA large subunit methyltransferase G | 1.559636 | 0.002078 |
| **CmoA** | Carboxy-S-adenosyl-L-methionine synthase | 1.560088 | 0.001516 |
| **NudJ** | Phosphatase NudJ | 1.56079 | 0.091488 |
| **RplN** | 50S ribosomal protein L14 | 1.562042 | 0.000357 |
| **BglF\_2** | PTS beta-glucoside transporter subunit IIABC | 1.563229 | 0.006484 |
| **NuoE** | NADH dehydrogenase I subunit E | 1.563779 | 0.0004 |
| **RpsE** | 30S ribosomal protein S5 | 1.564817 | 0.000448 |
| **Wzt** | ABC transporter ATP-binding protein | 1.56483 | 0.041858 |
| **YhjQ** | Cellulose synthase operon protein YhjQ | 1.565433 | 0.13551 |
| **RpoH** | RNA polymerase sigma factor RpoH | 1.565891 | 0.003496 |
| **RpsR** | 30S ribosomal protein S18 | 1.566233 | 0.001888 |
| **MraY** | Phospho-N-acetylmuramoyl-pentapeptide-transferase | 1.566669 | 0.001276 |
| **LipA** | Lipoyl synthase | 1.567911 | 0.000823 |
| **MalZ** | Maltodextrin glucosidase | 1.568947 | 0.01245 |
| **Irp1** | High-molecular-weight nonribosomal peptide/polyketide synthetase 1 | 1.570937 | 0.568741 |
| **AtpD** | ATP synthase subunit beta | 1.572629 | 0.000008 |
| **GlpK\_1** | Carbohydrate kinase | 1.575014 | 0.57194 |
| **EntC** | Isochorismate synthase | 1.58542 | 0.022175 |
| **PlsB** | Glycerol-3-phosphate acyltransferase | 1.586466 | 0.002752 |
| **NrdD** | Anaerobic ribonucleoside-triphosphate reductase | 1.588822 | 0.010836 |
| **NqrC** | Na(+)-translocating NADH-quinone reductase subunit C | 1.596277 | 0.019004 |
| **GJJ01\_27620** | DNA polymerase III subunit theta | 1.59632 | 0.127706 |
| **SelA** | L-seryl-tRNA(Sec) selenium transferase | 1.596978 | 0.00106 |
| **BANRA\_02570** | Protein PaaI | 1.600138 | 0.001866 |
| **MtnB** | Methylthioribulose-1-phosphate dehydratase | 1.600353 | 0.437192 |
| **PflB** | Formate C-acetyltransferase | 1.601837 | 0.00053 |
| **YeiG** | S-formylglutathione hydrolase | 1.602382 | 0.005007 |
| **DegA\_2** | LacI family DNA-binding transcriptional regulator | 1.604563 | 0.07145 |
| **DhaR** | Acetoin catabolism regulatory protein | 1.606493 | 0.263273 |
| **LivF** | High-affinity branched-chain amino acid transport ATP-binding protein | 1.609709 | 0.023008 |
| **Cca** | Multifunctional CCA protein | 1.610727 | 0.00267 |
| **YheT** | Hydrolase | 1.611843 | 0.112523 |
| **LdcA** | Muramoyltetrapeptide carboxypeptidase | 1.616133 | 0.012806 |
| **RsfS** | Ribosomal silencing factor RsfS | 1.61862 | 0.003997 |
| **LpxB** | Lipid-A-disaccharide synthase | 1.623743 | 0.088218 |
| **MiaB** | tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase | 1.625201 | 0.000292 |
| **GJJ01\_13315** | GNAT family N-acetyltransferase | 1.625416 | 0.254256 |
| **DmlR\_9** | LysR family transcriptional regulator | 1.629018 | 0.225455 |
| **RplC** | 50S ribosomal protein L3 | 1.62982 | 0.000179 |
| **PstC** | Phosphate transport system permease protein | 1.631441 | 0.051123 |
| **FhuC** | Car(A)\_1\_M80346 | 1.631674 | 0.001542 |
| **TrpR** | Trp operon repressor | 1.633097 | 0.008469 |
| **TtdT** | Anion permease | 1.636104 | 0.013641 |
| **BioD\_2** | ATP-dependent dethiobiotin synthetase BioD | 1.638023 | 0.001462 |
| **RplO** | 50S ribosomal protein L15 | 1.639217 | 0.000782 |
| **AroL** | Shikimate kinase 1 | 1.640329 | 0.003153 |
| **GJJ01\_06720** | Metal-dependent hydrolase | 1.642617 | 0.004791 |
| **BANRA\_03124** | ISNCY family transposase | 1.64562 | 0.030647 |
| **HcaR\_1** | Hca operon transcriptional activator | 1.649102 | 0.097808 |
| **LpxT** | Lipid A 1-diphosphate synthase | 1.65152 | 0.000195 |
| **BANRA\_00262** | Uncharacterized protein | 1.653836 | 0.024064 |
| **TruC** | TruC protein | 1.654097 | 0.001221 |
| **NarH** | Nitrate reductase subunit beta | 1.654123 | 0.005889 |
| **YgjP** | DUF45 domain-containing protein | 1.654957 | 0.000436 |
| **RpsD** | 30S ribosomal protein S4 | 1.655362 | 0.00004 |
| **UraH** | 5-hydroxyisourate hydrolase | 1.656371 | 0.048408 |
| **MoaB** | Molybdenum cofactor biosynthesis protein B | 1.658417 | 0.092679 |
| **SufS** | Cysteine desulfurase | 1.658839 | 0.023294 |
| **MtnK** | Methylthioribose kinase | 1.659449 | 0.000406 |
| **PabA** | Aminodeoxychorismate synthase component 2 | 1.677112 | 0.251819 |
| **BANRA\_01373** | DNA-binding protein | 1.681879 | 0.072401 |
| **BaeS** | Histidine kinase | 1.681985 | 0.048465 |
| **Gcd** | Gcd protein | 1.682341 | 0.004077 |
| **EnvC** | Murein hydrolase activator EnvC | 1.683521 | 0.015584 |
| **TrkA** | Trk system potassium uptake protein TrkA | 1.685457 | 0.067697 |
| **YciN** | DUF2498 domain-containing protein | 1.691468 | 0.026031 |
| **CsrD** | Lipoprotein | 1.694111 | 0.004702 |
| **FdhD** | Sulfur carrier protein FdhD | 1.698198 | 0.082197 |
| **YbbH\_4** | HTH-type transcriptional regulator HexR | 1.702189 | 0.003158 |
| **FeoA** | Fe(2+) transport protein A | 1.7041 | 0.005898 |
| **EntE** | (2,3-dihydroxybenzoyl)adenylate synthase | 1.705187 | 0.000481 |
| **OmpW** | Outer membrane protein OmpW | 1.706998 | 0.031832 |
| **YjcD** | Guanine-hypoxanthine permease | 1.707234 | 0.040079 |
| **DacB** | D-alanyl-D-alanine carboxypeptidase | 1.710029 | 0.015333 |
| **PolA** | DNA polymerase I | 1.711175 | 0.000172 |
| **TsgA** | Protein TsgA homolog | 1.714399 | 0.001734 |
| **YfiR** | TetR family transcriptional regulator | 1.715405 | 0.001217 |
| **AceE** | Pyruvate dehydrogenase E1 component | 1.717303 | 0.00001 |
| **Mqo** | Probable malate:quinone oxidoreductase | 1.717959 | 0.003682 |
| **RhlE** | ATP-dependent RNA helicase RhlE | 1.719062 | 0.000002 |
| **HolE\_1** | DNA polymerase III subunit theta | 1.720015 | 0.012269 |
| **B4U21\_25500** | UPF0441 protein B4U21\_25500 | 1.725125 | 0.002191 |
| **BANRA\_01179** | Membrane protein | 1.726206 | 0.00158 |
| **NorR** | Anaerobic nitric oxide reductase transcription regulator NorR | 1.727087 | 0.002415 |
| **FtsN** | Cell division protein FtsN | 1.727836 | 0.000315 |
| **Rph** | Ribonuclease PH | 1.72856 | 0.016426 |
| **RplX** | 50S ribosomal protein L24 | 1.73161 | 0.000517 |
| **RplJ** | 50S ribosomal protein L10 | 1.733155 | 0.000123 |
| **EXT45\_28075** | Recombinase | 1.734304 | 0.264061 |
| **MnmG** | tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG | 1.738878 | 0.039148 |
| **YbiX** | PKHD-type hydroxylase B6R99\_16635 | 1.741282 | 0.297593 |
| **AtpG** | ATP synthase gamma chain | 1.741696 | 0.00012 |
| **RecR** | Recombination protein RecR | 1.743897 | 0.001814 |
| **FolE2** | GTP cyclohydrolase FolE2 | 1.746387 | 0.003394 |
| **TyrR** | Transcriptional regulatory protein TyrR | 1.748097 | 0.00077 |
| **IlvB\_2** | Thiamine pyrophosphate enzyme | 1.748475 | 0.046768 |
| **Livk** | High-affinity branched-chain amino acid ABC transporter substrate-binding protein LivK | 1.752419 | 0.137917 |
| **B4U25\_35990** | LacI family DNA-binding transcriptional regulator | 1.752665 | 0.024754 |
| **RplQ** | 50S ribosomal protein L17 | 1.757042 | 0.000981 |
| **YbcJ** | Ribosome-associated protein | 1.75724 | 0.006671 |
| **SrmB** | ATP-dependent RNA helicase SrmB | 1.75808 | 0.000748 |
| **MrdA** | Peptidoglycan D,D-transpeptidase MrdA | 1.759157 | 0.003431 |
| **RpsH** | 30S ribosomal protein S8 | 1.762205 | 0.000463 |
| **ExbB** | Biopolymer transport protein ExbB | 1.765326 | 0.00106 |
| **MbtH** | Cytoplasmic protein YbdZ | 1.767316 | 0.112038 |
| **MhpD\_2** | 2-keto-4-pentenoate hydratase | 1.768555 | 0.134856 |
| **DmsB** | Anaerobic dimethyl sulfoxide reductase chain B | 1.77742 | 0.114053 |
| **YiiF** | CopG family transcriptional regulator | 1.779578 | 0.019123 |
| **ClpS** | ATP-dependent Clp protease adapter protein ClpS | 1.78108 | 0.000646 |
| **SdaC\_1** | HAAAP family serine/threonine permease | 1.78321 | 0.037849 |
| **PagP** | Lipid A palmitoyltransferase PagP | 1.784267 | 0.023708 |
| **HelD** | DNA helicase | 1.788999 | 0.065155 |
| **B4U21\_15950** | GMC family oxidoreductase | 1.789104 | 0.016633 |
| **RplE** | 50S ribosomal protein L5 | 1.79099 | 0.001096 |
| **RpsA** | 30S ribosomal protein S1 | 1.794288 | 0.000271 |
| **FccA** | Urocanate reductase | 1.795368 | 0.000021 |
| **MukF** | Chromosome partition protein MukF | 1.79545 | 0.00626 |
| **GpmI** | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 1.796387 | 0.000562 |
| **MoeZ** | tRNA uridine(34) hydroxylase | 1.80165 | 0.000164 |
| **YbfE** | LexA regulated protein | 1.80175 | 0.00035 |
| **MreB** | Cell shape-determining protein MreB | 1.804843 | 0.000906 |
| **UhpA\_2** | DNA-binding response regulator | 1.807836 | 0.016646 |
| **RsmE** | Ribosomal RNA small subunit methyltransferase E | 1.808605 | 0.000558 |
| **RpsG** | 30S ribosomal protein S7 | 1.809661 | 0.000295 |
| **RplP** | 50S ribosomal protein L16 | 1.81066 | 0.000186 |
| **RsmC** | Ribosomal RNA small subunit methyltransferase C | 1.813449 | 0.00042 |
| **RlmN** | Dual-specificity RNA methyltransferase RlmN | 1.813923 | 0.000007 |
| **BepD** | MdtA/MuxA family multidrug efflux RND transporter periplasmic adaptor subunit | 1.816548 | 0.008727 |
| **TolC** | Outer membrane channel protein | 1.81749 | 0.099614 |
| **LipB** | Octanoyltransferase | 1.819705 | 0.00164 |
| **Ipk** | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase | 1.820808 | 0.00039 |
| **YibH\_2** | Auxiliary transport protein, membrane fusion protein (MFP) family | 1.821525 | 0.000674 |
| **BarA** | Histidine kinase | 1.824501 | 0.00891 |
| **RavA** | ATPase RavA | 1.829864 | 0.000852 |
| **YhhW\_1** | Pirin family protein | 1.836376 | 0.046767 |
| **CysD** | Sulfate adenylyltransferase subunit 2 | 1.840102 | 0.329519 |
| **FocA** | Formate channel 1 | 1.840965 | 0.037329 |
| **RplV** | 50S ribosomal protein L22 | 1.841588 | 0.000013 |
| **YqhC** | AraC family transcriptional regulator | 1.843127 | 0.096139 |
| **AroQ** | 3-dehydroquinate dehydratase | 1.849103 | 0.094892 |
| **EpmA** | Elongation factor P--(R)-beta-lysine ligase | 1.85387 | 0.001104 |
| **CoaA** | Pantothenate kinase | 1.854803 | 0.00067 |
| **IscA** | Iron-binding protein IscA | 1.860325 | 0.004048 |
| **MalT** | HTH-type transcriptional regulator MalT | 1.873099 | 0.001727 |
| **SirB1** | Protein SirB1 | 1.880772 | 0.004981 |
| **SuhB\_2** | Inositol monophosphatase | 1.881133 | 0.00276 |
| **AaeA** | p-hydroxybenzoic acid efflux pump subunit AaeA | 1.881504 | 0.020919 |
| **GltC\_2** | LysR family transcriptional regulator | 1.882934 | 0.192832 |
| **MetQ\_3** | Lipoprotein | 1.883622 | 0.005923 |
| **RplK** | 50S ribosomal protein L11 | 1.886262 | 0.000087 |
| **DmlR\_2** | HTH-type transcriptional regulator DmlR | 1.887731 | 0.155839 |
| **NirB** | NirB protein | 1.89094 | 0.000137 |
| **BaeR** | DNA-binding response regulator | 1.891236 | 0.055833 |
| **YdjA** | Putative NAD(P)H nitroreductase | 1.893617 | 0.000255 |
| **RapA** | RNA polymerase-associated protein RapA | 1.904796 | 0.000309 |
| **RimM** | Ribosome maturation factor RimM | 1.915902 | 0.000046 |
| **PdhR** | Pyruvate dehydrogenase complex repressor | 1.917536 | 0.000198 |
| **RpmC** | 50S ribosomal protein L29 | 1.92156 | 0.000061 |
| **NtpA** | Dihydroneopterin triphosphate diphosphatase | 1.923676 | 0.004465 |
| **TrpE** | Anthranilate synthase component 1 | 1.927021 | 0.001262 |
| **MscL** | Large-conductance mechanosensitive channel | 1.928514 | 0.000344 |
| **Gpt** | Xanthine-guanine phosphoribosyltransferase | 1.929255 | 0.00799 |
| **FhuA** | Ferric hydroxamate uptake | 1.931714 | 0.019246 |
| **UgpC** | ABC transporter | 1.935317 | 0.170665 |
| **AceF** | Acetyltransferase component of pyruvate dehydrogenase complex | 1.940297 | 0.000019 |
| **ArtM** | Arginine ABC transporter | 1.943326 | 0.085722 |
| **TusC** | Protein TusC | 1.946889 | 0.013199 |
| **YajD** | Cytoplasmic protein | 1.947354 | 0.022287 |
| **ArgI** | Ornithine carbamoyltransferase | 1.950222 | 0.012825 |
| **RplU** | 50S ribosomal protein L21 | 1.952338 | 0.00002 |
| **GJJ01\_14600** | Alcohol dehydrogenase | 1.962454 | 0.137476 |
| **Rnt** | Ribonuclease T | 1.962753 | 0.006646 |
| **StpA** | DNA-binding protein | 1.969607 | 0.000048 |
| **TtcA** | tRNA-cytidine(32) 2-sulfurtransferase | 1.97273 | 0.000945 |
| **Lgt** | Phosphatidylglycerol--prolipoprotein diacylglyceryl transferase | 1.975106 | 0.012716 |
| **FeoB** | Ferrous iron transport protein B | 1.975771 | 0.000895 |
| **RpsS** | 30S ribosomal protein S19 | 1.983366 | 0.000233 |
| **AzoR\_2** | FMN-dependent NADH-azoreductase | 1.98379 | 0.000285 |
| **RafA** | Alpha-galactosidase | 1.996071 | 0.024234 |
| **MetL** | Bifunctional aspartokinase/homoserine dehydrogenase | 1.997104 | 0.009795 |
| **SstT** | Serine/threonine transporter SstT | 1.997891 | 0.000088 |
| **RlmM** | Ribosomal RNA large subunit methyltransferase M | 2.011849 | 0.001095 |
| **RplW** | 50S ribosomal protein L23 | 2.019854 | 0.000029 |
| **LamB\_3** | Maltoporin | 2.020749 | 0.010949 |
| **AdhE** | Aldehyde-alcohol dehydrogenase | 2.025335 | 0.000004 |
| **EntH** | Proofreading thioesterase EntH | 2.032558 | 0.00234 |
| **PotD** | Putrescine-binding periplasmic protein | 2.03493 | 0.035076 |
| **DnaK\_1** | Chaperone protein DnaK | 2.040341 | 0.000008 |
| **RpsI** | 30S ribosomal protein S9 | 2.041983 | 0.000028 |
| **TatE** | Probable Sec-independent protein translocase protein TatE | 2.043726 | 0.000042 |
| **LpxP** | Lipid A biosynthesis palmitoleoyltransferase | 2.052455 | 0.185622 |
| **DppB\_1** | ABC transporter permease subunit | 2.053847 | 0.221373 |
| **EPB11\_22935** | GNAT family N-acetyltransferase | 2.059089 | 0.000213 |
| **MscS2** | Miniconductance mechanosensitive channel MscM | 2.059251 | 0.000485 |
| **RpiR** | MurR/RpiR family transcriptional regulator | 2.068097 | 0.126222 |
| **Nth** | Endonuclease III | 2.074001 | 0.009065 |
| **HemN\_1** | Heme chaperone HemW | 2.081404 | 0.00926 |
| **ChbF\_1** | 6-phospho-beta-glucosidase | 2.084432 | 0.044229 |
| **PflB** | Formate C-acetyltransferase | 2.093699 | 0.000552 |
| **FabD\_1** | Malonyl CoA-acyl carrier protein transacylase | 2.122309 | 0.053347 |
| **CyoB** | Cytochrome bo(3) ubiquinol oxidase subunit 1 | 2.122529 | 0.000588 |
| **YgiQ** | UPF0313 protein B6R99\_11700 | 2.124835 | 0.008092 |
| **TrxC** | Thioredoxin 2 | 2.134233 | 0.000725 |
| **ArgE** | Acetylornithine deacetylase | 2.135326 | 0.000114 |
| **CedA** | Cell division activator CedA | 2.140627 | 0.01736 |
| **YhbU\_1** | Collagenase-like protease | 2.140923 | 0.002567 |
| **RuvC** | Crossover junction endodeoxyribonuclease RuvC | 2.141019 | 0.043143 |
| **MenC** | o-succinylbenzoate synthase | 2.144194 | 0.000414 |
| **YhjH\_2** | Cyclic diguanylate phosphodiesterase | 2.145659 | 0.220157 |
| **YehS** | DUF1456 domain-containing protein | 2.151399 | 0.001293 |
| **GrcA** | Autonomous glycyl radical cofactor | 2.151728 | 0.000295 |
| **RpsK** | 30S ribosomal protein S11 | 2.173438 | 0.000091 |
| **Tsx** | Nucleoside-specific channel-forming protein Tsx | 2.176457 | 0.006869 |
| **RecJ** | Single-stranded-DNA-specific exonuclease RecJ | 2.177853 | 0.000886 |
| **CbiA** | Cobyrinate a,c-diamide synthase | 2.181772 | 0.00007 |
| **RafR** | HTH-type transcriptional regulator RafR | 2.194736 | 0.00092 |
| **CusR** | Copper response regulator transcription factor CusR | 2.19494 | 0.134761 |
| **GlpR\_2** | DeoR faimly transcriptional regulator | 2.208174 | 0.00096 |
| **CysA\_2** | Sulfate/thiosulfate import ATP-binding protein CysA | 2.209301 | 0.014194 |
| **OadA** | Oxaloacetate decarboxylase | 2.210083 | 0.000006 |
| **BL124\_00024955** | Glycosyltransferase family 9 protein | 2.214218 | 0.036244 |
| **GJJ01\_24875** | Phage tail tape measure protein | 2.216653 | 0.00087 |
| **YfiH\_2** | Laccase domain protein yfiH | 2.217183 | 0.178853 |
| **RnhB** | Ribonuclease HII | 2.235692 | 0.006008 |
| **PheP** | Phenylalanine transporter | 2.251867 | 0.005591 |
| **NirD** | NirD protein | 2.262206 | 0.044901 |
| **FolB** | 7,8-dihydroneopterin aldolase | 2.267619 | 0.000018 |
| **FabZ** | 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | 2.280111 | 0.000019 |
| **MnmC** | tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC | 2.286753 | 0.007178 |
| **DmsA\_2** | Anaerobic dimethyl sulfoxide reductase subunit A | 2.290555 | 0.031336 |
| **EptB** | Kdo(2)-lipid A phosphoethanolamine 7''-transferase | 2.295478 | 0.000504 |
| **MdtK** | Multidrug resistance protein MdtK | 2.296095 | 0.084468 |
| **HigA-2** | Antitoxin HigA-2 | 2.299354 | 0.016721 |
| **MrcB** | Penicillin-binding protein 1B | 2.319527 | 0.000048 |
| **GlrK** | Histidine kinase | 2.326 | 0.026569 |
| **DcuD** | Anaerobic C4-dicarboxylate transporter DcuC | 2.330103 | 0.052435 |
| **YbaB** | Nucleoid-associated protein B4U21\_03855 | 2.330908 | 0.000027 |
| **ComR** | Bacterial regulatory proteins, tetR family | 2.334617 | 0.041113 |
| **HolA** | DNA polymerase III subunit delta | 2.340535 | 0.000107 |
| **CobS** | Adenosylcobinamide-GDP ribazoletransferase | 2.344313 | 0.004373 |
| **C2U49\_27255** | LacI family DNA-binding transcriptional regulator | 2.347021 | 0.176025 |
| **YpjD** | CcsA-like protein | 2.349141 | 0.00297 |
| **TmcA** | GNAT family N-acetyltransferase | 2.354824 | 0.041393 |
| **BetP** | BetT protein | 2.361902 | 0.108794 |
| **Def** | Peptide deformylase | 2.373513 | 0.00035 |
| **RpsQ** | 30S ribosomal protein S17 | 2.395454 | 0.000435 |
| **PotA\_3** | Spermidine/putrescine import ATP-binding protein PotA | 2.400163 | 0.048287 |
| **BdcA** | Oxidoreductase | 2.403073 | 0.000369 |
| **RpsO** | 30S ribosomal protein S15 | 2.424409 | 0.000452 |
| **AccD** | Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta | 2.432996 | 0.000146 |
| **YgdR\_2** | Membrane protein | 2.453397 | 0.225548 |
| **LysP** | Amino acid permease | 2.466425 | 0.000858 |
| **YdgI** | Amino acid permease | 2.530506 | 0.014464 |
| **DD581\_11815** | Elongation factor Tu (Fragment) | 2.532635 | 0.001829 |
| **YfnB** | 2-haloalkanoic acid dehalogenase | 2.550547 | 0.005419 |
| **SoxR** | Redox-sensitive transcriptional activator SoxR | 2.553747 | 0.001327 |
| **PotB** | PotB protein | 2.557444 | 0.000292 |
| **Fiu** | Catecholate siderophore receptor Fiu | 2.572812 | 0.032033 |
| **HexR** | HexR protein | 2.584873 | 0.000539 |
| **Hfq** | RNA-binding protein Hfq | 2.631325 | 0.000398 |
| **B4U21\_17300** | DUF2058 domain-containing protein | 2.633088 | 0.000054 |
| **YncA** | GNAT family N-acetyltransferase | 2.63699 | 0.008669 |
| **B4U21\_16785** | Ion transporter | 2.659725 | 0.079696 |
| **TerB** | Tellurium resistance membrane protein TerB | 2.684546 | 0.004002 |
| **NuoH** | NADH-quinone oxidoreductase subunit H | 2.686746 | 0.001706 |
| **NuoM** | NADH dehydrogenase I subunit M | 2.698228 | 0.000095 |
| **HcaT** | 3-phenylpropionate MFS transporter | 2.713763 | 0.079902 |
| **UbiC** | Chorismate pyruvate-lyase | 2.724322 | 0.000129 |
| **BL124\_00021250** | TonB-dependent receptor | 2.737865 | 0.043848 |
| **ExuR** | ExuR protein | 2.747183 | 0.013122 |
| **ArsC** | Arsenate reductase | 2.754157 | 0.000916 |
| **YfcB** | 50S ribosomal protein L3 glutamine methyltransferase | 2.874821 | 0.000505 |
| **NupX** | Nucleoside permease | 2.881831 | 0.001904 |
| **FhuB** | Fe(3+)-hydroxamate ABC transporter permease FhuB | 2.893739 | 0.009383 |
| **YifK** | Amino acid permease | 2.906191 | 0.000305 |
| **YhhV** | Antitoxin | 2.967039 | 0.003195 |
| **Fis** | DNA-binding protein Fis | 2.968407 | 0.002502 |
| **YhbU\_3** | Ubiquinone biosynthesis protein UbiU | 2.968866 | 0.002548 |
| **YdhC** | Bcr/CflA family efflux transporter | 2.98384 | 0.102256 |
| **IscR** | HTH-type transcriptional regulator IscR | 3.004428 | 0.000048 |
| **MetE** | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase | 3.01663 | 0.012974 |
| **BL124\_00033400** | UPF0149 protein BL124\_00033400 | 3.027268 | 0.007692 |
| **WbaP** | UDP-Gal::undecaprenolphosphate Gal-1-P transferase | 3.03881 | 0.000118 |
| **NarK** | Nitrate/nitrite transporter | 3.081599 | 0.000368 |
| **LsrR** | LsrR, transcriptional repressor of lsr operon | 3.096841 | 0.002512 |
| **RfaH** | Transcription antitermination protein RfaH | 3.13163 | 0.006507 |
| **RbsC** | RbsC protein | 3.178122 | 0.001382 |
| **NemA** | N-ethylmaleimide reductase | 3.193323 | 0.000089 |
| **IsiB** | Flavodoxin | 3.214876 | 0.01251 |
| **Fim\_1** | Fimbrial protein | 3.240534 | 0.004359 |
| **GlpC** | Anaerobic glycerol-3-phosphate dehydrogenase subunit C | 3.247958 | 0.000432 |
| **DeaD** | ATP-dependent RNA helicase DeaD | 3.266184 | 0.00001 |
| **HscB** | Co-chaperone protein HscB | 3.278164 | 0.001092 |
| **YncE\_2** | Antigen Lp49 | 3.320257 | 0.001028 |
| **MenA** | 1,4-dihydroxy-2-naphthoate octaprenyltransferase | 3.337725 | 0.000074 |
| **RbsR** | Ribose operon transcriptional repressor RbsR | 3.339158 | 0.000405 |
| **BANRA\_03067** | Amine oxidase, flavin-containing | 3.339239 | 0.066788 |
| **GJJ01\_00155** | Acetyltransferase YafP | 3.374015 | 0.074881 |
| **Kup** | Low affinity potassium transport system protein kup | 3.428788 | 0.000123 |
| **TcyL** | Cystine ABC transporter | 3.546004 | 0.001191 |
| **Wza** | Integral outer membrane lipoprotein | 3.561825 | 0.092533 |
| **NudC** | NAD-capped RNA hydrolase NudC | 3.569819 | 0.169116 |
| **UbiJ** | Ubiquinone biosynthesis accessory factor UbiJ | 3.611191 | 0.000236 |
| **YhjX** | Inner membrane protein yhjX | 3.626972 | 0.039617 |
| **BVX91\_07400** | Glycosyltransferase | 3.64601 | 0.114922 |
| **BrnQ** | Branched-chain amino acid transport system carrier protein | 3.686054 | 0.001326 |
| **RecN** | DNA repair protein RecN | 3.695094 | 0.00008 |
| **IlvB** | Acetolactate synthase | 3.81049 | 0.002032 |
| **DtpT** | Di-/tripeptide transporter | 3.873392 | 0.00004 |
| **AccB** | Biotin carboxyl carrier protein of acetyl-CoA carboxylase | 4.011628 | 0.000001 |
| **RecQ** | DNA helicase | 4.016875 | 0.000489 |
| **RcsA** | Transcriptional regulatory protein RcsA | 4.172624 | 0.002099 |
| **PriA** | Primosomal protein N' | 4.194054 | 0.003564 |
| **YaeE** | D-methionine ABC transporter permease MetI | 4.338075 | 0.000032 |
| **Hha** | Hemolysin expression modulating protein | 4.51068 | 0.016135 |
| **MenD** | 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase | 4.880206 | 0.000359 |
| **XynB\_2** | Beta-xylosidase | 4.880335 | 0.000385 |
| **PlaP** | APC family permease | 4.992996 | 0.000231 |
| **LptB\_3** | ABC transporter ATP-binding protein | 5.02985 | 0.002172 |
| **MalP\_2** | Alpha-1,4 glucan phosphorylase | 5.062167 | 0.001254 |
| **DnaE** | DNA polymerase III subunit alpha | 5.155331 | 0.000613 |
| **GlpB** | Anaerobic glycerol-3-phosphate dehydrogenase subunit B | 5.210341 | 0.001593 |
| **BtuF** | Vitamin B12-binding protein | 5.350788 | 0.000078 |
| **YahK** | Alcohol dehydrogenase catalytic domain-containing protein | 5.554869 | 0.002519 |
| **Fsa** | Fructose-6-phosphate aldolase | 5.782794 | 0.000532 |
| **CadB** | Arginine/agmatine antiporter | 5.991591 | 0.003256 |
| **YbbM** | ABC-type uncharacterized transport system, permease component | 6.000384 | 0.000427 |
| **ZnuC** | Zinc import ATP-binding protein ZnuC | 6.058259 | 0.032729 |
| **C4Y50\_024620** | Cobalamin biosynthesis protein CobW | 6.2951 | 0.036742 |
| **CsdE** | Cysteine desulfurase sulfur acceptor subunit CsdE | 6.756937 | 0.001824 |
| **MoaD** | MoaD protein | 6.87882 | 0.000197 |
| **YneE** | Ibestrophin | 6.958729 | 0.000014 |
| **YaeJ** | Aminoacyl-tRNA hydrolase | 6.988485 | 0.000529 |
| **MsbA\_1** | Cysteine/glutathione ABC transporter ATP-binding protein/permease CydC | 7.049462 | 0.00007 |
| **DusB** | tRNA-dihydrouridine synthase B | 7.173647 | 0.000535 |
| **Tam** | Trans-aconitate 2-methyltransferase | 7.525914 | 0.000184 |
| **GarR\_1** | 2-hydroxy-3-oxopropionate reductase | 8.224097 | 0.000041 |
| **YhbT** | Ubiquinone biosynthesis accessory factor UbiT | 9.443405 | 0.00019 |
| **YejM** | Inner membrane protein YejM | 9.547558 | 0.000043 |
| **DinG\_1** | ATP-dependent helicase | 9.985891 | 0.000444 |
| **YgfY** | FAD assembly factor SdhE | 10.655565 | 0.000011 |
| **SecE** | Protein translocase subunit SecE | 11.556173 | 0.000652 |
| **YbeD** | UPF0250 protein B4U21\_05195 | 11.970744 | 0.000095 |
| **FrmA\_1** | S-(hydroxymethyl)glutathione dehydrogenase | 12.041462 | 0 |
| **B4U21\_17310** | Cold-shock' DNA-binding domain | 13.584165 | 0.000129 |
| **YijO** | Helix-turn-helix domain-containing protein | 14.891831 | 0.000485 |
| **RpmI** | 50S ribosomal protein L35 | 211.055101 | 0.000001 |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Origin** | **Add Na+** | **Add HPO3¯** | **Lose HPO3¯** | **Add 1 Ara4N and lose HPO3¯** | **Add 1 Ara4N** | **Add 1 Ara4N and add Na+** | **Add 2 Ara4N** | **Add 2 Ara4N and add Na+** | **Add 1 pEtN** | **Add 1 pEtN and lose HPO3¯** |
| **1797 (P1)** | ND | ND | 1717 | 1848 | 1928 | ND | 2059 | ND | ND | ND |
| **1825 (P2)** | 1847 | ND | 1745 | 1876 | 1956 | 1978 | 2087 | 2109 | 1947 | 1867 |
| **1841 (P3)** | ND | 1921 | 1761 | 1892 | ND | ND | 2103 | ND | ND | ND |

**Supplementary Table 6.** Lipid A modifications presented in this study (*m/z*).

**ND,** Not detected

**Supplementary Table 7.** Chemical structures of lipid A presented in this study.

|  |  |
| --- | --- |
| ***m/z*** | **structure** |
| **1717** |  |
| **1797** |  |
| **1848** |  |
| **1928** |  |
| **2059** |  |
| **1745** |  |
| **1825** |  |
| **1847** | Na+ |
| **1876** |  |
| **1956** |  |
| **1978** | Na+ |
| **2087** |  |
| **2109** | Na+ |
| **1947** | or |
| **1867** | or |
| **1841** |  |
| **1921** | or |
| **1761** |  |
| **1892** |  |
| **2103** |  |