

GEM: Cloacimonadota

Pathway Features

- Flagellar hook-capping protein FlgD
- Predicted ATP-dependent Lon-type protease
- Signal recognition particle GTPase FtsY
- Uncharacterized conserved protein, contains caspase domain
- Coenzyme F420-reducing hydrogenase, beta subunit
- tRNA(Leu) C34 or U34 (ribose-2'-O)-methylase TrmL, contains SPOUT domain
- Copper oxidase (laccase) domain
- O-acetyl-ADP-ribose deacetylase (regulator of RNase III), contains Macro domain
- DNA-binding beta-propeller fold protein YncE
- Pyruvate carboxylase
- Alanyl-tRNA synthetase
- TPP-dependent indolepyruvate ferredoxin oxidoreductase, alpha subunit
- Putative GTP cyclohydrolase 1 type 2, NIF3 family
- Signal transduction histidine kinase ComP
- Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain
- Zn-dependent oligopeptidase, M3 family
- Ribosomal protein L9
- Thymidylate kinase
- tRNA A37 threonylcarbamoyladenine synthetase subunit TsaC/SUA5/YrdC
- Serine/threonine protein phosphatase PrpC
- Predicted transcriptional regulator, contains an HTH and PUA-like domains
- Uncharacterized membrane protein YckC, RDD family
- Palmitoleoyl-ACP: Kdo2-lipid-IV acyltransferase (lipid A biosynthesis)
- Ribosomal protein L2
- Chaperonin GroEL (HSP60 family)
- Nicotinate-nucleotide adenyltransferase NadD
- ABC-type transport system involved in cytochrome c biogenesis, ATPase component
- CRISPR-Cas system type III CMR-effector complex subunit Cmr1, RAMP superfamily Cas7 group
- Fatty acid-binding protein DegV (function unknown)
- Uncharacterized membrane protein
- 4-Hydroxy-3-methylbut-2-enyl diphosphate reductase IspH
- 16S rRNA G966 N2-methylase RsmD
- Uncharacterized conserved protein, contains Zn-finger domain of CDGSH type
- Trehalose-6-phosphate phosphatase
- ABC-type uncharacterized transport system, auxiliary component
- Predicted epimerase YddE/YHI9, PhzF superfamily
- Recombinational DNA repair protein RecR
- DNA mismatch repair ATPase MutL
- 2-iminoacetate synthase ThiH/Menaquinone biosynthesis enzymes MqnC and MqnE
- DNA uptake channel protein ComEC C-terminal domain, metallo-beta-lactamase superfamily
- Mu-like prophage host-nuclease inhibitor protein Gam
- ABC-type uncharacterized transport system involved in gliding motility, auxiliary component
- Aminoglycoside N3'-acetyltransferase
- Histidyl-tRNA synthetase
- DNA-binding transcriptional regulator, MerR family
- Uncharacterized membrane protein YhaH, DUF805 family
- UDP-N-acetylmuramoylalanine-D-glutamate ligase
- Mu-like prophage FluMu protein gp28
- Predicted Zn-dependent protease YjaZ, DUF2268 family
- Protein kinase association domain CaMKII_AD, NTF2-like superfamily

