**Supplementary Table 1 –** *Mo*-CBP3-PepI group unique proteinsidentified by ESI-LC-MS/MS

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Protein Name** | **ID Uniprot** | | | **Organism Reference** | | | **Cellular Compartment** | | |
| **Carbohydrate metabolism** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| 3-dehydro-D-guloside 4-epimerase | P76044 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| D-xylonate dehydratase YjhG | P39358 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Apulose kinase | Q6D5T8 | | | *Pectobacterium atrosepticum* (strain SCRI 1043 / ATCC BAA-672) | | | Cytoplasm | | |
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| ***Lipid metabolism*** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| 7alpha-hydroxysteroid dehydrogenase | P0AET8 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta | P0A9Q5 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Fatty acid oxidation complex subunit alpha | P21177 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| 3-ketoacyl-CoA thiolase | Q48GW4 | | | *Pseudomonas savastanoi pv. phaseolicola* (strain 1448A / Race 6) | | | Cytoplasm | | |
| Lipid-A-disaccharide synthase | B7V7U5 | | | *Pseudomonas aeruginosa* (strain LESB58) | | | Cytoplasm | | |
| Glycerol-3-phosphate acyltransferase | Q1GYU3 | | | *Methylobacillus flagellatus* (strain KT / ATCC 51484 / DSM 6875) | | | Plasma membrane | | |
| 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | B9DY11 | | | *Clostridium kluyveri* (strain NBRC 12016) | | | Cytoplasm | | |
| 4-hydroxy-2-oxovalerate aldolase 1 | Q47G67 | | | *Dechloromonas aromatica* (strain RCB) | | | Cytoplasm | | |
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| ***Cell Redox Homeostasis*** |  | | |  | | |  | | |
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| Hydroxylamine reductase | P75825 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Periplasmic serine endoprotease DegP | P0C0V0 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Protein-methionine-sulfoxide reductase catalytic subunit MsrP | P76342 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Catalase-peroxidase | Q1GCU3 | | | *Ruegeria sp.* (strain TM1040) | | | Cytoplasm | | |
| ***Stress and Defense Response*** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| Probable L,D-transpeptidase YcbB | P22525 | | | *Escherichia coli (strain K12)* | | | Plasma membrane | | |
| Zinc resistance-associated protein | P0AAA9 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Chaperone protein HtpG | P0A6Z3 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Co-chaperonin GroES | B5F2K9 | | | *Salmonella agona (strain SL483)* | | | Cytoplasm | | |
| ATP-dependent Clp protease ATP-binding subunit ClpX | Q2RU44 | | | *Rhodospirillum rubrum* (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIMB 8255 / S1) | | | Cytoplasm | | |
| Chaperone protein DnaJ | Q5FGQ8 | | | *Ehrlichia ruminantium* (strain Gardel) | | | Cytoplasm | | |
| ***Energy and Metabolism*** |  | | |  | | |  | | |
| Multiphosphoryl transfer protein 1 | P77439 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnG | P16685 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| 1-deoxy-D-xylulose 5-phosphate reductoisomerase | P45568 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Aspartate ammonia-lyase | Q8XDS0 | | | *Escherichia coli* O157:H7 | | | Cytoplasm | | |
| Trehalose synthase | Q1ARU5 | | | *Rubrobacter xylanophilus* (strain DSM 9941 / NBRC 16129 / PRD-1) | | | Cytoplasm | | |
| Cytochrome bc1 complex Rieske iron-sulfur subunit | Q9X807 | | | *Streptomyces coelicolor* (strain ATCC BAA-471 / A3(2) / M145) | | | Plasma membrane | | |
| Fructose-1,6-bisphosphatase class 1 2 | B2JVN8 | | | *Paraburkholderia phymatum* (strain DSM 17167 / CIP 108236 / LMG 21445 / STM815) | | | Cytoplasm | | |
| 1,4-alpha-glucan branching enzyme GlgB | A7FNX5 | | | *Yersinia pseudotuberculosis serotype O:1b* (strain IP 31758) | | | Cytoplasm | | |
| ATP synthase subunit a | Q4FPE9 | | | *Pelagibacter ubique* (strain HTCC1062) | | | Plasma membrane | | |
| Glycogen synthase | B1I4F5 | | | *Desulforudis audaxviator* (strain MP104C) | | | Cytoplasm | | |
| Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex | P09062 | | | *Pseudomonas putida* | | | Cytoplasm | | |
| Dihydroorotate dehydrogenase (quinone) | A5CS38 | | | *Clavibacter michiganensis subsp. michiganensis* (strain NCPPB 382) | | | Plasma membrane | | |
| Enolase | Q98Q50 | | | *Mycoplasmopsis pulmonis* (strain UAB CTIP) | | | Extracellular | | |
|  |  | | |  | | |  | | |
| NAD kinase | Q39JD3 | | | *Burkholderia lata* (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) | | | Cytoplasm | | |
| ***DNA metabolism*** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| UvrABC system protein B | P0A8F8 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| DNA-3-methyladenine glycosylase 2 | P04395 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| UvrABC system protein A | P0A698 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Probable endonuclease 4 | P75457 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| UvrABC system protein C | Q5P080 | | | *Aromatoleum aromaticum* (strain EbN1) | | | Cytoplasm | | |
| DNA recombination protein RmuC | P0AG71 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| Prophage integrase IntA | P32053 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| Holliday junction ATP-dependent DNA helicase RuvA | P75243 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Tyrosine recombinase XerD | Q88MV0 | | | *Pseudomonas putida* (strain ATCC 47054 / DSM 6125 / CFBP 8728 / NCIMB 11950 / KT2440) | | | Cytoplasm | | |
| ***Cell wall organization and structural maintenance*** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| Soluble lytic murein transglycosylase | P0AGC3 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| D-alanyl-D-alanine carboxypeptidase DacB | P24228 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Cell shape-determining protein MreB | P0A9X4 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Probable L,D-transpeptidase ErfK/SrfK | P39176 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Cell shape-determining protein MreC | P16926 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Membrane-bound lytic murein transglycosylase A | P0A935 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Murein tetrapeptide carboxypeptidase | | | P76008 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Murein DD-endopeptidase MepH | | | P76190 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Bifunctional protein GlmU | | | Q0BSR5 | | | *Granulibacter bethesdensis* (strain ATCC BAA-1260 / CGDNIH1) | | | Cytoplasm | | |
| Sensor protein LytS | | | Q5HLG3 | | | *Staphylococcus epidermidis* (strain ATCC 35984 / RP62A) | | | Plasma membrane | | |
| UDP-N-acetylglucosamine 1-carboxyvinyltransferase | | | A8GW63 | | | *Rickettsia bellii (strain OSU 85-389)* | | | Cytoplasm | | |
| Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase | | | Q9X1N5 | | | *Thermotoga maritima* (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) | | | Plasma membrane | | |
| D-alanine--D-alanine ligase | | | Q3IFY2 | | | *Pseudoalteromonas translucida* (strain TAC 125) | | | Cytoplasm | | |
| Inner membrane protein YdcZ | | | P76111 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Flagellar basal-body rod protein FlgG | | | P24500 | | | *Bacillus subtilis* (strain 168) | | | Unknown | | |
| Flagellin | | | Q06968 | | | *Salmonella berta* | | | Extracellular | | |
| Cell division protein FtsZ | | | P0A9A6 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Probable septum site-determining protein MinC | | | Q63RS4 | | | *Burkholderia pseudomallei* (strain K96243) | | | Cytoplasm | | |
| Cytadherence high molecular weight protein 3 | | | Q50360 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | cytoplasm | | |
|  | | |  | | |  | | |  | | |
| ***Protein Biosynthesis and Metabolism*** | | |  | | |  | | |  | | |
|  | | |  | | |  | | |  | | |
| 50S ribosomal protein L3 | | | P60438 | | | *Escherichia coli* (strain K12) | | | Ribosome | | |
| 30S ribosomal protein S17 | | | P0AG63 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| 50S ribosomal protein L4 | | | P75579 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Ribosome | | |
| 30S ribosomal protein S2 | | | A1TN69 | | | *Acidovorax citrulli* (strain AAC00-1) | | | Cytoplasm | | |
| 50S ribosomal protein L14 | | | A9BH95 | | | *Petrotoga mobilis* (strain DSM 10674 / SJ95) | | | Ribosome | | |
| 30S ribosomal protein S11 | | | A3N380 | | | *Actinobacillus pleuropneumoniae serotype 5b* (strain L20) | | | Ribosome | | |
| 30S ribosomal protein S5 | | | Q5P315 | | | *Aromatoleum aromaticum* (strain EbN1) | | | Small ribosomal unit | | |
| 30S ribosomal protein S6 | | | Q3JEJ6 | | | *Nitrosococcus oceani* (strain ATCC 19707 / BCRC 17464 / JCM 30415 / NCIMB 11848 / C-107) | | | Ribosome | | |
| 30S ribosomal protein S3 | | | Q8R7W0 | | | *Caldanaerobacter subterraneus subsp. tengcongensis* (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) | | | Ribosome | | |
| 50S ribosomal protein L28 | | | Q5PAC9 | | | *Anaplasma marginale* (strain St. Maries) | | | Ribosome | | |
| 50S ribosomal protein L24 | | | A9KJI3 | | | *Lachnoclostridium phytofermentans* (strain ATCC 700394 / DSM 18823 / ISDg) | | | Ribosome | | |
| Chromophore lyase CpcS/CpeS 2 | | | Q10XT3 | | | *Trichodesmium erythraeum* (strain IMS101) | | | Cytoplasm | | |
| Aspartate aminotransferase | | | P00509 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| D-amino acid dehydrogenase | | | P0A6J5 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Bifunctional protein TrpGD | | | P00904 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Elongation factor P--(R)-beta-lysine ligase | | | B7LC16 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| 4-aminobutyrate aminotransferase PuuE | | | P50457 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Acetolactate synthase isozyme 1 large subunit | | | P08142 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Cystathionine gamma-synthase | | | P00935 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Glutamate synthase [NADPH] large chain | | | P09831 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Glutamate decarboxylase beta | | | P69910 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Ornithine carbamoyltransferase | | | A7ZVD3 | | | *Escherichia coli* O157:H7 | | | Cytoplasm | | |
| Aspartate aminotransferase | | | Q56114 | | | *Salmonella typhi* | | | Cytoplasm | | |
| GMP synthase [glutamine-hydrolyzing] | | | A3MZV8 | | | *Actinobacillus pleuropneumoniae serotype 5b* (strain L20) | | | Cytoplasm | | |
| Chorismate synthase | | | Q1QQ46 | | | *Nitrobacter hamburgensis* (strain DSM 10229 / NCIMB 13809 / X14) | | | Cytoplasm | | |
| 3-dehydroquinate dehydratase | | | B4RCS3 | | | *Phenylobacterium zucineum* (strain HLK1) | | | Cytoplasm | | |
| Diaminopimelate epimerase | | | A1SAP5 | | | *Shewanella amazonensis* (strain ATCC BAA-1098 / SB2B) | | | Cytoplasm | | |
| Arginine biosynthesis bifunctional protein ArgJ | | | Q81M96 | | | *Bacillus anthracis* | | | Cytoplasm | | |
| 4-hydroxy-tetrahydrodipicolinate reductase | | | A9HE99 | | | *Gluconacetobacter diazotrophicus* (strain ATCC 49037 / DSM 5601 / CCUG 37298 / CIP 103539 / LMG 7603 / PAl5) | | | Cytoplasm | | |
| Tryptophan synthase beta chain | | | Q13EQ2 | | | *Rhodopseudomonas palustris* (strain BisB5) | | | Cytoplasm | | |
| Acetolactate synthase large subunit IlvB1 | | | P9WG41 | | | *Mycobacterium tuberculosis* (strain ATCC 25618 / H37Rv) | | | Cytoplasm | | |
| Glycine--tRNA ligase beta subunit | | | A4J7C9 | | | *Desulfotomaculum reducens* (strain MI-1) | | | Cytoplasm | | |
| o-succinylbenzoate synthase | | | Q838J7 | | | *Enterococcus faecalis* (strain ATCC 700802 / V583) | | | Cytoplasm | | |
| Ketol-acid reductoisomerase (NADP(+)) | | | Q17X66 | | | *Helicobacter acinonychis* (strain Sheeba) | | | Cytoplasm | | |
| Glycine cleavage system H protein | | | A3QHI1 | | | *Shewanella loihica* (strain ATCC BAA-1088 / PV-4) | | | Cytoplasm | | |
| Cysteine synthase A | | | P0ABK6 | | | *Escherichia coli* O157:H7 | | | Cytoplasm | | |
| Diaminopimelate decarboxylase | | | Q8K9C4 | | | *Buchnera aphidicola subsp. Schizaphis graminum* (strain Sg) | | | Cytoplasm | | |
| 3-phosphoshikimate 1-carboxyvinyltransferase | | | B2U886 | | | *Ralstonia pickettii* (strain 12J) | | | Cytoplasm | | |
| Histidinol-phosphate aminotransferase | | | B9KDN6 | | | *Campylobacter lari* (strain RM2100 / D67 / ATCC BAA-1060) | | | Cytoplasm | | |
| Pyridoxal 5'-phosphate synthase subunit PdxT | | | Q9KGN5 | | | *Alkalihalobacillus halodurans* (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) | | | Cytoplasm | | |
| Kynurenine formamidase | | | Q2T0N2 | | | *Burkholderia thailandensis* (strain ATCC 700388 / DSM 13276 / CIP 106301 / E264) | | | Cytoplasm | | |
| Cytosol non-specific dipeptidase | | | P15288 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Dipeptidyl carboxypeptidase | | | P24171 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| ATP-dependent Clp protease proteolytic subunit | | | Q928C4 | | | *Listeria innocua serovar 6a* (strain ATCC BAA-680 / CLIP 11262) | | | Cytoplasm | | |
| Protease HtpX homolog | | | B4S7I8 | | | *rosthecochloris aestuarii* (strain DSM 271 / SK 413) | | | Plasma membrane | | |
| Carbamoyl dehydratase HypE | | | P24193 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
|  | | |  | | |  | | |  | | |
| Cysteine--tRNA ligase | | | P75423 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Leucine--tRNA ligase | | | P75398 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Serine--tRNA ligase | | | P75107 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Valine--tRNA ligase | | | P75304 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Glutamyl-tRNA(Gln) amidotransferase subunit A | | | P75534 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Phenylalanine--tRNA ligase alpha subunit | | | Q5GTJ5 | | | *Wolbachia sp. subsp. Brugia malayi* (strain TRS) | | | Cytoplasm | | |
| Valine--tRNA ligase | | | P36420 | | | *Lactobacillus casei* | | | Cytoplasm | | |
| Proline--tRNA ligase | | | B8CW65 | | | *Halothermothrix orenii* (strainH 168 / OCM 544 / DSM 9562*)* | | | Cytoplasm | | |
| Alanine--tRNA ligase | | | Q03YQ2 | | | *Leuconostoc mesenteroides subsp. mesenteroides* (strain ATCC 8293 / DSM 20343 / BCRC 11652 / CCM 1803 / JCM 6124 / NCDO 523 / NBRC 100496 / NCIMB 8023 / NCTC 12954 / NRRL B-1118 / 37Y) | | | Cytoplasm | | |
| Threonine--tRNA ligase | | | B0TT20 | | | *Shewanella halifaxensis* (strain HAW-EB4) | | | Cytoplasm | | |
| Peptide chain release factor 1 | | | B8HB03 | | | *Pseudarthrobacter chlorophenolicus* (strain ATCC 700700 / DSM 12829 / CIP 107037 / JCM 12360 / KCTC 9906 / NCIMB 13794 / A6) | | | Cytoplasm | | |
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| ***Regulation Factor and RNA Processing*** | | |  | | |  | | |  | | |
|  | | |  | | |  | | |  | | |
| Multifunctional CCA protein | | | P06961 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Ribosomal RNA small subunit methyltransferase D | | | P0ADX9 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Ribonuclease 3 | | P0A7Y0 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| tRNA threonylcarbamoyladenosine dehydratase | | Q46927 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase | | P0AEI1 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative pre-16S rRNA nuclease | | P57114 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Ribonuclease Y | | P75506 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| tRNA-specific 2-thiouridylase MnmA | | A7I2L9 | | | *Campylobacter hominis* (strain ATCC BAA-381 / LMG 19568 / NCTC 13146 / CH001A) | | | Cytoplasm | | |
| Ribosomal RNA small subunit methyltransferase A | | A4YJT3 | | | *Bradyrhizobium sp.* (strain BTAi1 / ATCC BAA-1182) | | | Cytoplasm | | |
| Ribosomal protein S12 methylthiotransferase RimO | | Q7VKK2 | | | *Haemophilus ducreyi* (strain 35000HP / ATCC 700724) | | | Cytoplasm | | |
| Probable RNA 2'-phosphotransferase | | Q395F2 | | | *Burkholderia lata* (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) | | | Cytoplasm | | |
| tRNA uridine (34) hydroxylase | | Q7UFS5 | | | *Rhodopirellula baltica* (strain DSM 10527 / NCIMB 13988 / SH1) | | | Cytoplasm | | |
| tRNA modification GTPase MnmE | | A5VA82 | | | *Rhizorhabdus wittichii* (strain DSM 6014 / CCUG 31198 / JCM 15750 / NBRC 105917 / EY 4224 / RW1) | | | Cytoplasm | | |
| Elongation factor Ts | | A8MHH0 | | | *Alkaliphilus oremlandii* (strain OhILAs) | | | Cytoplasm | | |
| Ribosomal RNA large subunit methyltransferase H | | Q2NUV2 | | | *Sodalis glossinidius* (strain morsitans) | | | Cytoplasm | | |
| Ribonuclease Z | | A6LU82 | | | *Clostridium beijerinckii* (strain ATCC 51743 / NCIMB 8052) | | | Cytoplasm | | |
| Elongation factor Tu | | A7HBL7 | | | *Anaeromyxobacter sp.* (strain Fw109-5) | | | Cytoplasm | | |
| GTPase Der | | A1SU43 | | | *Psychromonas ingrahamii* (strain 37) | | | Cytoplasm | | |
| Elongation factor G 2 | | Q3IJW9 | | | *Pseudoalteromonas translucida* (strain TAC 125) | | | Cytoplasm | | |
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| ***Regulation of transcription*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Uxu operon transcriptional regulator | | P39161 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| HTH-type transcriptional regulator ZntR | | P0ACS5 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Psp operon transcriptional activator | | P37344 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Propionate catabolism operon regulatory protein | | P77743 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Sugar fermentation stimulation protein B | | P0ACH1 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| DNA polymerase I | | P00582 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| OriC-binding nucleoid-associated protein | | P64467 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| DNA-directed RNA polymerase subunit alpha | | Q50295 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Biofilm growth-associated repressor | | Q8UAA8 | | | *Agrobacterium fabrum* (strain C58 / ATCC 33970) | | | Cytoplasm | | |
| Transcriptional regulatory protein PrrA | | Q50136 | | | *Mycobacterium leprae* (strain TN) | | | Cytoplasm | | |
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| ***DNA replication*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Beta sliding clamp | | P0A988 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Anaerobic ribonucleoside-triphosphate reductase | | P28903 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Ribonucleoside-diphosphate reductase subunit alpha | | P78027 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| LexA repressor | | O33927 | | | *Thermotoga maritima* (strain ATCC 43589 / DSM 3109 / JCM 10099 / NBRC 100826 / MSB8) | | | Cytoplasm | | |
| Flap endonuclease Xni | | A1S8B8 | | | *Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)* | | | Cytoplasm | | |
| Chromosomal replication initiator protein DnaA | | Q1MSG8 | | | *Lawsonia intracellularis* (strain PHE/MN1-00) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Cell signaling*** | |  | | |  | | |  | | |
| Signal recognition particle protein | | P0AGD7 | | | *Escherichia coli* (strain K12) | | | Ribosome | | |
| Bacteriophage adsorption protein A | | P31600 | | | *Escherichia coli* (strain K12) | | | Cell outer membrane | | |
| Sensor protein EvgS | | P30855 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Sensor histidine kinase EnvZ | | P0AEJ4 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
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| ***Ion assimilation*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Ferric iron reductase protein FhuF | | P39405 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Periplasmic nitrate reductase | | P33937 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Anaerobic nitric oxide reductase flavorubredoxin | | A0KEJ1 | | | *Aeromonas hydrophila subsp. hydrophila* (strain ATCC 7966 / DSM 30187 / BCRC 13018 / CCUG 14551 / JCM 1027 / KCTC 2358 / NCIMB 9240 / NCTC 8049) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| ***Transferase*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| 3-oxoadipyl-CoA/3-oxo-5,6-dehydrosuberyl-CoA thiolase | | P0C7L2 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Trehalose-6-phosphate synthase | | P31677 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Propionyl-CoA:succinate CoA transferase | | P52043 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative phosphotransferase enzyme IIB component MPN\_268 | | P75507 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Ubiquinone biosynthesis O-methyltransferase | | A8LQ43 | | | *Dinoroseobacter shibae* (strain DSM 16493 / NCIMB 14021 / DFL 12) | | | Cytoplasm | | |
| tRNA-cytidine (32) 2-sulfurtransferase | | A4G9W3 | | | *Herminiimonas arsenicoxydans* | | | Cytoplasm | | |
| Probable transaldolase | | A5GBY8 | | | *Geotalea uraniireducens* (strain Rf4) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Nucleotide metabolism*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Nucleoside diphosphate kinase | | A8AD67 | | | *Citrobacter koseri* (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) | | | Cytoplasm | | |
| Probable dihydroorotate dehydrogenase A (fumarate) | | P59626 | | | *Enterococcus faecalis* (strain ATCC 700802 / V583) | | | Cytoplasm | | |
| Uridine phosphorylase | | O08444 | | | *Klebsiella aerogenes* | | | Cytoplasm | | |
| Thymidylate kinase | | C4KZW9 | | | *Exiguobacterium sp.* (strain ATCC BAA-1283 / AT1b) | | | Cytoplasm | | |
| Thymidylate synthase | | A7MXJ9 | | | *Vibrio campbellii* (strain ATCC BAA-1116 / BB120) | | | Cytoplasm | | |
| Adenosine deaminase | | P22333 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Allantoinase | | Q9RV76 | | | *Deinococcus radiodurans* (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) | | | Cytoplasm | | |
| Putative carbamate hydrolase RutD | | Q32HQ2 | | | *Shigella dysenteriae serotype 1* (strain Sd197) | | | Unknown | | |
| Dihydroorotate dehydrogenase B (NAD(+)) | | Q8EUY2 | | | *Mycoplasma penetrans* (strain HF-2) | | | Cytoplasm | | |
| Probable glycine dehydrogenase (decarboxylating) subunit 1 | | B5Y9D4 | | | *Coprothermobacter proteolyticus* (strain ATCC 35245 / DSM 5265 / OCM 4 / BT) | | | Cytoplasm | | |
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| ***Transmembrane transporters*** | |  | | |  | | |  | | |
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| Protein TonB | | P02929 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Sodium/pantothenate symporter | | P16256 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Proline-specific permease ProY | | P0AAE2 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| D-allose import ATP-binding protein AlsA | | P32721 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Glutamate/aspartate import ATP-binding protein GltL | | P0AAG3 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| L-cystine-binding protein TcyJ | | P0AEM9 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Inner membrane metabolite transport protein YdjE | | P38055 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Outer membrane porin C | | P06996 | | | *Escherichia coli* (strain K12) | | | Cell outer membrane | | |
| Miniconductance mechanosensitive channel YbdG | | P0AAT4 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Polyamine export protein | | P0AE45 | | | *Escherichia coli* (strain K12) | | | Cell outer membrane | | |
| Putative nucleoside permease NupX | | P33021 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| AI-2 transport protein TqsA | | P0AFS5 | | | *Escherichia coli* (strain K12) | | | Cell inner membrane | | |
| Multiphosphoryl transfer protein | | P32670 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Flagellar biosynthetic protein FlhB | | P76299 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| p-hydroxybenzoic acid efflux pump subunit AaeA | | P46481 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Nitrate/nitrite transporter NarU | | P37758 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Phosphate import ATP-binding protein PstB | | P75186 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Methionine import ATP-binding protein MetN | | Q8RFN2 | | | *Fusobacterium nucleatum subsp. nucleatum* (strain ATCC 25586 / DSM 15643 / BCRC 10681 / CIP 101130 / JCM 8532 / KCTC 2640 / LMG 13131 / VPI 4355) | | | Plasma membrane | | |
| Probable TonB-dependent receptor NMB0964 | | Q9JZN9 | | | *Neisseria meningitidis serogroup B* (strain MC58) | | | Plasma membrane | | |
| Probable membrane transporter protein YdhB | | O05493 | | | *Bacillus subtilis* (strain 168) | | | Plasma membrane | | |
| Putative multidrug export ATP-binding/permease protein SA1683 | | Q7A4T3 | | | *Staphylococcus aureus* (strain N315) | | | Plasma membrane | | |
| Protein translocase subunit SecA | | Q9K6W8 | | | *Alkalihalobacillus halodurans* (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) | | | Cytoplasm | | |
| C4-dicarboxylate-binding periplasmic protein DctP | | Q9HU18 | | | *Pseudomonas aeruginosa* (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) | | | Periplasmic space | | |
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| ***Isoprene biosynthesis*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) | | Q6G104 | | | *Bartonella quintana* (strain Toulouse) | | | Cytoplasm | | |
| Bifunctional enzyme IspD/IspF | | A5V2U9 | | | *Rhizorhabdus wittichii* (strain DSM 6014 / CCUG 31198 / JCM 15750 / NBRC 105917 / EY 4224 / RW1) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Light dependent process*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Light-independent protochlorophyllide reductase subunit B | | Q132N3 | | | *Rhodopseudomonas palustris* (strain BisB5) | | | Cytoplasm | | |
| Protein Thf1 | | Q8YZ41 | | | *Nostoc sp.* (strain PCC 7120 / SAG 25.82 / UTEX 2576) | | | Cytoplasm | | |
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| ***Pathogenesis*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Cytolysin RtxA | | A1YKW7 | | | *Kingella kingae* | | | Extracellular | | |
| Putative colanic acid biosynthesis glycosyl transferase WcaI | | P32057 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Lipopolysaccharide 1,2-N-acetylglucosaminetransferase | | P27242 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Unknown*** | |  | | |  | | |  | | |
| Oxidoreductase UcpA | | P37440 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative inactive recombination-promoting nuclease-like protein YjiQ | | P0DP22 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Lipoprotein YfjS | | O52982 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Protein YhfA | | P0ADX1 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Hydrogenase-4 component I | | P77668 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Probable ATP-dependent helicase lhr | | P30015 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Hydrogenase-4 component J | | P77453 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Insertion element IS150 protein InsJ | | P19768 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Protein YrdA | | P0A9W9 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Probable cyclic di-GMP phosphodiesterase PdeI | | P75800 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Probable ATP-dependent RNA helicase MG425 homolog | | P75172 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Putative adhesin P1-like protein MPN\_370 | | P75411 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Extracellular | | |
| UPF0134 protein MPN\_675 | | P75117 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Unknown | | |
| Translation initiation factor IF-2 | | C5CDZ4 | | | *Kosmotoga olearia* (strain ATCC BAA-1733 / DSM 21960 / TBF 19.5.1) | | | Cytoplasm | | |
| NAD(P)H dehydrogenase (quinone) | | B9M9X5 | | | *Acidovorax ebreus* (strain TPSY) | | | Unknown | | |
| General stress protein 26 | | P80238 | | | *Bacillus subtilis* (strain 168) | | | Unknown | | |
| 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase | | P73191 | | | *Synechocystis sp.* (strain PCC 6803 / Kazusa) | | | Cytoplasm | | |
| UPF0102 protein Sama\_3355 | | A1SB01 | | | *Shewanella amazonensis* (strain ATCC BAA-1098 / SB2B) | | | Cytoplasm | | |
| Oligoribonuclease | | Q2L2P5 | | | *Bordetella avium* (strain 197N) | | | Cytoplasm | | |
| UPF0229 protein Meso\_0256 | | Q11LR5 | | | *Chelativorans sp.* (strain BNC1) | | | Cytoplasm | | |
| Quinone-reactive Ni/Fe-hydrogenase large chain | | P31883 | | | *Wolinella succinogenes* (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) | | | Plasma membrane | | |
| Lipoprotein LpqB | | Q47LZ | | | *Thermobifida fusca* (strain YX) | | | Plasma membrane | | |
|  | |  | | |  | | |  | | |

**Supplementary Table 2 –** DMSO group unique proteinsidentified by ESI-LC-MS/MS



|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Protein Name** | **ID uniprot** | | | **Organism Reference** | | | **Cellular Compartment** | | |
| **Carbohydrate metabolism** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| Maltodextrin phosphorylase | P00490 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| L-fuculokinase | P11553 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Hexitol phosphatase B | P77247 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative beta-xylosidase | P77713 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| Lactaldehyde dehydrogenase | P25553 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| 3-oxo-tetronate kinase | Q46889 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| dTDP-4-amino-4,6-dideoxygalactose transaminase | P27833 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Sulfoquinovose isomerase | P32140 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative 1-phosphofructokinase | P75038 | | | *Mycoplasma pneumoniae (strain ATCC 29342 / M129)* | | | Plasma membrane | | |
| Transaldolase | Q66ET5 | | | *Yersinia pseudotuberculosis serotype I* (strain IP32953) | | | Cytoplasm | | |
| 5-oxoprolinase subunit A | A0JR24 | | | *Arthrobacter sp.* (strain FB24) | | | Unknown | | |
| ***Cell Redox Homeostasis*** |  | | |  | | |  | | |
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| Alkyl hydroperoxide reductase C | P0AE08 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Alkyl hydroperoxide reductase subunit F | P35340 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Probable NADH oxidase | P75389 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| ***Stress and Defense Response*** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| ATP-dependent RNA helicase DeaD | P0A9P6 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase | P77690 | | | *Escherichia coli (strain K12)* | | | Cytoplasm | | |
| Multidrug resistance protein MdtN | P32716 | | | *Escherichia coli (strain K12)* | | | Plasma membrane | | |
| UPF0194 membrane protein YbhG | P75777 | | | *Escherichia coli (strain K12)* | | | Plasma membrane | | |
| Probable multidrug resistance protein EmrK | P52599 | | | *Escherichia coli (strain K12)* | | | Plasma membrane | | |
| Chaperone protein ClpB | Q88VX7 | | | *Escherichia coli (strain K12)* | | | Cytoplasm | | |
| Protein GrpE | P78017 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Chaperonin GroEL | P78012 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Co-chaperonin GroES | A7ZCV1 | | | *Campylobacter concisus* (strain 13826) | | | Cytoplasm | | |
| Chaperone protein DnaK | C4K3I6 | | | *Hamiltonella defensa subsp. Acyrthosiphon pisum* (strain 5AT) | | | Cytoplasm | | |
| Chaperone protein ClpB | Q88VX7 | | | *Lactiplantibacillus plantarum* (strain ATCC BAA-793 / NCIMB 8826 / WCFS1) | | | Cytoplasm | | |
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|  |  | | |  | | |  | | |
| ***Energy and Metabolism*** |  | | |  | | |  | | |
| Pyruvate dehydrogenase E1 component | P0AFG8 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Phosphoglucomutase | P36938 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Glucose-6-phosphate isomerase | P0A6T1 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Acyl carrier protein | P0A6A8 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Citrate synthase | P0ABH7 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Cytochrome bo(3) ubiquinol oxidase subunit 1 | P0ABI8 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Phosphoglycerate kinase | P0A799 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Formate hydrogenlyase subunit 7 dehydrogenase C2 | P16433 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Glutathione-specific gamma-glutamylcyclotransferase | P39163 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| NADH-quinone oxidoreductase subunit I | P0AFD6 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Galactokinase | P0A6T3 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Fructose-bisphosphate aldolase | P75089 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Enolase | P75189 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Acetate kinase | P75245 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Phosphoglycerate kinase | A7MJQ4 | | | *Cronobacter sakazakii* (strain ATCC BAA-894) | | | Cytoplasm | | |
| Adenylate kinase | A5FZU4 | | | *Acidiphilium cryptum* (strain JF-5) | | | Cytoplasm | | |
| Glyceraldehyde-3-phosphate dehydrogenase | Q07234 | | | *Buchnera aphidicola subsp. Schizaphis graminum* (strain Sg) | | | Cytoplasm | | |
| Phosphoenolpyruvate synthase | P23538 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| methylglyoxal synthase | P0A731 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Phosphoribosyl 1,2-cyclic phosphate phosphodiesterase | P16692 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Malate dehydrogenase | B1XHK9 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| Phosphoenolpyruvate carboxylase | A1U2U4 | | | *Marinobacter nauticus* (strain ATCC 700491 / DSM 11845 / VT8) | | | Cytoplasm | | |
| Dihydroorotate dehydrogenase (quinone) | Q8DLB7 | | | *Thermosynechococcus vestitus* (strain IAM M-273 / NIES-2133 / BP-1) | | | Cytoplasm | | |
| Glycerol kinase | B9JZR4 | | | *Agrobacterium vitis* (strain S4 / ATCC BAA-846) | | | Cytoplasm | | |
| NADPH-Fe(3+) oxidoreductase subunit alpha | Q74FU6 | | | *Geobacter sulfurreducens* (strain ATCC 51573 / DSM 12127 / PCA) | | | Cytoplasm | | |
|  |  | | |  | | |  | | |
| ATP synthase subunit delta | A6H2D8 | | | *Flavobacterium psychrophilum* (strain ATCC 49511 / DSM 21280 / CIP 103535 / JIP02/86) | | | Plasma membrane | | |
| Glucokinase | C5BCK8 | | | *Edwardsiella ictaluri* (strain 93-146) | | | Cytoplasm | | |
| 1,4-alpha-glucan branching enzyme GlgB | Q04KG8 | | | *Streptococcus pneumoniae serotype 2* (strain D39 / NCTC 7466) | | | Cytoplasm | | |
| PTS system glucose-specific EIICBA component | P20166 | | | *Bacillus subtilis* (strain 168) | | | Plasma membrane | | |
| Phosphoglycerate kinase | Q47XD4 | | | *Colwellia psychrerythraea* (strain 34H / ATCC BAA-681) | | | Cytoplasm | | |
| Succinate--CoA ligase [ADP-forming] subunit beta | A4W879 | | | *Enterobacter sp.* (strain 638) | | | Cytoplasm | | |
| ATP synthase gamma chain | Q3IK49 | | | *Pseudoalteromonas translucida* (strain TAC 125) | | | Plasma membrane | | |
| ***DNA metabolism*** |  | | |  | | |  | | |
|  |  | | |  | | |  | | |
| DNA base-flipping protein | P0AFP2 | | | *Escherichia coli (strain K12)* | | | Unknown | | |
| Transcription-repair-coupling factor | P30958 | | | *Escherichia coli (strain K12)* | | | Cytoplasm | | |
| Exodeoxyribonuclease I | Q2A0L0 | | | *Escherichia coli (strain K12)* | | | Cytoplasm | | |
| Formamidopyrimidine-DNA glycosylase | P42371 | | | *Lactococcus lactis subsp. cremoris* | | | Cytoplasm | | |
| DNA repair protein RecN | P17894 | | | *Bacillus subtilis (strain 168)* | | | Cytoplasm | | |
| DNA mismatch repair protein MutS | Q38YR4 | | | *Latilactobacillus sakei subsp. sakei* (strain 23K) | | | Cytoplasm | | |
| Protein RecA | Q05358 | | | *Legionella pneumophila* | | | Cytoplasm | | |
| DNA utilization protein HofM | P45753 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| RecBCD enzyme subunit RecB | P08394 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| 5'-3' exonuclease | P75403 | | | Mycoplasma pneumoniae (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Exodeoxyribonuclease 7 large subunit | Q2RIB5 | | | *Moorella thermoacetica* (strain ATCC 39073 / JCM 9320) | | | Cytoplasm | | |
| Crossover junction endodeoxyribonuclease RuvC | Q820F5 | | | *Streptomyces avermitilis* (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) | | | Cytoplasm | | |
| ***Cell signaling*** |  | | |  | | |  | | |
| *Signal recognition particle receptor FtsY* | P75362 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Methyl-accepting chemotaxis protein I | P02942 | | | *Escherichia coli* (strain K12) | | | Cell inner membrane | | |
|  |  | | |  | | |  | | |
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|  | | |  | | |  | | |  | | |
| ***Protein Biosynthesis and Metabolism*** | | |  | | |  | | |  | | |
|  | | |  | | |  | | |  | | |
| 50S ribosomal protein L14 | | | P0ADY3 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
|  | | |  | | |  | | |  | | |
| 50S ribosomal protein L27 | | | P0ABI8 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Protein NrdI | | | P0A772 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| 50S ribosomal protein L16 | | | P41204 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| 50S ribosomal protein L17 | | | Q59547 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Ribosome | | |
| 50S ribosomal protein L22 | | | A8AQL2 | | | *Citrobacter koseri* (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) | | | Ribosome | | |
| 50S ribosomal protein L29 | | | Q6A6M8 | | | *Cutibacterium acnes* (strain DSM 16379 / KPA171202) | | | Ribosome | | |
| 50S ribosomal protein L22 | | | Q3KLH4 | | | *Chlamydia trachomatis serovar A* (strain ATCC VR-571B / DSM 19440 / HAR-13) | | | Ribosome | | |
| Pup--protein ligase | | | D1BS28 | | | *Xylanimonas cellulosilytica* (strain DSM 15894 / CECT 5975 / LMG 20990 / XIL07) | | | Cytoplasm | | |
| 50S ribosomal protein L6 | | | Q88XX1 | | | *Lactiplantibacillus plantarum* (strain ATCC BAA-793 / NCIMB 8826 / WCFS1) | | | Ribosome | | |
| 50S ribosomal protein L30 | | | B9K8A4 | | | *Thermotoga neapolitana* (strain ATCC 49049 / DSM 4359 / NBRC 107923 / NS-E) | | | Ribosome | | |
| 30S ribosomal protein S11 | | | Q9PJN3 | | | *Chlamydia muridarum* (strain MoPn / Nigg) | | | Ribosome | | |
| Ribosome-recycling factor | | | C3MBQ5 | | | *Sinorhizobium fredii* (strain NBRC 101917 / NGR234) | | | Cytoplasm | | |
| LexA repressor | | | B8HG97 | | | *Pseudarthrobacter chlorophenolicus* (strain ATCC 700700 / DSM 12829 / CIP 107037 / JCM 12360 / KCTC 9906 / NCIMB 13794 / A6) | | | Cytoplasm | | |
| 50S ribosomal protein L15 | | | Q6CZY9 | | | *Pectobacterium atrosepticum* (strain SCRI 1043 / ATCC BAA-672) | | | Ribosome | | |
| Protein translocase subunit SecA | | | Q8K9C4 | | | *Buchnera aphidicola subsp. Schizaphis graminum* (strain Sg) | | | Plasma membrane | | |
| 30S ribosomal protein S4 | | | B0C9F5 | | | *Acaryochloris marina* (strain MBIC 11017) | | | Ribosome | | |
| 30S ribosomal protein S11 | | | B3WAJ3 | | | *Lacticaseibacillus casei* (strain BL23) | | | Ribosome | | |
| 5,10-methylenetetrahydrofolate reductase | | | P0AEZ1 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| S-adenosylmethionine synthase | | | B7UHY9 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| D-cysteine desulfhydrase | | | P76316 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative aminodehydroquinate synthase | | | Q3J830 | | | *Amycolatopsis mediterranei* (strain S699) | | | Cytoplasm | | |
| Glutamate mutase epsilon subunit | | | Q05509 | | | *Clostridium tetanomorphum* | | | Cytoplasm | | |
| N-acetyl-gamma-glutamyl-phosphate reductase | | | A5WH78 | | | *Psychrobacter sp.* (strain PRwf-1) | | | Cytoplasm | | |
| Tyrosine phenol-lyase | | | Q9CMK9 | | | *Pasteurella multocida* (strain Pm70) | | | Cytoplasm | | |
| 3-dehydroquinate synthase | | | A3PC83 | | | *Prochlorococcus marinus* (strain MIT 9301) | | | Cytoplasm | | |
| 3-isopropylmalate dehydratase large subunit | | | Q7VAV9 | | | *Prochlorococcus marinus* (strain SARG / CCMP1375 / SS120) | | | Cytoplasm | | |
| Phosphoribosyl-ATP pyrophosphatase | | | B1M0Q0 | | | *Methylobacterium radiotolerans* (strain ATCC 27329 / DSM 1819 / JCM 2831 / NBRC 15690 / NCIMB 10815 / 0-1) | | | Cytoplasm | | |
|  | | |  | | |  | | |  | | |
| 1D-myo-inositol 2-acetamido-2-deoxy-alpha-D-glucopyranoside deacetylase | | | D6Y7M2 | | | *Thermobispora bispora* (strain ATCC 19993 / DSM 43833 / CBS 139.67 / JCM 10125 / KCTC 9307 / NBRC 14880 / R51) | | | Cytoplasm | | |
| Chorismate synthase | | | Q0S0N2 | | | *Rhodococcus jostii* (strain RHA1) | | | Cytoplasm | | |
| 3-phosphoshikimate 1-carboxyvinyltransferase | | | B9MQK4 | | | *Caldicellulosiruptor bescii* (strain ATCC BAA-1888 / DSM 6725 / Z-1320) | | | Cytoplasm | | |
| Glycine cleavage system H protein | | | A1T9T8 | | | *Mycolicibacterium vanbaalenii* (strain DSM 7251 / JCM 13017 / BCRC 16820 / KCTC 9966 / NRRL B-24157 / PYR-1) | | | Cytoplasm | | |
| Selenide, water dikinase | | | C4ZDB0 | | | *Agathobacter rectalis* (strain ATCC 33656 / DSM 3377 / JCM 17463 / KCTC 5835 / VPI 0990) | | | Cytoplasm | | |
| Serine hydroxymethyltransferase | | | A6VXM6 | | | *Marinomonas sp.* (strain MWYL1) | | | Cytoplasm | | |
| Imidazole glycerol phosphate synthase subunit HisH | | | P60601 | | | *Rhodopseudomonas palustris* (strain ATCC BAA-98 / CGA009) | | | Cytoplasm | | |
| Glutamine synthetase | | | P10583 | | | *Azospirillum brasilense* | | | Cytoplasm | | |
| Arginine biosynthesis bifunctional protein ArgJ | | | Q67KC5 | | | *Symbiobacterium thermophilum* (strain T / IAM 14863) | | | Cytoplasm | | |
| 3-phosphoshikimate 1-carboxyvinyltransferase | | | B8D9A1 | | | *Buchnera aphidicola subsp. Acyrthosiphon pisum* (strain 5A) | | | Cytoplasm | | |
| Dihydroxy-acid dehydratase | | | Q2SA20 | | | *Hahella chejuensis* (strain KCTC 2396) | | | Cytoplasm | | |
| Carbamoyl-phosphate synthase small chain | | | B2URJ0 | | | *Akkermansia muciniphila* (strain ATCC BAA-835 / DSM 22959 / JCM 33894 / BCRC 81048 / CCUG 64013 / CIP 107961 / Muc) | | | Cytoplasm | | |
| Phosphoribosyl-AMP cyclohydrolase | | | P62392 | | | *Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni* (strain Fiocruz L1-130) | | | Cytoplasm | | |
| Argininosuccinate synthase | | | Q63U95 | | | *Burkholderia pseudomallei* (strain K96243) | | | Cytoplasm | | |
| Glycine--tRNA ligase beta subunit | | | P00961 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Phosphoenolpyruvate-dependent phosphotransferase system | | | P37177 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Methionyl-tRNA formyltransferase | | | P75235 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| GTPase Era | | | Q97JI5 | | | *Clostridium acetobutylicum* (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) | | | Plasma membrane | | |
| ***Regulation Factor and RNA Processing*** | | |  | | |  | | |  | | |
|  | | |  | | |  | | |  | | |
| Ribosomal RNA large subunit methyltransferase K/L | | | P0A8I8 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| tRNA-modifying protein YgfZ | | | P75810 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| RNA 2'-phosphotransferase | | | P39380 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| Ribonuclease J | | P75497 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Elongation factor Tu 1 | | P0CE47 | | | *Escherichia coli O139:H28* (strain E24377A / ETEC) | | | Cytoplasm | | |
| Elongation factor G | | Q492B1 | | | *Blochmannia pennsylvanicus* (strain BPEN) | | | Cytoplasm | | |
| Phenylalanine--tRNA ligase alpha subunit | | Q88WM8 | | | *Lactiplantibacillus plantarum* (strain ATCC BAA-793 / NCIMB 8826 / WCFS1) | | | Cytoplasm | | |
| Phenylalanine--tRNA ligase beta subunit | | P59505 | | | *Buchnera aphidicola subsp. Baizongia pistaciae* (strain Bp) | | | Cytoplasm | | |
| Elongation factor 4 | | C3K6G8 | | | *Pseudomonas fluorescens* (strain SBW25) | | | Cytoplasm | | |
| tRNA modification GTPase MnmE | | Q1MPF1 | | | *Lawsonia intracellularis* (strain PHE/MN1-00) | | | Cytoplasm | | |
| ***Transferase*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| L-carnitine CoA-transferase | | P31572 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Phosphate acetyltransferase EutD | | P77218 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Protein adenylyltransferase SelO | | Q0THC2 | | | *Escherichia coli* (strain K12) | | | Unknown | | |
| 3-methyl-2-oxobutanoate hydroxymethyltransferase | | P31057 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase | | P36562 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative acetyltransferase MPN\_114 | | P75448 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Ornithine carbamoyltransferase | | Q93JF1 | | | *Streptomyces coelicolor (*strain ATCC BAA-471 / A3(2) / M145) | | | Cytoplasm | | |
| Sulfate adenylyltransferase | | A5D5R7 | | | *Pelotomaculum thermopropionicum* (strain DSM 13744 / JCM 10971 / SI) | | | Cytoplasm | | |
| 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase | | Q1LTH3 | | | *Baumannia cicadellinicola subsp. Homalodisca coagulata* | | | Unknown | | |
| 1-deoxy-D-xylulose-5-phosphate synthase | | A3MYS9 | | | *Actinobacillus pleuropneumoniae serotype 5b* (strain L20) | | | Cytoplasm | | |
| Phosphatidylglycerol--prolipoprotein diacylglyceryl transferase | | Q8NNU2 | | | *Corynebacterium glutamicum* (strain ATCC 13032 / DSM 20300 / BCRC 11384 / JCM 1318 / LMG 3730 / NCIMB 10025) | | | Cytoplasm | | |
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| ***Light dependent process*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Light-independent protochlorophyllide reductase subunit N | | Q7V2D5 | | | *Prochlorococcus marinus subsp. pastoris* (strain CCMP1986 / NIES-2087 / MED4) | | | Cytoplasm | | |
| Glutamyl-tRNA reductase | | A5UU33 | | | *Roseiflexus sp.* (strain RS-1) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Transmembrane transporters***  p-hydroxybenzoic acid efflux pump subunit AaeB | | P46481 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| D-galactose-binding periplasmic protein | | P0AEE5 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Inner membrane transport protein RhmT | | P76470 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Putative outer membrane porin protein NmpC | | P21420 | | | *Escherichia coli* (strain K12) | | | Cell outer membrane | | |
| Thiosulfate-binding protein | | P16700 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Oligopeptide transport ATP-binding protein OppF | | P75551 | | | Mycoplasma pneumoniae (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Spermidine/putrescine import ATP-binding protein PotA | | P75059 | | | Mycoplasma pneumoniae (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Phosphate import ATP-binding protein PstB 1 | | Q8RCU0 | | | *Caldanaerobacter subterraneus subsp. tengcongensis* (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) | | | Plasma membrane | | |
| Fe(3+) ions import ATP-binding protein FbpC 2 | | Q6D2F6 | | | *Pectobacterium atrosepticum* (strain SCRI 1043 / ATCC BAA-672) | | | Plasma membrane | | |
|  | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| ***DNA replication***  DNA adenine methylase | | P0AEE8 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| 50S ribosomal protein L2 | | P60422 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Probable DNA helicase II homolog | | P75437 | | | Mycoplasma pneumoniae (strain ATCC 29342 / M129) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Regulation of transcription*** | |  | | |  | | |  | | |
| Arabinose operon regulatory protein | | P0A9E0 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| HTH-type transcriptional regulator GadX | | P37639 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Periplasmic protein TorT | | P38683 | | | *Escherichia coli* (strain K12) | | | Periplasmic space | | |
| DNA-directed RNA polymerase subunit alpha | | P0A7Z4 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative acyl-CoA dehydrogenase AidB | | P33224 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Antitoxin VapB2 | | O07227 | | | *Mycobacterium tuberculosis* (strain ATCC 25618 / H37Rv) | | | Unknown | | |
| HTH-type transcriptional regulator BetI | | B7VQ27 | | | *Vibrio atlanticus* (strain LGP32) | | | Cytoplasm | | |
| Catabolite control protein A | | O07329 | | | *Streptococcus mutans serotype c* (strain ATCC 700610 / UA159) | | | Cytoplasm | | |
| DNA-directed RNA polymerase subunit beta' | | Q0BUQ5 | | | *Granulibacter bethesdensis* (strain ATCC BAA-1260 / CGDNIH1) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Antibiotics biosynthesis*** | |  | | |  | | |  | | |
|  | |  | | |  | | |  | | |
| Cytochrome P-450 monooxygenase DoxA | | Q93MI2 | | | *Streptomyces peucetius subsp. caesius* | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Nucleotide metabolism*** | |  | | |  | | |  | | |
| Allantoate amidohydrolase | | P77425 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Bifunctional protein FolD | | P75096 | | | *Mycoplasma pneumoniae (strain ATCC 29342 / M129)* | | | Cytoplasm | | |
| Thymidylate kinase | | Q6FZU8 | | | *Bartonella quintana (strain Toulouse)* | | | Cytoplasm | | |
| dTTP/UTP pyrophosphatase | | Q82ZA4 | | | *Enterococcus faecalis* (strain ATCC 700802 / V583) | | | Cytoplasm | | |
| Phosphoribosylamine--glycine ligase | | P15640 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Phosphotransferase RcsD | | P39838 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| DNA translocase FtsK 2 | | Q8XWX9 | | | *Ralstonia solanacearum (strain GMI1000)* | | | Plasma membrane | | |
| Dihydroorotase | | P96081 | | | *Thermus aquaticus* | | | Cytoplasm | | |
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| ***Pathogenesis*** | |  | | |  | | |  | | |
| LPS-assembly protein LptD | | P31554 | | | *Escherichia coli* (strain K12) | | | Cell outer membrane | | |
| 3-deoxy-D-manno-octulosonic acid kinase | | Q9PBJ1 | | | *Xylella fastidiosa (strain 9a5c)* | | | Plasma membrane | | |
| T-DNA border endonuclease VirD2 | | P18592 | | | *Agrobacterium fabrum* (strain C58 / ATCC 33970) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| ***Cell wall organization and structural maintenance*** | |  | | |  | | |  | | |
| D-alanyl-D-alanine dipeptidase | | P77790 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| 1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD | | P13016 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Membrane-bound lytic murein transglycosylase F | | P0AGC5 | | | *Escherichia coli* (strain K12) | | | Cell outer membrane | | |
| Undecaprenyl-diphosphatase | | G0FS62 | | | *Amycolatopsis mediterranei* (strain S699) | | | Plasma membrane | | |
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| ***Lipid metabolism*** | |  | | |  | | |  | | |
| Acyl carrier protein phosphodiesterase | | B1XEZ2 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Crotonobetainyl-CoA reductase | | P60584 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
|  | |  | | |  | | |  | | |
| Bifunctional polymyxin resistance protein ArnA | | P77398 | | | *Escherichia coli* (strain K12) | | | Protein containing complex | | |
| Long-chain-fatty-acid--CoA ligase | | P69451 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Medium/long-chain-fatty-acid--[acyl-carrier-protein] ligase MbtM | | P0A4X9 | | | *Mycobacterium bovis* (strain ATCC BAA-935 / AF2122/97) | | | Plasma membrane | | |
| Phosphatidylglycerol--prolipoprotein diacylglyceryl transferase | | Q17X31 | | | *Helicobacter acinonychis* (strain Sheeba) | | | Plasma membrane | | |
| ***Unknown*** | |  | | |  | | |  | | |
| Putative lipoprotein YfiB | | P07021 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Putative aminopeptidase FrvX | | P32153 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Probable ATP-binding protein YheS | | P63389 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Ureidoglycolate dehydrogenase (NAD(+)) | | W1F386 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Inner membrane protein YbjJ | | P75810 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| Probable lipoprotein YiaD | | P37665 | | | *Escherichia coli* (strain K12) | | | Plasma membrane | | |
| tRNA-dihydrouridine(20/20a) synthase | | P32695 | | | *Escherichia coli* (strain K12) | | | Cytoplasm | | |
| Putative phosphatase MPN\_427 | | P75360 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Putative MgpC-like protein MPN\_092 | | P75600 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Unknown | | |
| Probable ATP-dependent RNA helicase MG308 homolog | | P75335 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Phosphoenolpyruvate-protein phosphotransferase | | P75168 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| Putative esterase/lipase 1 | | P75333 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Unknown | | |
| ATP synthase subunit alpha | | Q50329 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Acyl carrier protein homolog | | P75378 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Plasma membrane | | |
| Protein MPN\_376 | | P75405 | | | *Mycoplasma pneumoniae* (strain ATCC 29342 / M129) | | | Cytoplasm | | |
| UPF0597 protein DP0591 | | Q6AQQ3 | | | *Desulfotalea psychrophila* (strain LSv54 / DSM 12343) | | | Cytoplasm | | |
| L-lactate oxidase | | C0XIJ3 | | | *Lentilactobacillus hilgardii* (strain ATCC 8290) | | | Cytoplasm | | |
| Flagellin | | P06175 | | | *Salmonella rubislaw* | | | Extracellular | | |
| 5-methylthioadenosine/S-adenosylhomocysteine deaminase | | A4J675 | | | *Desulfotomaculum reducens* (strain MI-1) | | | Cytoplasm | | |
| Surface layer protein | | P38538 | | | *Brevibacillus choshinensis* | | | Extracellular | | |
| ESX-5 secretion system protein EccA5 | | P63745 | | | *Mycobacterium bovis* (strain ATCC BAA-935 / AF2122/97) | | | Cytoplasm | | |
| Protein adenylyltransferase SelO | | Q1H0D2 | | | *Methylobacillus flagellatus* (strain KT / ATCC 51484 / DSM 6875) | | | Cytoplasm | | |
| Sugar fermentation stimulation protein homolog | | A6W2V7 | | | *Marinomonas sp.* (strain MWYL1) | | | Cytoplasm | | |
| Phase 2 flagellin | | P52615 | | | *Salmonella abortus-equi* | | | Extracellular | | |
| Putative membrane protein insertion efficiency factor | | Q11JM2 | | | *Chelativorans sp.* (strain BNC1) | | | Plasma membrane | | |
| UPF0358 protein BH2626 | | Q9K9L9 | | | *Alkalihalobacillus halodurans* (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) | | | Cytoplasm | | |
| UPF0114 protein PC1\_0431 | | C6DJS4 | | | *Pectobacterium carotovorum subsp. carotovorum* (strain PC1) | | | Plasma membrane | | |
| D-threo-3-hydroxyaspartate dehydratase | | B2DFG5 | | | *Delftia sp.* (strain HT23) | | | Cytoplasm | | |
| Methionine import ATP-binding protein MetN 1 | | Q63H29 | | | *Bacillus cereus (strain ZK / E33L)* | | | Plasma membrane | | |
| FHA domain-containing protein FhaB | | A0QNG6 | | | *Mycolicibacterium smegmatis* (strain ATCC 700084 / mc(2)155) | | | Plasma membrane | | |
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