**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*** |  |  |  |
|  |  |  |  |
| 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 |
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| ***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 |
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| ***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 |
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| ***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 |
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| ***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*** |  |  |  |
|  |  |  |  |
| 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 |
|  |  |  |  |
|  |  |  |  |
| ***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 |
|  |  |  |  |
|  |  |  |  |
| ***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*** |  |  |  |
|  |  |  |  |
| 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 |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| ***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 |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |
| ***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 |
|  |  |  |  |
|  |  |  |  |
| ***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 |
|  |  |  |  |
|  |  |  |  |
| ***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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