

Pathway Features

- Uncharacterized conserved protein YpmB, contains C-terminal PepSY domain
- Uncharacterized conserved protein, contains Zn-finger domain of CHY type
- Predicted ATPase, archaeal AAA+ ATPase superfamily
- Predicted house-cleaning noncanonical NTP pyrophosphatase, all-alpha NTP-PPase (MazG) superfamily
- Uncharacterized protein, contains DUF2185 domain
- Multidrug resistance efflux pump EmrA
- Folypolyglutamate synthase/Dihydropteroate synthase
- Uncharacterized conserved protein YhaN, contains AAA domain
- ABC-type transport system involved in cytochrome c biogenesis, permease component
- GTP-binding protein EngB required for normal cell division
- Sensor histidine kinase DipB regulating citrate/malate metabolism
- 3'-5' exoribonuclease YhaM, can participate in 23S rRNA maturation, HD superfamily
- Membrane protein TolA involved in colicin uptake
- LPS O-antigen chain length determinant protein, WzzB/FepE family
- Aldehyde, CO or xanthine dehydrogenase, Mo-binding subunit
- ABC-type Fe3+-citrate transport system, periplasmic component
- Thioester reductase domain of alpha aminoacidate reductase Lys2 and NRPSs
- Serine protease inhibitor ecotin
- DNA-directed RNA polymerase, subunit F
- Uncharacterized protein with cyclophilin fold, contains DUF369 domain
- Transcription factor homologous to NACalpha-BTF3
- ABC-type microcin C transport system, permease component YejE
- Ubiquitin-protein ligase
- Iron-sulfur cluster repair protein YtfE, RIC family, contains ScdAN and hemerythrin domains
- Transcriptional regulator, contains Arc/MetJ-type RHH (ribbon-helix-helix) DNA-binding domain
- Membrane-bound lytic murein transglycosylase
- Uncharacterized membrane protein YedE/YeeE, contains two sulfur transport domains
- Isopenicillin N synthase and related dioxygenases
- Methionine aminopeptidase
- 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase LspG/GcpE
- Two-component response regulator, AmiR/NasT family, consists of REC and RNA-binding antiterminator (ANTAR) domains
- Adenylate cyclase class IV, CYTH domain (includes archaeal enzymes of unknown function)
- ABC-type polysaccharide transport system, permease component
- Outer membrane receptor for monomeric catechols
- Lysozyme M1 (1,4-beta-N-acetylmuramidase), GH25 family
- Predicted membrane chloride channel, bestrophin family
- Molybdopterin-binding protein MopI
- Tetraacyldisaccharide-1-P 4'-kinase (Lipid A 4'-kinase)
- Ribosomal protein L3
- Dihydropteroate synthase
- FAD:protein FMN transferase ApbE
- DNA/RNA endonuclease G, NUC1
- Predicted nucleic acid-binding OB-fold protein
- Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family
- Uncharacterized conserved protein containing a metal-binding domain
- Uncharacterized conserved protein YutD, DUF1027 family
- Chorismate synthase
- Uncharacterized conserved protein, UPF0297 family
- Uncharacterized conserved protein, DUF505 domain
- Formylmethanofuran dehydrogenase subunit D

