Manuscript for Cyanobacteria: A novel Species

Project 3

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# 1. Abstract

*Cyanobacteria are a diverse group of Gram-negative oxygen-evolving photoautotrophic prokaryotes which play an important role in biological nitrogen fixation. These prokaryotes produce two metabolites: primary metabolites, essential for survival, and secondary metabolites required for auxiliary purposes–stress responses, defense mechanisms, metal carrying, and signaling. These secondary metabolites can include compounds that act as hormones, antibiotics, allelochemicals, and toxins. This is important because antibiotic resistance in bacteria and fungi is becoming a problem due to resistant pathogenic bacteria. Both species of cyanobacteria used in this experiment belong to a Genera with known toxin, antibiotic, and/or fungi-producing species. Thus we aim to expand upon this work by investigating these newly identified species and their production of secondary metabolites. Specifically, we aim to 1) identify both novel cyanobacteria by doing whole genome sequencing and creating phylogenetic trees based on known conserved regions as well as 16s phylogenetic trees, 2) investigate secondary metabolites by annotating the genome sequenced, 3) test the reactivity of the antimicrobial and/or antifungal compounds produced by the cyanobacteria against Gram-Positive bacteria, Gram-Negative bacteria, and a fungal species, and to evaluate the potential toxicity of both species using an Artemia salina bioassay.*

# 2. Introduction

## 2.1 General Background Information

**1.1 Beginning of life, Cyanobacteria**

Cyanobacteria or Cyanophyta are an ancient group of oxygenic photosynthesizers estimated to have originated around 3.0 ga. The appearance of cyanobacteria led to the Great Oxygenation Event (GOE) approximately 2.4 billion years ago, thus greatly modifying the Earth and its atmospheres(Guéguen & Maréchal, 2021). These changes gave rise to new ecosystems due to the difference in climate, the reduction of atmospheric carbon dioxide, and the increased sunlight. Through acquiring the chloroplast and mitochondria via primary endosymbiosis, the rise of eukaryotes can be dated back to approximately ~1,200 million years ago (Shih & Matzke, 2013). A second oxygenation event can be seen during the Neoproterozoic Oxygenation Event (NOE) approximately 800-600 million years ago due to the rise of algae.

 Since 2009, there are approximately 150 genera and over 2,000 species of cyanobacteria (Vincent, 2009). Cyanobacteria are morphologically diverse, ranging from unicellular to multicellular. They can be filamentous, coccoid, trichal, and some can have differential cells such as heterocysts or akinetes. These are Gram-Negative bacteria originally described under the Botanical, and it wasn’t until 1978 that scientists proposed systems to resolve the classification of cyanobacteria and place them under the bacteriological code (Walter et al., 2017). Currently, there is a formal system that is a compromise between the Bacteriological and Botanical Codes for species and is based on botanical taxonomic criteria and includes bacteriological and molecular information (Palinska & Surosz, 2014).  Their morphological diversity provided a challenge for scientists regarding classification. Still, their biochemical and physiological properties allowed them to live almost anywhere in extreme environments such as hypersaline lakes and calderas on active volcanoes.

**1.2 Microbial Diversity and Housekeeping genes**

Locations such as the Hawaiian Archipelago provide a unique biodiversity hotspot due to the geographical isolation of these islands and the tropical climates year around. Well documented studies on microorganism communities and interactions are limited and there are still locations in which there has been little anthropogenic activity. Such locations provide ideally pristine habitats for the study of microbial diversity and potentially discovery of novel species. Locations such as underwater hydrothermal vents and lava calderas provide unique niches for organisms to thrive.

However, to thrive in such environments, these organisms must have adapted a way to obtain energy. With the rise of cyanobacteria (blue-green algae), Chlorophyta (green algae), Rhodophyta (red algae), Bacillariophyta (diatoms), and Plantae (photosynthetic eukaryotes) can also be broken down into two types of photophosphorylation: oxygenic phosphorylation and anoxygenic phosphorylation. Cyanobacteria and Eukaryotes fall under oxygenic phosphorylation, and produce O2 from H2O using chlorophyll as a light harvester and are considered photoautotrophs since they utilize light as energy and will fix CO2.

The process of gaining energy is a cycle called the Calvin-Benson-Bassham (CBB). This process is a reductive pentose phosphate pathway that assimilates CO2. Ribulose- 1,5-bisphosphate carboxylase/oxygenase (RubisCO) is one of the major enzymatic activities unique to the Calvin cycle and is also the CBB enzyme responsible for the fixation for CO2 (Hirota et al., 2002). These genes encoding RubisCO are broken down into Ribulose bisphosphate carboxylase large chain (cbbL) and Ribulose bisphosphate carboxylase small chain (cbbS). While the compromise between the Botanical and Bacteriological Code for new species includes, phylogenetic analyses investigate the sequence divergence of the 16s rRNA gene, construction of the secondary structure of the 16s - 23s region, morphological description, and description of the thylakoid structure, recently papers like (Mareš et al., 2019),  (Xie, Jäger, & Potts, 1989), and (Walter et al., 2017) have been published using additional housekeeping genes to help resolve placement of species within a Genera.

Gene transcription is directed through the DNA-dependent RNA polymerase, which in bacteria, is formed by a core RNA polymerase broken down into the sigma factors: α, β, β′, and σ.  The DNA-directed RNA polymerase subunit β (rpoB)and the DNA-directed RNA polymerase subunit β′ (rpoC and rpoC2) are adjacent to each other and are transcribed from the major promoter (Xie, Wen - Qin et al. 1989 ). Due to the 16s rRNA region lacking sensitivity for evolutionary changes, these additional housekeeping genes are being added to studies more recently.

Novel species of cyanobacteria were sampled from a volcano caldera located on Kiluea, HI in 2008. Three species of cyanobacteria have been isolated from a consortium of organisms growing in a mat on the cave wall.  We sequenced the cyanobacteria, all three of which were novel species, so following the compromise between the Botanical and Bacteriological Code, we will describe the morphology of the organisms, construct a secondary structure of the 16s - 23s region, and do a phylogenetic analysis of the whole genomes, rpoB gene, rpoC gene, rpoC2 gene, cbbL gene, and cbbS gene. We would also like to investigate the production of antibiotics and inhibitory genes of these novel species.

## 2.2 Description of data and data source

*Novel species was discovered from Big Ell Cave located on Kilauea, Hawaii in 2008. Mutliple samples were taken from 2008 - 2018 in order to get an idea of the effects of a volcanic eruption on the biodiversity within the caldera. Samples were isolated to obtain what we are calling JS1 (Gleobacter violaceus), JS2 (Fischerella sp), and JS3 (Leptolygnbya sp). GitHub repository (https://github.com/Yokohime/Chiyoko\_ZOOL710\_project3.git) has the raw data, coding scripts for cleaning and analysis.*

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| Figure.1: Location of caldera located on Kiluea, HI. |

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| Figure.2: Image of mat sampled from within Big Ell cave containing JS1 (purple) , JS2 (green) , JS3 (green), and including a multitude of other bacteria. |

## 2.3 Questions/Hypotheses to be addressed

*Aims of this project include to address the following:*

* 1. Are these unknown cyanobacteria novel Species, Genera, or Family?
  2. Do these novel cyanobacteria–Leptolyngbya sp. and Fischerella sp.–produce any toxic secondary metabolites or any that inhibit the survival of another organism?
  3. If these species produce any toxic or inhibitory secondary metabolites, are they novel?

# 3. Methods

After extracting the DNA, Illumina and MinION sequencing was done in the Advanced Studies in Genomics, Proteomics, and Bioinformatics (ASGPB) located at the University of Hawai’i at Manoa, Life Science Building 320. Genomic data for all available Fischerella species were obtained from National Center for Biotechnologu Information (NCBI). Genomes were annotated using Ulana, a Prokka pipeline written by Ethan Hill of Iolani High School. Using Rstudio, the annotations were cleaned and organized to extract the annotated genes of interest. Genes for the rpoB, rpoC, rpoC2,cbbL, and cbbS genes were extracted from the genome and aligned using MUSCLE 3.8 which can be accessed on European Molecular Biology Laboratory (EMBL-EBI):https://www.ebi.ac.uk/Tools/msa/.

## 3.1 Data acquisition, import and cleaning

\*Data was obtained from field samples of a mat found in a volcanic calderea on the island, Hawai’i in 2008. DNA was extracted and sequenced at the facilities located at the University of Hawai’i at Manoa. The whole genome was annotated and cleaned and can be found under under the Raw\_data folder.

**Cleaning script**

*Data was uploaded, checked for errors, and then organized to extract the data of interest. Comparison between each species was made in terms of what genes each species shared between each other as well as what genes were shared between all species. Cleaning script can be found here: https://github.com/Yokohime/Chiyoko\_ZOOL710\_project3/blob/main/Code/Processing\_Code/ProcessingData.R*

# 4. Results

## 4.1 Exploratory/Descriptive analysis

# 5. 16s

#|echo: FALSE  
 knitr::include\_graphics("Images/16S\_Tree.png")

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| --- |
| Maximum-likelihood tree based on the 16S gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
 knitr::include\_graphics("Images/16S\_Matrix.png")

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| The sume of the branch lengths for the 16S gene for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 6. rpoB

#|echo: FALSE  
knitr::include\_graphics("Images/rpoB\_Tree.png")

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| Maximum-likelihood tree based on the rpoB gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

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| The sume of the branch lengths for the rpoB gene for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 7. rpoC

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| Maximum-likelihood tree based on the rpoC gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/rpoC\_Matrix.png")

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| The sume of the branch lengths for the rpoC gene for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 8. rpoC2

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| Maximum-likelihood tree based on the rpoC2 gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/rpoC2\_Matrix.png")

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| Percent Identity based on the rpoC2 gene for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 9. rpo Genes concatenated

#|echo: FALSE  
knitr::include\_graphics("Images/rpo\_Gene\_Tree.png")

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| Maximum-likelihood tree based on the rpo gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/rpo\_Gene\_Matrix.png")

|  |
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| The sume of the branch lengths for the rpo genes for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 10. cbbL

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| Maximum-likelihood tree based on the cbbL gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/cbbL\_Matrix.png")

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| The sume of the branch lengths for the cbbL gene for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 11. cbbS

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| Maximum-likelihood tree based on the cbbS gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/cbbS\_Matrix.png")

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| The sume of the branch lengths for the cbbS gene for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 12. All genes combined

#|echo: FALSE  
knitr::include\_graphics("Images/cbb\_Tree.png")

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| Maximum-likelihood tree based on the cbbLand cbbS gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/cbb\_Matrix.png")

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| The sume of the branch lengths for the cbb genes for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 13. All genes combined

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| Maximum-likelihood tree based on the 16S rRNA, rpoB, rpoC, rpoC2, cbbL,and cbbS gene sequences of all available Fischerella species. Bootstrap values after 1,000 replicates are expressed as percentages.Gleobacter violaceus PCC 7421 was used as an outgroup. The scale bar indicates the fraction of nucleotide substitutions per site. |

#|echo: FALSE  
knitr::include\_graphics("Images/All\_Genes\_Matrix.png")

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| The sume of the branch lengths for the rpoB, rpoC, rpoC2, cbbL, cbbS, and 16S rRNA genes for all 7 species of Ficherella sp. and Gleobactor vialoceus. |

# 14. Products of JS2

::: {#tbl-Products of JS2 .cell tbl-cap=‘List of products produced based on the genes present in JS2.’} ::: {.cell-output-display} | |x | |:—-|:——————————————————————————————————————-| |1 |Chromosomal replication initiator protein DnaA | |2 |Beta sliding clamp | |3 |Adaptive-response sensory-kinase SasA | |4 |50S ribosomal protein L33 | |5 |Ribonuclease R | |6 |Neopullulanase | |7 |Manganese transport system membrane protein MntB | |8 |Manganese transport system ATP-binding protein MntB | |9 |Periplasmic zinc-binding protein TroA | |10 |putative adenylyltransferase/sulfurtransferase MoeZ | |11 |tRNA 2-selenouridine synthase | |12 |Nucleoside triphosphate pyrophosphohydrolase/pyrophosphatase MazG | |13 |Cytochrome b6-f complex iron-sulfur subunit | |14 |Gamma-glutamyl phosphate reductase | |15 |Salicylate biosynthesis isochorismate synthase | |16 |1 | |17 |4-dihydroxy-2-naphthoate octaprenyltransferase | |18 |L-Ala-D/L-Glu epimerase | |19 |2-succinylbenzoate–CoA ligase | |21 |4-dihydroxy-2-naphthoyl-CoA hydrolase | |22 |Hercynine oxygenase | |23 |Inner membrane ABC transporter permease protein YdcV | |24 |Sensor histidine kinase RcsC | |25 |Glucose–fructose oxidoreductase | |26 |Aminopyrimidine aminohydrolase | |27 |LL-diaminopimelate aminotransferase | |28 |Thioredoxin 2 | |29 |Phage shock protein A | |31 |Nucleoside triphosphate pyrophosphatase | |32 |Putative acetyltransferase | |33 |UDP-N-acetylmuramoylalanine–D-glutamate ligase | |34 |Glycine–tRNA ligase beta subunit | |35 |tRNA-Gly(tcc) | |37 |5’/3’-nucleotidase SurE | |38 |Divalent metal cation transporter MntH | |39 |Orange carotenoid-binding protein | |40 |Glucose 1-dehydrogenase | |41 |putative zinc-binding alcohol dehydrogenase | |43 |Cocaine esterase | |44 |Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB | |45 |8-oxoguanine deaminase | |46 |Serine/threonine-protein kinase PknD | |47 |Endoribonuclease MazF9 | |48 |Ribose-5-phosphate isomerase A | |49 |Deoxyhypusine synthase-like protein | |50 |Cobalt-precorrin-5B C(1)-methyltransferase | |51 |Precorrin-6A reductase | |52 |D-alanyl-D-alanine dipeptidase | |53 |IS1 family transposase ISNpu9 | |54 |IS1 family transposase ISMae3 | |55 |Putative nucleoside permease NupX | |56 |Squalene–hopene cyclase | |57 |RNA polymerase sigma factor SigA2 | |58 |Polyamine aminopropyltransferase | |59 |S-adenosylmethionine decarboxylase proenzyme | |60 |Serine/threonine-protein kinase B | |62 |Glucose/mannose transporter GlcP | |63 |Octanoyltransferase | |64 |Ribosome hibernation promotion factor | |65 |Outer membrane protein A | |66 |tRNA-specific adenosine deaminase | |67 |Transcriptional regulatory protein LnrK | |69 |Gamma-glutamyl-hercynylcysteine sulfoxide hydrolase | |70 |Ammonia channel | |71 |Magnesium-protoporphyrin O-methyltransferase | |72 |N-acetylglucosamine-6-phosphate deacetylase | |73 |N5-carboxyaminoimidazole ribonucleotide mutase | |75 |4-hydroxy-3-methylbut-2-enyl diphosphate reductase | |76 |Ammonium transporter | |78 |S-adenosylmethionine synthase | |79 |Phosphoribulokinase | |80 |Ferredoxin–NADP reductase | |81 |Homoserine dehydrogenase | |82 |Fructose-1 | |83 |6-bisphosphatase class 1 | |84 |Transaldolase | |85 |Glucose-6-phosphate 1-dehydrogenase | |86 |Cobyrinate a | |87 |c-diamide synthase | |88 |Translation initiation factor IF-3 | |89 |CRISPR-associated exonuclease Cas4 | |90 |CRISPR-associated exonuclease Cas4/endonuclease Cas1 fusion | |91 |CRISPR-associated endoribonuclease Cas2 | |92 |IS4 family transposase IS8402 | |93 |IS630 family transposase ISAcma28 | |95 |tRNA 5-hydroxyuridine methyltransferase | |96 |putative adenylyl-sulfate kinase | |97 |Endonuclease V | |98 |Ubiquinone biosynthesis O-methyltransferase | |99 |mitochondrial | |100 |Vitamin B12 import ATP-binding protein BtuD | |101 |Thiol:disulfide interchange protein DsbD | |102 |Cytochrome c biogenesis protein CcsB | |103 |NADPH-dependent 7-cyano-7-deazaguanine reductase | |104 |Protein translocase subunit SecA | |105 |2-methoxy-6-polyprenyl-1 | |106 |4-benzoquinol methylase | |108 |Bifunctional riboflavin kinase/FMN adenylyltransferase | |109 |Ribonuclease BN | |110 |5’-nucleotidase SurE | |111 |Phenylalanine–tRNA ligase alpha subunit | |113 |ATP-dependent RNA helicase DbpA | |114 |2-isopropylmalate synthase | |116 |3-mercaptopyruvate sulfurtransferase | |117 |tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC | |119 |Bifunctional protein GlmU | |120 |Isoaspartyl peptidase/L-asparaginase | |121 |Dihydroorotate dehydrogenase (quinone) | |122 |Corrinoid adenosyltransferase | |123 |1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase | |124 |Serine/threonine exchanger SteT | |125 |23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD | |126 |Alkaline phosphatase synthesis transcriptional regulatory protein SphR | |127 |Sensor protein SphS | |128 |Phosphate-specific transport system accessory protein PhoU | |129 |Regulatory protein CysR | |130 |putative protein | |133 |Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase | |134 |FO synthase | |135 |Photosystem II lipoprotein Psb27 | |136 |putative protein YqgN | |137 |GDP-L-fucose synthase | |138 |GDP-mannose 4 | |139 |6-dehydratase | |140 |D-inositol-3-phosphate glycosyltransferase | |141 |Ribonuclease H | |142 |CDP-diacylglycerol–glycerol-3-phosphate 3-phosphatidyltransferase | |143 |Aspartate ammonia-lyase | |144 |Aliphatic amidase expression-regulating protein | |145 |High-affinity branched-chain amino acid transport system permease protein LivH | |146 |Lipopolysaccharide export system ATP-binding protein LptB | |148 |Putative transport protein | |149 |Bifunctional protein FolD protein | |150 |Farnesyl diphosphate synthase | |151 |Ycf54-like protein | |152 |Pyridoxine 5’-phosphate synthase | |153 |Glutathione import ATP-binding protein GsiA | |154 |Glutaminase 1 | |155 |Endolytic peptidoglycan transglycosylase RlpA | |156 |Bifunctional pantoate ligase/cytidylate kinase | |157 |N-acetylmuramic acid 6-phosphate etherase | |158 |CRISPR system Cms protein Csm4 | |159 |CRISPR system Cms endoribonuclease Csm3 | |160 |putative UbiX-like flavin prenyltransferase | |162 |ATP-dependent Clp protease proteolytic subunit | |163 |putative molybdenum cofactor guanylyltransferase | |164 |Acetolactate synthase small subunit | |165 |Putative pterin-4-alpha-carbinolamine dehydratase | |166 |Dihydroanticapsin 7-dehydrogenase | |167 |N-acetylcysteine deacetylase | |168 |ATP-dependent dethiobiotin synthetase BioD 1 | |170 |Ribose-phosphate pyrophosphokinase | |171 |putative beta-lactamase YbxI | |172 |Chloride/fluoride channel protein | |174 |DNA gyrase subunit A | |175 |Apolipoprotein N-acyltransferase | |176 |Alkaline phosphatase D | |178 |2-succinyl-6-hydroxy-2 | |179 |4-cyclohexadiene-1-carboxylate synthase | |180 |Endo-1 | |181 |4-beta-xylanase Z | |182 |Phosphatidylglycerol lysyltransferase | |183 |Trehalose transport system permease protein SugB | |184 |Oligosaccharides import ATP-binding protein MsmX | |186 |putative manganese catalase | |188 |Bis(5’-nucleosyl)-tetraphosphatase | |189 |symmetrical | |192 |Isopentenyl-diphosphate delta-isomerase | |193 |Protease 4 | |194 |DNA primase | |195 |Pullulanase | |196 |Dihydrolipoyl dehydrogenase | |197 |Indole-3-glycerol phosphate synthase | |199 |Glutathione transport system permease protein GsiC | |200 |Adenine phosphoribosyltransferase | |201 |Biosynthetic peptidoglycan transglycosylase | |202 |Lipoprotein signal peptidase | |203 |Phosphate transport system permease protein PstC | |204 |Phosphate transport system permease protein PstA | |205 |Phosphate import ATP-binding protein PstB 3 | |207 |Peptidoglycan-associated lipoprotein | |208 |putative transporter | |209 |Bicarbonate transport ATP-binding protein CmpD | |210 |Glutamate/aspartate import solute-binding protein | |211 |Zinc-transporting ATPase | |212 |3’ | |213 |5’-cyclic adenosine monophosphate phosphodiesterase CpdA | |214 |Phosphoadenosine phosphosulfate reductase | |215 |Tyrocidine synthase 3 | |217 |Glucose 1-dehydrogenase 1 | |220 |Sulfur carrier protein FdhD | |221 |Cell division coordinator CpoB | |222 |Sugar fermentation stimulation protein A | |223 |Aldehyde dehydrogenase | |224 |thermostable | |225 |2-iminobutanoate/2-iminopropanoate deaminase | |226 |4-alpha-glucanotransferase | |227 |Lipopolysaccharide core heptosyltransferase RfaQ | |228 |2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | |229 |Segregation and condensation protein B | |230 |Putative serine protease HhoB | |231 |4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin) | |232 |phosphoglycerate mutase GpmB | |233 |Glucokinase | |234 |Lysine–tRNA ligase | |235 |putative transcriptional regulatory protein | |236 |Ubiquinone hydroxylase UbiL | |237 |Ion-translocating oxidoreductase complex subunit D | |238 |Peptidoglycan-N-acetylglucosamine deacetylase | |239 |Proton extrusion protein PcxA | |240 |tRNA-Thr(tgt) | |241 |Ornithine carbamoyltransferase | |242 |Transcription regulator LexA | |243 |4-diphosphocytidyl-2-C-methyl-D-erythritol kinase | |244 |Ribosomal RNA small subunit methyltransferase A | |245 |Argininosuccinate synthase | |246 |30S ribosomal protein S6 | |247 |Serine hydroxymethyltransferase | |248 |Putative competence-damage inducible protein | |249 |Glutamate 5-kinase | |250 |HTH-type transcriptional regulator BetI | |251 |Photosystem I iron-sulfur center | |252 |Glutamine–fructose-6-phosphate aminotransferase [isomerizing] | |253 |putative alcohol dehydrogenase AdhA | |255 |Carbonic anhydrase | |257 |Putative non-heme bromoperoxidase BpoC | |258 |Formamidase | |259 |4 | |260 |4’-diapolycopene aldehyde oxidase | |261 |Histidine–tRNA ligase | |262 |3-keto-5-aminohexanoate cleavage enzyme | |264 |RutC family protein YjgH | |265 |Allantoinase | |266 |Putative NADP-dependent oxidoreductase YfmJ | |268 |Xaa-Pro aminopeptidase | |271 |Protein DedA | |272 |Deaminated glutathione amidase | |273 |Phosphopantetheine adenylyltransferase | |274 |Phosphatidylglycerol–prolipoprotein diacylglyceryl transferase | |275 |Cobalt-precorrin-4 C(11)-methyltransferase | |276 |putative flavin reductase | |277 |putative dual-specificity RNA methyltransferase RlmN | |278 |UvrABC system protein C | |279 |Polar-differentiation response regulator DivK | |280 |Secreted effector protein PipB2 | |281 |HTH-type transcriptional regulator BenM | |282 |Dihydroxy-acid dehydratase | |283 |[Ribosomal protein S18]-alanine N-acetyltransferase | |284 |Galactitol 2-dehydrogenase | |285 |IS701 family transposase ISAcma37 | |287 |Putative universal stress protein | |288 |K(+)/H(+) antiporter NhaP | |289 |putative nicotinate-nucleotide pyrophosphorylase [carboxylating] | |290 |putative glycerol-3-phosphate dehydrogenase 2 [NAD(P)+] | |291 |ATP-dependent zinc metalloprotease FtsH 2 | |292 |Glutamate–tRNA ligase | |293 |tRNA-Asp(gtc) | |294 |Protein YeeZ | |295 |Chaperone protein DnaJ | |296 |Phospho-2-dehydro-3-deoxyheptonate aldolase | |298 |23S ribosomal RNA | |299 |tRNA-Ala(tgc) | |300 |16S ribosomal RNA | |301 |(S)-ureidoglycine–glyoxylate transaminase | |303 |Outer membrane protein assembly factor BamA | |304 |Photosystem I assembly protein Ycf3 | |305 |putative diguanylate cyclase DgcE | |306 |Anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase | |307 |Peptide methionine sulfoxide reductase MsrB | |308 |Formylglycine-generating enzyme | |309 |N-acetylgalactosamine-6-O-sulfatase | |311 |Chromosome partition protein Smc | |312 |Peroxiredoxin | |313 |Co-chaperone protein DjlA | |314 |Bacterial dynamin-like protein | |317 |Putative cystathionine beta-synthase | |318 |Ferredoxin | |319 |2Fe-2S | |320 |Putative cytochrome P450 135B1 | |327 |Heterocyst differentiation ATP-binding protein HepA | |328 |dTDP-4-dehydrorhamnose 3 | |329 |5-epimerase | |330 |ADP-L-glycero-D-manno-heptose-6-epimerase | |331 |L-2-hydroxyglutarate dehydrogenase | |332 |Glucose-1-phosphate cytidylyltransferase | |334 |Serine/threonine-protein phosphatase 3 | |336 |Phenylalanine–tRNA ligase beta subunit | |337 |Modification methylase DpnIIA | |338 |N-(5’-phosphoribosyl)anthranilate isomerase | |339 |Carboxyvinyl-carboxyphosphonate phosphorylmutase | |341 |UDP-N-acetylmuramoyl-L-alanyl-D-glutamate–2 | |342 |6-diaminopimelate ligase | |343 |Ribonuclease D | |344 |Thiosulfate sulfurtransferase GlpE | |345 |D-erythronate 4-phosphate dehydrogenase | |346 |Cytochrome b6-f complex subunit 7 | |347 |NAD kinase | |348 |Response regulator MprA | |350 |50S ribosomal protein L35 | |351 |50S ribosomal protein L20 | |352 |ABC transporter glutamine-binding protein GlnH | |353 |Penicillin-binding protein 4\* | |354 |Light-independent protochlorophyllide reductase subunit B | |355 |Aerobic cobaltochelatase subunit CobN | |356 |Phosphoglycerate kinase | |358 |Tryptophan synthase alpha chain | |359 |NAD(P)H-quinone oxidoreductase subunit L | |360 |Pyridinium-3 | |361 |5-bisthiocarboxylic acid mononucleotide nickel insertion protein | |362 |putative protein YciO | |363 |Ribosome-binding factor A | |364 |Magnetosome protein MamM | |366 |Phytochrome-like protein cph1 | |367 |Sporulation initiation inhibitor protein Soj | |372 |Threonine synthase | |373 |GTP 3’ | |374 |8-cyclase | |376 |Putative gamma-glutamylcyclotransferase YkqA | |377 |Methanethiol oxidase | |378 |Glutathione-regulated potassium-efflux system protein KefB | |379 |Maltogenic alpha-amylase | |380 |Hybrid peroxiredoxin hyPrx5 | |381 |Phosphate-import ATP-binding protein PhnC | |382 |putative ABC transporter phosphite binding protein PhnD1 | |383 |Protease HtpX | |384 |UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 | |385 |tRNA-Leu(cag) | |386 |23S rRNA (uridine(2479)-2’-O)-methyltransferase | |387 |Lipid II isoglutaminyl synthase (glutamine-hydrolyzing) subunit MurT | |388 |Serine acetyltransferase | |389 |S-methyl-5’-thioadenosine phosphorylase | |391 |putative FAD-linked oxidoreductase | |393 |Macrolide export ATP-binding/permease protein MacB | |394 |tRNA dimethylallyltransferase | |395 |DNA gyrase subunit B | |396 |RNA polymerase sigma factor RpoD | |400 |Multidrug resistance protein MdtA | |402 |putative multidrug ABC transporter permease YbhR | |403 |putative multidrug ABC transporter permease YbhS | |404 |putative multidrug ABC transporter ATP-binding protein YbhF | |405 |Colistin resistance protein EmrA | |406 |putative ABC transporter ATP-binding protein YknY | |411 |Phosphoglycolate phosphatase | |412 |Epoxyqueuosine reductase | |415 |Anti-sigma F factor | |416 |Regulator of RpoS | |417 |Transcriptional regulatory protein LiaR | |418 |N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase | |422 |Beta-barrel assembly-enhancing protease | |425 |Virginiamycin A acetyltransferase | |426 |Urease accessory protein UreE | |427 |Urease accessory protein UreF | |428 |Acetyltransferase | |430 |putative ABC transporter ATP-binding protein | |431 |Tol-Pal system protein TolQ | |432 |Tol-Pal system protein TolR | |433 |Mercuric reductase | |434 |N-acetyl-alpha-D-glucosaminyl L-malate synthase | |436 |Nitrate import permease protein NrtB | |437 |tRNA-Val(tac) | |438 |Alcohol dehydrogenase | |439 |tRNA-Thr(cgt) | |441 |30S ribosomal protein S20 | |442 |D-aminoacyl-tRNA deacylase | |443 |DNA-directed RNA polymerase subunit beta | |444 |DNA-directed RNA polymerase subunit beta’ | |446 |Histidinol dehydrogenase | |447 |Polyphosphate kinase | |448 |Oxygen regulatory protein NreC | |449 |Protein-glutamate methylesterase/protein-glutamine glutaminase | |451 |Sporulation-control protein spo0M | |452 |RNA polymerase-associated protein RapA | |453 |Polyribonucleotide nucleotidyltransferase | |456 |protein kinase UbiB | |457 |malonic semialdehyde reductase RutE | |458 |Cis-3-alkyl-4-alkyloxetan-2-one decarboxylase | |459 |Glycine oxidase | |460 |Putative epoxidase LasC | |462 |Superoxide dismutase [Fe] | |464 |Uracil phosphoribosyltransferase | |465 |GTP cyclohydrolase-2 | |466 |RNA 3’-terminal phosphate cyclase | |473 |Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase | |474 |Voltage-gated ClC-type chloride channel ClcB | |475 |HTH-type transcriptional regulator IscR | |476 |Cobalamin biosynthesis protein CobD | |477 |Bifunctional protein PyrR | |479 |Haloalkane dehalogenase | |480 |Photosystem II reaction center Psb28 protein | |481 |tRNA (cytidine/uridine/adenosine-2’-O-)-methyltransferase TrmJ | |482 |Protease HtpX | |483 |Aspartate–tRNA ligase | |484 |Putative tyrosine-protein kinase in cps region | |486 |CDP-paratose 2-epimerase | |487 |UDP-N-acetyl-D-mannosaminuronic acid transferase | |491 |Sucrose synthase | |494 |Phosphoserine aminotransferase | |498 |Calcium-transporting ATPase 1 | |499 |Chemotaxis protein methyltransferase | |507 |Phosphate-binding protein PstS | |508 |5-methylthioadenosine/S-adenosylhomocysteine deaminase | |510 |Transcriptional regulatory protein TcrA | |512 |Glutathione biosynthesis bifunctional protein GshAB | |513 |Cyanophycinase | |514 |Tol-Pal system protein TolB | |515 |Chaperone protein dnaK2 | |516 |Spore protein SP21 | |517 |ATP-dependent zinc metalloprotease FtsH 4 | |520 |NAD(P)H-quinone oxidoreductase subunit K 1 | |526 |Lipopolysaccharide assembly protein B | |528 |High-affinity Na(+)/H(+) antiporter NhaS3 | |529 |Efflux pump membrane transporter BepE | |531 |Tyrosine phenol-lyase | |532 |3-phenylpropionate/cinnamic acid dioxygenase ferredoxin subunit | |533 |Protein CbbY | |534 |Galactokinase | |535 |1-carboxybiuret hydrolase subunit AtzE | |536 |Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta | |537 |Prepilin peptidase PppA | |538 |3-isopropylmalate dehydrogenase | |539 |Bacitracin transport ATP-binding protein BcrA | |540 |Putative multidrug resistance protein MdtD | |541 |IS200/IS605 family transposase ISAsp19 | |542 |Succinate–CoA ligase [ADP-forming] subunit alpha | |543 |putative iron export permease protein FetB | |544 |dTDP-3-amino-3 | |546 |6-trideoxy-alpha-D-glucose transaminase | |547 |Cytochrome b559 subunit beta | |548 |Cytochrome b559 subunit alpha | |549 |Ycf48-like protein | |550 |Anaerobic nitric oxide reductase flavorubredoxin | |551 |NAD(P)H-quinone oxidoreductase subunit 3 | |553 |NAD(P)H-quinone oxidoreductase subunit J | |557 |30S ribosomal protein S15 | |559 |Cyclohexadienyl dehydrogenase | |560 |Undecaprenyl-diphosphatase | |564 |Protein SrpB | |565 |Glycogen phosphorylase | |566 |S-formylglutathione hydrolase | |567 |7-carboxy-7-deazaguanine synthase | |569 |Isonitrile hydratase | |570 |HTH-type transcriptional regulator MalT | |572 |Linear gramicidin dehydrogenase LgrE | |573 |Selenide | |574 |water dikinase | |575 |6-carboxy-5 | |576 |6 | |577 |7 | |578 |8-tetrahydropterin synthase | |582 |Protein Thf1 | |583 |Phycocyanobilin lyase CpcT | |584 |Oxygen-dependent coproporphyrinogen-III oxidase | |585 |Iron-sulfur cluster carrier protein | |586 |putative peptidoglycan glycosyltransferase FtsW | |590 |UDP-glucose 4-epimerase | |591 |UDP-glucose 6-dehydrogenase TuaD | |592 |HTH-type transcriptional activator RhaR | |594 |Alkaline phosphatase synthesis transcriptional regulatory protein PhoP | |595 |Protein PatA | |597 |tRNA(Ile)-lysidine synthase | |598 |Cytochrome c biogenesis protein CcsA | |599 |Carbon dioxide-concentrating mechanism protein CcmK | |600 |Carbon dioxide-concentrating mechanism protein CcmK | |601 |Cyclic AMP receptor protein | |602 |Rubredoxin | |604 |2-phosphosulfolactate phosphatase | |608 |Transketolase | |611 |Putative lipid kinase BmrU | |612 |3-dehydroquinate synthase | |613 |Superoxide dismutase [Cu-Zn] | |614 |Biotin synthase | |615 |[Ribosomal protein S5]-alanine N-acetyltransferase | |616 |Protein adenylyltransferase SelO | |618 |Cell division topological specificity factor | |619 |Septum site-determining protein MinD | |620 |septum site-determining protein MinC | |621 |Glutamate dehydrogenase | |622 |Apocarotenoid-15 | |623 |15’-oxygenase | |624 |Folate-biopterin transporter | |625 |3-oxoacyl-[acyl-carrier-protein] synthase 2 | |626 |Photosystem I assembly protein Ycf4 | |627 |Photosystem II D2 protein | |628 |Photosystem II CP43 reaction center protein | |630 |Putative ribosomal N-acetyltransferase YdaF | |634 |N-ethylmaleimide reductase | |635 |putative HTH-type transcriptional regulator | |636 |Anaerobic regulatory protein | |637 |Exoenzyme S synthesis regulatory protein ExsA | |638 |Bifunctional ligase/repressor BirA | |639 |Riboflavin synthase | |641 |Menaquinone reductase | |642 |Ribosome-recycling factor | |643 |Uridylate kinase | |644 |(E)-2-((N-methylformamido)methylene)succinate hydrolase | |645 |Polyisoprenyl-teichoic acid–peptidoglycan teichoic acid transferase TagU | |646 |Ribulose-phosphate 3-epimerase | |648 |Multidrug resistance protein EbrB | |649 |Beta-hexosaminidase | |651 |Trans-2 | |652 |3-dihydro-3-hydroxyanthranilate isomerase | |653 |15-cis-phytoene desaturase | |654 |15-cis-phytoene synthase | |655 |tRNA-Ser(gct) | |656 |Aerobic respiration control sensor protein ArcB | |657 |Dodecaprenyl-phosphate galacturonate synthase | |658 |DNA mismatch repair protein MutL | |660 |Adenosine deaminase | |663 |Adenylosuccinate synthetase | |665 |Ferredoxin-thioredoxin reductase | |666 |variable chain | |667 |Protein QmcA | |668 |Zinc uptake regulation protein | |669 |Phosphoribosylformylglycinamidine synthase subunit PurS | |670 |Phosphoribosylformylglycinamidine synthase subunit PurQ | |671 |GTPase HflX | |672 |putative glutaredoxin | |673 |Glutathione synthetase | |674 |Cell division protein FtsZ | |675 |Cell division protein FtsQ | |676 |Photosystem II manganese-stabilizing polypeptide | |677 |RNA polymerase sigma-F factor | |679 |4-alpha-glucan branching enzyme | |680 |Small ribosomal subunit biogenesis GTPase RsgA | |682 |Chaperone protein DnaK | |683 |Protein GrpE | |684 |Twitching mobility protein | |685 |Type II secretion system protein F | |686 |Endonuclease MutS2 | |687 |putative oxidoreductase/MSMEI\_1564 | |688 |Thioredoxin 1 | |689 |IS701 family transposase ISNpu6 | |690 |Thiol-disulfide oxidoreductase ResA | |692 |Glucose-1-phosphate adenylyltransferase | |693 |Peptide deformylase | |694 |Cell division protein FtsX | |695 |Leucyl/phenylalanyl-tRNA–protein transferase | |696 |30S ribosomal protein S14 | |697 |Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase | |698 |2-haloacrylate reductase | |700 |Signal recognition particle receptor FtsY | |701 |Transcription antitermination protein NusB | |703 |Chaperone protein HtpG | |704 |Chaperone protein ClpB 1 | |706 |Lactoylglutathione lyase | |707 |Mitomycin biosynthesis 6-O-methyltransferase | |708 |Oxygen-dependent choline dehydrogenase | |711 |ATP-dependent RNA helicase RhlE | |712 |Thiamine-monophosphate kinase | |713 |Glyceraldehyde-3-phosphate dehydrogenase 2 | |714 |Nicotinate-nucleotide adenylyltransferase | |715 |UDP-N-acetylmuramate–L-alanine ligase | |716 |UDP-N-acetylenolpyruvoylglucosamine reductase | |717 |Thioredoxin-like protein | |718 |Nitrate import ATP-binding protein NrtD | |719 |Putative aliphatic sulfonates transport permease protein SsuC | |721 |Hydrogenase maturation factor HypB | |722 |Hydrogenase maturation factor HypA | |723 |Agmatinase | |724 |putative cytosol aminopeptidase | |725 |Selenocysteine-containing peroxiredoxin PrxU | |726 |tRNA-Met(cat) | |727 |tRNA (cytidine(34)-2’-O)-methyltransferase | |728 |Glutamate–cysteine ligase | |729 |Acetoin utilization protein AcuC | |730 |UvrABC system protein A | |733 |Histidine decarboxylase | |734 |Urease subunit alpha | |735 |Urease subunit beta 1 | |736 |Urease subunit gamma | |737 |Urease accessory protein UreD | |740 |Photosystem II protein D1 2 | |741 |Photosystem II protein D1 1 | |742 |Phosphoenolpyruvate carboxylase | |745 |tRNA-Arg(tct) | |746 |2-hydroxy-6-oxo-2 | |747 |4-heptadienoate hydrolase | |748 |Branched-chain-amino-acid aminotransferase | |750 |Putative cytochrome P450 135A1 | |751 |Modification methylase HaeIII | |752 |Deoxyribose-phosphate aldolase 2 | |753 |DNA repair protein RecO | |755 |Recombination protein RecR | |756 |ABC transporter ATP-binding/permease protein YojI | |757 |Aurachin B dehydrogenase | |758 |3-oxoacyl-[acyl-carrier-protein] synthase 3 | |759 |Polyketide biosynthesis protein PksE | |760 |p-hydroxybenzoic acid efflux pump subunit AaeA | |761 |Lipoprotein-releasing system ATP-binding protein LolD | |765 |Bifunctional homocysteine S-methyltransferase/5 | |766 |10-methylenetetrahydrofolate reductase | |767 |Tryptophan–tRNA ligase | |771 |LPS-assembly protein LptD | |772 |Photosystem II reaction center protein I | |773 |ATP-dependent DNA helicase RecQ | |774 |Long-chain-fatty-acid–CoA ligase FadD15 | |775 |Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex | |776 |FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase | |777 |Putative xanthine dehydrogenase molybdenum-binding subunit XdhA | |778 |Autoinducer 2 import ATP-binding protein LsrA | |781 |Purine-binding protein | |782 |Lactose transport system permease protein LacF | |783 |Phosphoribosylglycinamide formyltransferase | |784 |Glutathione transferase FosA | |785 |Ferredoxin-1 | |786 |Aconitate hydratase B | |791 |tRNA-Ile(gat) | |793 |IS200/IS605 family transposase ISNsp2 | |796 |Glucosamine kinase | |797 |Glycogen operon protein GlgX | |798 |Malto-oligosyltrehalose trehalohydrolase | |799 |Hopanoid C-2 methylase | |803 |Phycocyanobilin:ferredoxin oxidoreductase | |804 |DNA polymerase III subunit alpha | |805 |Aerobic C4-dicarboxylate transport protein | |806 |DNA repair protein RecN | |810 |Response regulator rcp1 | |813 |2-(acetamidomethylene)succinate hydrolase | |814 |DNA polymerase III PolC-type | |815 |Cytochrome b6-f complex subunit 8 | |816 |ATP-dependent zinc metalloprotease FtsH | |817 |Membrane protein insertase YidC | |818 |Ribonuclease P protein component | |819 |50S ribosomal protein L34 | |820 |NAD(P) transhydrogenase subunit alpha part 1 | |821 |NAD(P) transhydrogenase subunit alpha | |822 |NAD(P) transhydrogenase subunit beta | |823 |Putative glutamine amidotransferase YafJ | |824 |Light-independent protochlorophyllide reductase iron-sulfur ATP-binding protein | |825 |Light-independent protochlorophyllide reductase subunit N | |826 |Lactococcin-G-processing and transport ATP-binding protein LagD | |827 |Hemolysin secretion protein D | |828 |chromosomal | |831 |NADH-quinone oxidoreductase subunit K | |832 |NAD(P)H-quinone oxidoreductase subunit I | |833 |NAD(P)H-quinone oxidoreductase subunit 1 | |834 |Citrate synthase | |835 |Alanine racemase 2 | |836 |tRNA-Leu(tag) | |837 |Glutamate-1-semialdehyde 2 | |838 |1-aminomutase | |839 |putative amino acid permease YhdG | |845 |Multidrug resistance protein Stp | |846 |Maltodextrin phosphorylase | |847 |Pyruvate kinase | |852 |Transcriptional regulatory protein WalR | |853 |Signal peptidase I T | |854 |Dihydroorotase | |855 |Fructose-bisphosphate aldolase class 1 | |856 |Aspartate aminotransferase | |857 |N5-carboxyaminoimidazole ribonucleotide synthase | |858 |putative zinc protease | |860 |Cobalt-precorrin-5A hydrolase | |861 |Phosphocholine transferase AnkX | |862 |putative sugar epimerase YhfK | |865 |Xylulose-5-phosphate phosphoketolase | |866 |Polyphosphate:ADP phosphotransferase | |867 |Phosphoglucomutase | |868 |Metalloprotease TldD | |869 |Putative monooxygenase | |870 |Methylthioribulose-1-phosphate dehydratase | |871 |2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase | |872 |Acireductone dioxygenase | |873 |Peptidoglycan D | |874 |D-transpeptidase MrdA | |875 |Fe/S biogenesis protein NfuA | |877 |Elongation factor 4 | |878 |Aminoglycoside N(6’)-acetyltransferase type 1 | |880 |Serine/threonine-protein kinase A | |883 |NAD(P)H-quinone oxidoreductase subunit 2 | |884 |chloroplastic | |885 |Protein-methionine-sulfoxide reductase heme-binding subunit MsrQ | |886 |ATP phosphoribosyltransferase regulatory subunit | |888 |Inositol-1-monophosphatase | |889 |Urease accessory protein UreG | |893 |O-acetylserine sulfhydrylase | |894 |Linear gramicidin synthase subunit D | |895 |Flavin-dependent trigonelline monooxygenase | |896 |oxygenase component | |897 |Linear gramicidin synthase subunit B | |900 |Alkanal monooxygenase alpha chain | |902 |Aspartate 1-decarboxylase | |903 |Phthiocerol synthesis polyketide synthase type I PpsE | |904 |Polyketide synthase PksL | |908 |Trans-aconitate 2-methyltransferase | |909 |D-alanine–D-alanyl carrier protein ligase | |913 |Multidrug export protein MepA | |914 |Protein MbtH | |915 |3-phenylpropionate-dihydrodiol/cinnamic acid-dihydrodiol dehydrogenase | |917 |putative siderophore-binding lipoprotein YfiY | |918 |Vitamin B12 transporter BtuB | |919 |Acyl carrier protein | |920 |Glutaryl-7-aminocephalosporanic-acid acylase | |921 |putative siderophore transport system permease protein YfiZ | |922 |putative siderophore transport system permease protein YfhA | |925 |putative siderophore transport system ATP-binding protein YusV | |926 |Glutamine transport ATP-binding protein GlnQ | |927 |Glutamine transport system permease protein GlnP | |928 |Ferrous iron permease EfeU | |929 |Cell division protein FtsP | |930 |Cobalt transport protein CbiM | |931 |Cadmium | |932 |cobalt and zinc/H(+)-K(+) antiporter | |933 |Cobalt transport protein CbiN | |934 |Cobalt transport protein CbiQ | |935 |Energy-coupling factor transporter ATP-binding protein EcfA3 | |937 |Maltose/maltodextrin import ATP-binding protein MalK | |938 |Ycf53-like protein | |940 |Isocitrate dehydrogenase [NADP] | |941 |Anthranilate synthase component 1 | |942 |Photosystem I reaction center subunit II | |944 |Glycogen synthase | |945 |Threonine–tRNA ligase | |946 |NAD(P)H-quinone oxidoreductase chain 4 1 | |947 |Homoserine kinase | |948 |Metallothiol transferase FosB | |950 |GDP-mannose-dependent alpha-mannosyltransferase | |951 |Phosphoribosylaminoimidazole-succinocarboxamide synthase | |953 |UDP-3-O-acyl-N-acetylglucosamine deacetylase | |954 |3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ | |955 |Acyl-[acyl-carrier-protein]–UDP-N-acetylglucosamine O-acyltransferase | |956 |Lipid-A-disaccharide synthase | |957 |ABC transporter ATP-binding protein YtrE | |959 |Histidine biosynthesis bifunctional protein HisB | |960 |Enoyl-[acyl-carrier-protein] reductase [NADH] FabI | |961 |Global nitrogen regulator | |962 |tRNA-Gly(gcc) | |963 |Protease PrtS | |964 |Vitamin B12-binding protein | |966 |Putative multidrug export ATP-binding/permease protein | |968 |1-pyrroline-5-carboxylate dehydrogenase | |972 |Linearmycin resistance ATP-binding protein LnrL | |973 |High-affinity branched-chain amino acid transport ATP-binding protein LivF | |974 |Elongation factor G | |976 |Glycerol kinase | |979 |Exodeoxyribonuclease | |982 |L-threonine dehydratase biosynthetic IlvA | |983 |L-arabinose transport system permease protein AraQ | |988 |Superoxide dismutase [Mn] 2 | |991 |tRNA-Ser(cga) | |992 |Glycine–tRNA ligase alpha subunit | |997 |Ribosomal large subunit pseudouridine synthase E | |1000 |UDP-N-acetylglucosamine 4-epimerase | |1001 |Phosphoribosylamine–glycine ligase | |1005 |putative ABC transporter ATP-binding protein YbiT | |1006 |HTH-type transcriptional activator CmpR | |1007 |putative protein kinase UbiB | |1008 |Protein phosphatase PrpC | |1010 |Anhydro-N-acetylmuramic acid kinase | |1011 |N-acetyltransferase Eis | |1012 |putative inner membrane transporter YhbE | |1014 |Putative diflavin flavoprotein A 3 | |1015 |Putative diflavin flavoprotein A 5 | |1016 |Glutathione hydrolase proenzyme | |1021 |Cysteine/Cysteine sulfinic acid decarboxylase | |1022 |Carboxylesterase 2 | |1023 |Bifunctional purine biosynthesis protein PurH | |1025 |Ca(2+)/H(+) antiporter | |1026 |Phosphoribosylformylglycinamidine cyclo-ligase | |1029 |DNA-binding transcriptional activator DevR/DosR | |1030 |Multidomain esterase | |1031 |IS200/IS605 family transposase ISAsp13 | |1032 |Demethylmenaquinone methyltransferase | |1033 |UvrABC system protein B | |1034 |D-3-phosphoglycerate dehydrogenase | |1035 |Ribosomal protein L11 methyltransferase | |1036 |putative cytochrome c oxidase subunit 1 | |1037 |Na(+)/H(+) antiporter NhaG | |1040 |Trehalose synthase/amylase TreS | |1041 |Gluconolactonase | |1042 |6’’‘-hydroxyparomomycin C oxidase | |1043 |Zinc transporter ZupT | |1046 |Sulfate/thiosulfate import ATP-binding protein CysA | |1047 |HTH-type transcriptional regulator CysL | |1048 |putative oxidoreductase | |1049 |Cytochrome c6 | |1051 |putative protein YyaP | |1052 |N | |1053 |N-dimethyltransferase OxyT | |1055 |Tyrosine recombinase XerD | |1056 |Ribonucleoside-diphosphate reductase subunit beta | |1057 |putative cysteine-rich protein YhjQ | |1059 |Flavodoxin | |1061 |Nickel and cobalt resistance protein CnrA | |1065 |putative membrane transporter protein | |1066 |Beta-lactamase hydrolase-like protein | |1070 |Transcriptional regulatory protein SrrA | |1071 |Sensor histidine kinase TmoS | |1073 |4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnE | |1074 |Polyprenol monophosphomannose synthase | |1077 |tRNA-Ala(cgc) | |1078 |Beta-phosphoglucomutase | |1082 |RNA-splicing ligase RtcB | |1085 |GMP synthase [glutamine-hydrolyzing] | |1086 |Ribosome-binding ATPase YchF | |1087 |Arginine decarboxylase | |1088 |tRNA-dihydrouridine synthase B | |1090 |acetoacetate decarboxylase | |1091 |Ferredoxin-3 | |1092 |Cytochrome c oxidase subunit 1 | |1093 |putative cytochrome c oxidase subunit 3 | |1096 |ISAzo13 family transposase ISMae28 | |1098 |Kynurenine formamidase | |1100 |Anthranilate phosphoribosyltransferase 2 | |1101 |Carbamoyl-phosphate synthase small chain | |1102 |Anti-sigma-B factor antagonist | |1103 |Mini-ribonuclease 3 | |1104 |23S rRNA (guanosine-2’-O-)-methyltransferase RlmB | |1111 |Ribosomal RNA small subunit methyltransferase F | |1113 |Competence protein ComM | |1114 |Purine nucleoside phosphoramidase | |1115 |Photosystem II protein D1 3 | |1117 |3’-5’ exonuclease DinG | |1118 |Peroxide operon regulator | |1120 |Threonine-phosphate decarboxylase | |1121 |DNA-binding protein HU | |1122 |Type 3 secretion system secretin | |1123 |Folylpolyglutamate synthase | |1124 |Photosystem II protein Y | |1125 |Protein YrdA | |1127 |Methionine aminopeptidase 1 | |1129 |NADH-quinone oxidoreductase subunit L | |1132 |Carbon dioxide concentrating mechanism protein CcmL | |1133 |Carbon dioxide concentrating mechanism protein CcmM | |1136 |tRNA modification GTPase MnmE | |1137 |Energy-coupling factor transporter ATP-binding protein EcfA2 | |1138 |Virulence protein | |1139 |dTDP-fucosamine acetyltransferase | |1140 |Anhydromuropeptide permease | |1141 |UDP-N-acetylmuramoyl-tripeptide–D-alanyl-D-alanine ligase | |1142 |Fructokinase | |1143 |Thermoresistant gluconokinase | |1144 |HTH-type transcriptional regulator MtrA | |1145 |3-isopropylmalate dehydratase small subunit 1 | |1146 |3-isopropylmalate dehydratase large subunit | |1148 |S-adenosylmethionine:tRNA ribosyltransferase-isomerase | |1149 |Pentapeptide repeat protein Rfr32 | |1150 |Acyl-homoserine lactone acylase QuiP | |1151 |3-oxoacyl-[acyl-carrier-protein] reductase FabG | |1153 |DNA mismatch repair protein MutS | |1154 |tRNA-Ala(ggc) | |1156 |Curved DNA-binding protein | |1158 |Cyclic pyranopterin monophosphate synthase | |1159 |tRNA-Arg(acg) | |1160 |Staphylopine export protein | |1162 |ATP-dependent DNA helicase PcrA | |1163 |RecBCD enzyme subunit RecB | |1164 |tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase | |1165 |D-alanine–D-alanine ligase | |1166 |Tn3 family transposase ISNpu13 | |1167 |ISKra4 family transposase ISCep1 | |1168 |2-hydroxy-6-oxo-6-phenylhexa-2 | |1169 |4-dienoate hydrolase | |1171 |7-dimethyl-8-ribityllumazine synthase | |1172 |Photosystem II reaction center protein Z | |1173 |A-adding tRNA nucleotidyltransferase | |1174 |1-deoxy-D-xylulose-5-phosphate synthase | |1175 |Methylthioribose-1-phosphate isomerase | |1177 |Serine/threonine-protein kinase C | |1178 |50S ribosomal protein L7/L12 | |1179 |50S ribosomal protein L10 | |1180 |50S ribosomal protein L1 | |1181 |50S ribosomal protein L11 | |1182 |Transcription termination/antitermination protein NusG | |1183 |Protein translocase subunit SecE | |1184 |tRNA-Trp(cca) | |1185 |50S ribosomal protein L19 | |1188 |GTPase Der | |1189 |GTPase Era | |1190 |Multidrug resistance protein MdtB | |1191 |Macrolide export protein MacA | |1192 |Putative phycocyanobilin lyase CpcS 2 | |1195 |Type III pantothenate kinase | |1197 |Alkaline phosphatase H | |1199 |30S ribosomal protein S2 | |1200 |Elongation factor Ts | |1202 |ECF RNA polymerase sigma factor SigX | |1203 |ATP-dependent DNA helicase RecG | |1207 |Glycine dehydrogenase (decarboxylating) | |1208 |Glycine cleavage system H protein | |1209 |Aminomethyltransferase | |1211 |tRNA-Arg(ccg) | |1213 |Threonine–tRNA ligase 2 | |1214 |Methylenetetrahydrofolate–tRNA-(uracil-5-)-methyltransferase TrmFO | |1215 |putative HTH-type transcriptional regulator YxaF | |1216 |Proline iminopeptidase | |1217 |Pyrophosphate–fructose 6-phosphate 1-phosphotransferase | |1219 |Acetyl-coenzyme A synthetase | |1222 |CC-adding tRNA nucleotidyltransferase | |1224 |30S ribosomal protein S1 | |1225 |Photosystem II reaction center protein T | |1226 |Photosystem II CP47 reaction center protein | |1227 |Dipeptide transport system permease protein DppB | |1228 |Putative serine protease HtrA | |1229 |Transcriptional regulatory protein DegU | |1230 |Cholesterol oxidase | |1231 |Diaminopimelate epimerase | |1232 |tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG | |1237 |Molybdopterin synthase catalytic subunit | |1238 |Spore photoproduct lyase | |1239 |DNA-directed RNA polymerase subunit omega | |1240 |tRNA-Pro(ggg) | |1242 |4-alpha-glucan branching enzyme GlgB | |1243 |putative PIN and TRAM-domain containing protein YacL | |1244 |Heme chaperone HemW | |1245 |ATP-dependent Clp protease adapter protein ClpS | |1246 |Histidinol-phosphate aminotransferase | |1247 |Acetophenone carboxylase delta subunit | |1248 |Acetophenone carboxylase gamma subunit | |1249 |2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase | |1250 |Dihydroneopterin aldolase | |1251 |putative ABC transporter-binding protein | |1252 |Trehalose transport system permease protein SugA | |1253 |Phosphoglucosamine mutase | |1254 |Heme oxygenase 1 | |1255 |P-loop guanosine triphosphatase YjiA | |1256 |dCTP deaminase | |1258 |Adenylate kinase | |1259 |Ribonuclease PH | |1260 |6-phosphogluconolactonase | |1264 |8-methylmenaquinol:fumarate reductase membrane anchor subunit | |1268 |Multidrug resistance protein MdtC | |1270 |Spermidine/putrescine transport system permease protein PotB | |1271 |Spermidine/putrescine-binding periplasmic protein | |1272 |Spermidine/putrescine import ATP-binding protein PotA | |1275 |Glutamyl-tRNA reductase | |1276 |D-fructose 1 | |1277 |6-bisphosphatase class 2/sedoheptulose 1 | |1278 |7-bisphosphatase | |1280 |Calcium-dependent protease | |1281 |putative protein RP812 | |1282 |Glutaredoxin 4 | |1288 |Putative anti-sigma factor antagonist | |1289 |Ribonuclease E | |1290 |Ribonuclease HII | |1291 |Bifunctional chorismate mutase/prephenate dehydratase | |1292 |Lon protease 2 | |1293 |30S ribosomal protein S10 | |1294 |Elongation factor Tu | |1296 |30S ribosomal protein S7 | |1297 |30S ribosomal protein S12 | |1299 |Ferredoxin-dependent glutamate synthase 2 | |1300 |N-glycosidase | |1301 |Cysteine desulfuration protein SufE | |1302 |Photosystem I reaction center subunit PsaK | |1303 |4-hydroxy-tetrahydrodipicolinate reductase | |1304 |Cobalt-precorrin-8 methylmutase | |1305 |Ribosomal RNA small subunit methyltransferase G | |1306 |Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase | |1310 |Hydroxyacylglutathione hydrolase GloB | |1311 |50S ribosomal protein L9 | |1314 |F420-dependent glucose-6-phosphate dehydrogenase | |1316 |Porphobilinogen deaminase | |1318 |Putative peroxiredoxin bcp | |1319 |1-deoxy-D-xylulose 5-phosphate reductoisomerase | |1320 |Succinate dehydrogenase flavoprotein subunit | |1325 |Putative mycofactocin system creatinine amidohydrolase family protein MftE | |1326 |UV DNA damage endonuclease | |1328 |Putative KHG/KDPG aldolase | |1332 |ATP-dependent zinc metalloprotease FtsH 3 | |1334 |Demethyl-4-deoxygadusol synthase | |1342 |Formyltetrahydrofolate deformylase | |1344 |Sec-independent protein translocase protein TatC | |1345 |L-aspartate oxidase | |1346 |aspartoacylase | |1347 |Argininosuccinate lyase | |1349 |5-biscarboxylic acid mononucleotide synthase | |1351 |2-C-methyl-D-erythritol 2 | |1352 |4-cyclodiphosphate synthase | |1353 |tRNA (guanine-N(1)-)-methyltransferase | |1355 |Cyanophycin synthetase | |1356 |Sec-independent protein translocase protein TatAy | |1359 |Phytochrome-like protein cph2 | |1371 |D-ribulose kinase | |1372 |Photosystem I reaction center subunit XII | |1374 |Disulfide-bond oxidoreductase YfcG | |1375 |Uroporphyrinogen decarboxylase | |1376 |Protease 2 | |1377 |Maltose/maltodextrin-binding periplasmic protein | |1378 |putative murein peptide carboxypeptidase | |1381 |3-phosphoshikimate 1-carboxyvinyltransferase 1 | |1382 |GTP cyclohydrolase 1 type 2 | |1383 |Isopenicillin N epimerase | |1384 |Glycerol dehydrogenase | |1386 |Aquaporin Z | |1387 |Glutaredoxin arsenate reductase | |1388 |Ribonuclease 3 | |1390 |Putative phosphoesterase YjcG | |1392 |Adenylosuccinate lyase | |1394 |Putative cation transport regulator ChaB | |1403 |Ferrochelatase | |1404 |Bifunctional adenosylcobalamin biosynthesis protein CobP | |1408 |Ribonuclease Z | |1413 |Cation/acetate symporter ActP | |1414 |Quinone oxidoreductase 1 | |1417 |Glutathione amide reductase | |1420 |Response regulator PleD | |1424 |Molybdopterin molybdenumtransferase | |1426 |putative serine/threonine-protein kinase PkwA | |1430 |Plastocyanin | |1431 |Cytochrome c-550 | |1435 |Hemin transport system permease protein HmuU | |1436 |Bicarbonate transporter BicA | |1437 |NAD(P)H-quinone oxidoreductase subunit N | |1438 |50S ribosomal protein L3 | |1439 |50S ribosomal protein L4 | |1440 |50S ribosomal protein L2 | |1441 |30S ribosomal protein S19 | |1442 |50S ribosomal protein L22 | |1443 |30S ribosomal protein S3 | |1444 |50S ribosomal protein L16 | |1445 |30S ribosomal protein S17 | |1446 |50S ribosomal protein L14 | |1447 |50S ribosomal protein L24 | |1448 |50S ribosomal protein L5 | |1449 |30S ribosomal protein S8 | |1450 |50S ribosomal protein L6 | |1451 |50S ribosomal protein L18 | |1452 |30S ribosomal protein S5 | |1453 |50S ribosomal protein L15 | |1454 |Protein translocase subunit SecY | |1456 |Translation initiation factor IF-1 | |1457 |30S ribosomal protein S13 | |1458 |30S ribosomal protein S11 | |1459 |DNA-directed RNA polymerase subunit alpha | |1460 |50S ribosomal protein L17 | |1461 |tRNA pseudouridine synthase A | |1462 |50S ribosomal protein L13 | |1463 |30S ribosomal protein S9 | |1464 |50S ribosomal protein L31 | |1465 |Peptide chain release factor 1 | |1466 |putative signaling protein | |1467 |DNA base-flipping protein | |1468 |N(1)-aminopropylagmatine ureohydrolase | |1469 |Hca operon transcriptional activator HcaR | |1470 |Dephospho-CoA kinase | |1471 |Uroporphyrinogen-III C-methyltransferase | |1475 |Homogentisate phytyltransferase | |1476 |2-methyl-6-phytyl-1 | |1477 |4-hydroquinone methyltransferase | |1478 |Ktr system potassium uptake protein B | |1479 |Ktr system potassium uptake protein A | |1481 |Pyrimidine 5’-nucleotidase YjjG | |1482 |Demethylphylloquinone reductase NdbB | |1485 |Cysteine desulfurase IscS | |1486 |GTP-binding protein TypA/BipA | |1489 |catalytic chain | |1490 |Lipopolysaccharide export system protein LptA | |1492 |Putative cytochrome P450 120 | |1499 |Nucleoid-associated protein YbaB | |1500 |Putative low molecular weight protein-tyrosine-phosphatase | |1501 |Histidine N-alpha-methyltransferase | |1502 |Ketol-acid reductoisomerase (NADP(+)) | |1503 |Aldo-keto reductase IolS | |1504 |IS701 family transposase ISAcma24 | |1506 |ATP phosphoribosyltransferase | |1507 |Carboxy-S-adenosyl-L-methionine synthase | |1508 |Multidrug resistance protein NorM | |1510 |Cytochrome bd-I ubiquinol oxidase subunit 2 | |1511 |Cytochrome bd-II ubiquinol oxidase subunit 1 | |1512 |Epoxide hydrolase A | |1513 |HTH-type transcriptional activator RhaS | |1514 |DNA replication and repair protein RecF | |1515 |Calcium-transporting ATPase | |1516 |Malonyl CoA-acyl carrier protein transacylase | |1518 |Phosphate acyltransferase | |1519 |tRNA-Pyl(cta) | |1520 |Lipopolysaccharide export system protein LptC | |1521 |Methionine–tRNA ligase | |1522 |Putative aminoacrylate hydrolase RutD | |1523 |HTH-type transcriptional regulator GltC | |1524 |Alpha-hemolysin translocation ATP-binding protein HlyB | |1528 |D-alanyl-D-alanine carboxypeptidase | |1529 |Ribosomal RNA small subunit methyltransferase E | |1530 |Extracellular esterase EstB | |1531 |Kojibiose phosphorylase | |1534 |Poly-beta-1 | |1535 |6-N-acetyl-D-glucosamine synthase | |1536 |Histone deacetylase-like amidohydrolase | |1539 |2 | |1540 |3-bisphosphoglycerate-independent phosphoglycerate mutase | |1542 |Heat-inducible transcription repressor HrcA | |1545 |3 | |1547 |5-tetrahydropyridine-2 | |1548 |6-dicarboxylate N-acetyltransferase | |1550 |Transcriptional regulatory protein OmpR | |1552 |Pyridoxine/pyridoxamine 5’-phosphate oxidase | |1553 |Soluble epoxide hydrolase | |1556 |Diacetylchitobiose uptake system permease protein DasC | |1557 |Aldehyde decarbonylase | |1558 |Long-chain acyl-[acyl-carrier-protein] reductase | |1559 |Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha | |1561 |GTP cyclohydrolase 1 | |1565 |Putative zinc metalloprotease Rip3 | |1567 |Hydrogenase maturation factor HybF | |1568 |Carbamoyl dehydratase HypE | |1569 |Hydrogenase maturation factor HypD | |1570 |Hydrogenase maturation factor HybG | |1571 |Carbamoyltransferase HypF | |1573 |Periplasmic [NiFe] hydrogenase small subunit | |1574 |Periplasmic [NiFeSe] hydrogenase large subunit | |1575 |D-lactate dehydrogenase | |1576 |NADP-dependent 3-hydroxy acid dehydrogenase YdfG | |1577 |UDP-N-acetylglucosamine–N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase | |1578 |Acetylornithine aminotransferase | |1587 |Bicarbonate-binding protein CmpA | |1588 |Bicarbonate transport system permease protein CmpB | |1589 |Bicarbonate transport ATP-binding protein CmpC | |1593 |Heme oxygenase HutZ | |1594 |1-deoxyxylulose-5-phosphate synthase YajO | |1595 |DNA protection during starvation protein | |1598 |Quercetin 2 | |1599 |3-dioxygenase | |1606 |Hydrogenase 2 maturation protease | |1607 |Molybdenum-pterin-binding protein 2 | |1610 |Protoheme IX farnesyltransferase | |1612 |heterocyst | |1613 |Protein HesB | |1615 |Protein HesA | |1617 |Nitrogenase-stabilizing/protective protein NifW 2 | |1618 |Nitrogenase molybdenum-iron protein beta chain | |1619 |Nitrogenase molybdenum-iron protein alpha chain | |1622 |Nitrogenase iron protein | |1624 |Cysteine desulfurase NifS | |1625 |FeMo cofactor biosynthesis protein NifB | |1627 |Manganese ABC transporter substrate-binding lipoprotein | |1628 |Oxidoreductase UcpA | |1629 |Protein PsbN | |1630 |Photosystem II reaction center protein H | |1631 |Sec-independent protein translocase protein TatA | |1632 |Peptidyl-tRNA hydrolase | |1633 |30S ribosomal protein S21 A | |1634 |Ribosomal RNA small subunit methyltransferase I | |1635 |Sulfofructose kinase | |1636 |3’(2’) | |1637 |5’-bisphosphate nucleotidase CysQ | |1638 |Putative hydro-lyase | |1646 |Choline transport ATP-binding protein OpuBA | |1647 |Carnitine transport permease protein OpuCD | |1648 |Aminodeoxychorismate/anthranilate synthase component 2 | |1650 |DNA repair protein RadA | |1655 |Ribosome maturation factor RimP | |1656 |Transcription termination/antitermination protein NusA | |1657 |Translation initiation factor IF-2 | |1661 |Chaperone SurA | |1662 |Chorismate synthase | |1663 |Glyoxylate/hydroxypyruvate reductase B | |1665 |Protein MtfA | |1667 |Photosystem II 12 kDa extrinsic protein | |1668 |Adenosyl-chloride synthase | |1673 |L-propargylglycine–L-glutamate ligase | |1674 |General stress protein 39 | |1675 |Magnesium transporter MgtE | |1689 |dITP/XTP pyrophosphatase | |1690 |Nitrogen regulatory protein P-II | |1691 |Endonuclease III | |1692 |Metalloprotease MmpA | |1693 |Serine–tRNA ligase | |1695 |Nicotine blue oxidoreductase | |1698 |Dihydropteroate synthase | |1699 |Triosephosphate isomerase | |1700 |Phosphoenolpyruvate synthase | |1701 |putative dolichyl-phosphate-mannose–protein mannosyltransferase | |1705 |tRNA (guanine-N(7)-)-methyltransferase | |1709 |tRNA-Leu(gag) | |1710 |Biotin carboxylase | |1711 |Photosystem II reaction center X protein | |1714 |tRNA 5-carboxymethoxyuridine methyltransferase | |1715 |Riboflavin biosynthesis protein RibBA | |1716 |N-acetyl-gamma-glutamyl-phosphate reductase | |1717 |Enolase | |1718 |Putative HMP/thiamine import ATP-binding protein YkoD | |1719 |Energy-coupling factor transporter transmembrane protein EcfT | |1720 |Flavin-dependent thymidylate synthase | |1721 |Putative glutamate–cysteine ligase 2 | |1722 |Peptidase E | |1723 |Tropinesterase | |1725 |Photosystem I P700 chlorophyll a apoprotein A2 1 | |1727 |Arginine biosynthesis bifunctional protein ArgJ | |1728 |Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B | |1729 |Putative membrane protein insertion efficiency factor | |1730 |Phytol kinase | |1731 |Nicotinate phosphoribosyltransferase pncB2 | |1733 |Glutamine-dependent NAD(+) synthetase | |1736 |FeS cluster assembly protein SufB | |1737 |putative ATP-dependent transporter SufC | |1738 |FeS cluster assembly protein SufD | |1739 |putative cysteine desulfurase | |1740 |Copper-exporting P-type ATPase | |1741 |IS200/IS605 family transposase ISAsp8 | |1744 |Epimerase family protein | |1747 |Cobyric acid synthase | |1751 |Imidazole glycerol phosphate synthase subunit HisF | |1752 |Holliday junction ATP-dependent DNA helicase RuvB | |1754 |Ribulose bisphosphate carboxylase small chain | |1755 |Ribulose bisphosphate carboxylase large chain | |1756 |3-methyl-2-oxobutanoate hydroxymethyltransferase | |1757 |HTH-type transcriptional activator HxlR | |1758 |Ribosome maturation factor RimM | |1759 |S-(hydroxymethyl)glutathione dehydrogenase | |1763 |Lipoyl synthase 2 | |1766 |Putative cytochrome P450 137 | |1767 |Germacrene A synthase | |1768 |Phosphomethylpyrimidine synthase | |1769 |Orotate phosphoribosyltransferase | |1771 |7-cyano-7-deazaguanine synthase | |1772 |Putative oxidoreductase YceM | |1777 |IS200/IS605 family transposase ISTel3 | |1780 |Thiamine-phosphate synthase | |1781 |GDP-mannose-dependent alpha-(1-6)-phosphatidylinositol monomannoside mannosyltransferase | |1789 |Tricorn protease | |1792 |D-inositol 3-phosphate glycosyltransferase | |1798 |Protein YdeP | |1800 |Response regulator SaeR | |1801 |tRNA threonylcarbamoyladenosine biosynthesis protein TsaE | |1802 |Gluconeogenesis factor | |1803 |Crossover junction endodeoxyribonuclease RuvC | |1806 |Aquaporin Z 2 | |1811 |Stage V sporulation protein D | |1812 |tRNA-Leu(caa) | |1816 |UDP-galactopyranose mutase | |1817 |Galactofuranosyltransferase GlfT2 | |1824 |tRNA-Gln(ttg) | |1826 |UDP-N-acetylglucosamine 2-epimerase | |1827 |Circadian clock protein KaiB | |1828 |Proline–tRNA ligase | |1829 |Transcriptional repressor SmtB | |1830 |Biotin carboxyl carrier protein of acetyl-CoA carboxylase | |1831 |Elongation factor P | |1832 |Inward rectifier potassium channel Kirbac3.1 | |1833 |ATP-dependent (S)-NAD(P)H-hydrate dehydratase | |1836 |Acetyl esterase | |1837 |Phycocyanobilin lyase CpcT | |1838 |tRNA-Cys(gca) | |1849 |Monoacylglycerol lipase | |1851 |putative 3-hydroxyacyl-CoA dehydrogenase | |1852 |3-ketoacyl-CoA thiolase | |1853 |Acyl-coenzyme A dehydrogenase | |1856 |6-hydroxy-D-nicotine oxidase | |1860 |Magnesium-chelatase 38 kDa subunit | |1861 |NAD(P)H-quinone oxidoreductase subunit H | |1862 |Ribosomal RNA small subunit methyltransferase H | |1871 |Teichoic acid translocation permease protein TagG | |1874 |2-deoxy-scyllo-inosamine dehydrogenase | |1876 |6-bisphosphatase/inositol-1-monophosphatase | |1877 |Protein PucC | |1879 |RNA helicase CrhR | |1880 |Ribosomal protein S12 methylthiotransferase RimO | |1881 |Vitamin K epoxide reductase | |1882 |ATP synthase subunit beta | |1883 |ATP synthase epsilon chain | |1885 |putative 30S ribosomal protein PSRP-3 | |1886 |Adenosylhomocysteinase | |1887 |N-acetylmuramic acid/N-acetylglucosamine kinase | |1889 |Valine–tRNA ligase | |1891 |5-bisthiocarboxylic acid mononucleotide synthase | |1892 |Allophycocyanin subunit alpha-B | |1893 |23S rRNA (uracil-C(5))-methyltransferase RlmCD | |1894 |Asparagine–tRNA ligase | |1896 |10 kDa chaperonin | |1897 |60 kDa chaperonin 1 | |1898 |IS200/IS605 family transposase ISTel2 | |1901 |Beta-monoglucosyldiacylglycerol synthase | |1902 |Putative mycofactocin radical SAM maturase MftC | |1903 |Phosphate-binding protein PstS 1 | |1906 |DNA-3-methyladenine glycosylase | |1911 |Fatty acyl-CoA reductase | |1912 |Ribosomal large subunit pseudouridine synthase B | |1917 |Cobalt-precorrin-6B C(15)-methyltransferase (decarboxylating) | |1918 |Putative phosphoribosyl transferase | |1919 |Large-conductance mechanosensitive channel | |1920 |Orotidine 5’-phosphate decarboxylase | |1921 |Tyrosine–tRNA ligase | |1922 |Penicillin-binding protein 2D | |1930 |Glutamyl-tRNA(Gln) amidotransferase subunit A | |1934 |Negative regulator of genetic competence ClpC/MecB | |1935 |Mycothiol acetyltransferase | |1936 |Diaminopimelate decarboxylase | |1937 |Diadenylate cyclase | |1938 |Ditrans | |1939 |polycis-undecaprenyl-diphosphate synthase ((2E | |1940 |6E)-farnesyl-diphosphate specific) | |1945 |H(+)/Cl(-) exchange transporter ClcA | |1948 |UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase | |1949 |Inosine-5’-monophosphate dehydrogenase | |1950 |Putative aminopeptidase YsdC | |1951 |Decarboxylase NovR | |1952 |Phosphatidylcholine-sterol acyltransferase | |1954 |Adenine DNA glycosylase | |1956 |Carbamoyl-phosphate synthase large chain | |1958 |Kynurenine 3-monooxygenase | |1959 |Tryptophan synthase beta chain | |1960 |putative protein YciH | |1962 |Methionyl-tRNA formyltransferase | |1963 |putative protein YqeN | |1966 |Renalase | |1970 |Protein YhgF | |1971 |Ribonuclease VapC11 | |1974 |Sulfur carrier protein TtuD | |1976 |Inner membrane amino-acid ABC transporter permease protein YhdY | |1977 |Putative amino-acid ABC transporter-binding protein YhdW | |1982 |Manganese-binding lipoprotein MntA | |1983 |Modification methylase BspRI | |1987 |16S/23S rRNA (cytidine-2’-O)-methyltransferase TlyA | |1988 |Phycobiliprotein beta chain | |1989 |Glutamine synthetase | |1996 |tRNA-Gly(ccc) | |1998 |DNA topoisomerase 1 | |1999 |Monomeric sarcosine oxidase | |2000 |Acetoin:2 | |2001 |6-dichlorophenolindophenol oxidoreductase subunit alpha | |2002 |Protein LacX | |2003 |plasmid | |2004 |tRNA-Lys(ttt) | |2005 |Fructose-bisphosphate aldolase | |2006 |3-octaprenyl-4-hydroxybenzoate carboxy-lyase | |2008 |Carbonic anhydrase 2 | |2011 |Mannosylfructose-phosphate phosphatase | |2012 |Holliday junction ATP-dependent DNA helicase RuvA | |2013 |8-amino-7-oxononanoate synthase | |2014 |Transcription-repair-coupling factor | |2017 |33 kDa chaperonin | |2018 |Putative serine protease HhoA | |2020 |4’-diapophytoene desaturase (4 | |2021 |4’-diapolycopene-forming) | |2023 |putative ketoamine kinase | |2027 |Photosystem I reaction center subunit III | |2033 |Phycobiliprotein ApcE | |2035 |Allophycocyanin beta chain | |2036 |Allophycocyanin alpha-B chain | |2038 |Light-dependent chlorophyll f synthase | |2042 |Photosystem I P700 chlorophyll a apoprotein A1 | |2043 |Photosystem I P700 chlorophyll a apoprotein A2 | |2044 |Photosystem I reaction center subunit XI | |2045 |Pyruvate-flavodoxin oxidoreductase | |2047 |Chemotaxis protein CheY | |2048 |Chemotaxis protein CheW | |2049 |Methyl-accepting chemotaxis protein | |2051 |Chemotaxis protein methyltransferase 1 | |2052 |Cytochrome b6 | |2053 |K(+)/H(+) antiporter NhaP2 | |2054 |tRNA-Glu(ttc) | |2056 |Metalloregulation DNA-binding stress protein | |2063 |tRNA-Arg(tcg) | |2064 |tRNA-Asn(att) | |2069 |Inner membrane transport protein YnfM | |2071 |Sugar phosphatase YidA | |2073 |Holo-[acyl-carrier-protein] synthase | |2075 |HTH-type transcriptional regulator DmlR | |2080 |HTH-type transcriptional regulator CatM | |2081 |Nuclease | |2083 |Heterocyst differentiation control protein | |2084 |Sorbitol dehydrogenase | |2090 |Malonate-semialdehyde dehydrogenase | |2091 |Polyphosphate glucokinase | |2092 |Putative protein-methionine-sulfoxide reductase subunit YedZ1 | |2094 |Oxygen-independent coproporphyrinogen III oxidase | |2100 |Glucosamine-6-phosphate deaminase 1 | |2103 |Divalent-cation tolerance protein CutA | |2105 |Sulfur carrier protein CysO | |2115 |Decaprenyl-phosphate phosphoribosyltransferase | |2118 |PGL/p-HBAD biosynthesis glycosyltransferase | |2119 |Zeaxanthin glucosyltransferase | |2123 |Precorrin-6Y C(5 | |2124 |15)-methyltransferase [decarboxylating] | |2125 |Sulfite reductase [ferredoxin] | |2126 |Precorrin-8X methylmutase | |2127 |Cobalamin biosynthesis protein CobIJ | |2128 |Siroheme synthase | |2131 |Multicopper oxidase mco | |2132 |Copper-exporting P-type ATPase B | |2133 |Soluble pyridine nucleotide transhydrogenase | |2134 |Cobalt-zinc-cadmium resistance protein CzcA | |2148 |Putative fluoride ion transporter CrcB | |2158 |4’-diaponeurosporen-aldehyde dehydrogenase | |2159 |Carotenoid cleavage oxygenase | |2161 |Nitrate import ATP-binding protein NrtC | |2162 |Nitrate/nitrite binding protein NrtA | |2169 |TRAP-T-associated universal stress protein TeaD | |2171 |Potassium-transporting ATPase ATP-binding subunit | |2176 |putative sporulation protein YtaF | |2180 |Molybdate-binding protein ModA | |2189 |Polyvinylalcohol dehydrogenase | |2197 |Putative transport protein YhhT | |2198 |D-aminopeptidase | |2199 |IS200/IS605 family transposase ISSoc10 | |2204 |Glucoamylase | |2205 |Manganese efflux system protein MneP | |2207 |Putative permease | |2209 |UDP-2 | |2210 |3-diacylglucosamine pyrophosphatase LpxG | |2220 |Glycerol-3-phosphate acyltransferase | |2221 |Intermembrane phospholipid transport system permease protein MlaE | |2222 |Putative signal peptide peptidase SppA | |2223 |Chorismate mutase AroH | |2227 |UTP–glucose-1-phosphate uridylyltransferase | |2228 |dTDP-4-dehydrorhamnose reductase | |2231 |Isochorismate synthase MenF | |2232 |Pyridoxal phosphate homeostasis protein | |2233 |Cell division protein SepF | |2234 |Pyrroline-5-carboxylate reductase | |2236 |30S ribosomal protein S4 | |2237 |Gamma-glutamylputrescine oxidoreductase | |2238 |N-acetylhexosamine 1-kinase | |2239 |Cellobiose 2-epimerase | |2244 |CRISPR-associated endoribonuclease Cas2 3 | |2245 |CRISPR-associated endonuclease Cas1 | |2246 |Thiosulfate reductase molybdopterin-containing subunit PhsA | |2248 |Sporulation kinase E | |2253 |Mercuric resistance operon regulatory protein | |2254 |putative copper-transporting ATPase PacS | |2257 |Leucine–tRNA ligase | |2258 |ECF RNA polymerase sigma factor SigE | |2261 |Single-stranded-DNA-specific exonuclease RecJ | |2262 |Photosystem II reaction center protein Ycf12 | |2263 |Shikimate kinase | |2266 |Acetylglutamate kinase | |2269 |Biosynthetic arginine decarboxylase | |2270 |Nucleoside diphosphate kinase | |2271 |NAD-dependent malic enzyme | |2273 |Acetolactate synthase large subunit | |2274 |Enterobactin exporter EntS | |2277 |Ribokinase | |2280 |Aspartate carbamoyltransferase | |2285 |L-threo-3-hydroxyaspartate ammonia-lyase | |2286 |putative RNA 2’-phosphotransferase | |2290 |dTDP-glucose 4 | |2291 |6-dehydratase 2 | |2293 |Peptide methionine sulfoxide reductase MsrA | |2298 |SsrA-binding protein | |2300 |Cytochrome b6-f complex iron-sulfur subunit 1 | |2301 |Cytochrome f | |2302 |Imidazole glycerol phosphate synthase subunit HisH | |2303 |Ribosomal RNA small subunit methyltransferase D | |2304 |Cytochrome b6-f complex subunit 5 | |2306 |3-diketo-5-methylthiopentyl-1-phosphate enolase | |2309 |Oligopeptidase A | |2310 |Isoleucine–tRNA ligase | |2314 |6-phosphogluconate dehydrogenase | |2315 |decarboxylating | |2317 |Alanine dehydrogenase | |2318 |Pyrimidine-specific ribonucleoside hydrolase RihB | |2319 |Phosphoribosylformylglycinamidine synthase subunit PurL | |2320 |Amidophosphoribosyltransferase | |2322 |Pyrimidine-specific ribonucleoside hydrolase RihA | |2323 |tRNA pseudouridine synthase B | |2326 |Flavohemoprotein | |2328 |Mannan endo-1 | |2329 |4-beta-mannosidase | |2331 |Aspartate–tRNA(Asp/Asn) ligase | |2335 |primosomal protein N’ | |2337 |Potassium-transporting ATPase potassium-binding subunit | |2339 |Potassium-transporting ATPase KdpC subunit | |2340 |Sensor protein KdpD | |2341 |DNA ligase | |2345 |Glyceraldehyde-3-phosphate dehydrogenase 1 | |2351 |NADH dehydrogenase-like protein | |2353 |Lactate utilization protein A | |2354 |tRNA-Thr(ggt) | |2355 |tRNA-Tyr(gta) | |2357 |IS701 family transposase ISNpu7 | |2361 |tRNA-Glu(ctc) | |2365 |tRNA-Phe(gaa) | |2366 |tRNA-Asn(gtt) | |2369 |tRNA-Pro(tgg) | |2371 |tRNA-Lys(ctt) | |2376 |tRNA-Leu(taa) | |2380 |tRNA-Ser(tga) | |2381 |Stage 0 sporulation protein J | |2383 |CRISPR-associated endonuclease Cas2 2 | |2384 |Replicative DNA helicase | |2385 |IS982 family transposase ISPasp2 | |2386 |PhoH-like protein | |2387 |30S ribosomal protein S21 | |2388 |30S ribosomal protein S16 | |2389 |Signal recognition particle protein | |2390 |Nitrate reductase | |2391 |Nitrate/nitrite transporter NrtP | |2394 |Anthranilate phosphoribosyltransferase | |2396 |Inorganic pyrophosphatase | |2398 |Sensory transduction protein regX3 | |2401 |Thermonuclease | |2403 |tRNA-Ser(gga) | |2404 |Aurachin C monooxygenase/isomerase | |2405 |Acylphosphatase | |2406 |Colistin resistance protein EmrB | |2409 |Transcriptional regulator SlyA | |2411 |Glucose-6-phosphate isomerase | |2414 |Glutathionyl-hydroquinone reductase YqjG | |2415 |2-hydroxy-3-oxopropionate reductase | |2416 |DNA adenine methyltransferase YhdJ | |2417 |Thiazole synthase | |2418 |(R)-citramalate synthase | |2419 |Putative two-component membrane permease complex subunit SMU\_747c | |2423 |Serine/threonine-protein kinase F | |2425 |DNA polymerase I | |2427 |Xylulose-5-phosphate/fructose-6-phosphate phosphoketolase | |2428 |Na(+)/H(+) antiporter ApNhaP | |2429 |Oligosaccharide 4-alpha-D-glucosyltransferase | |2430 |Methionine aminopeptidase | |2437 |2-phosphonomethylmalate synthase | |2440 |Daunorubicin/doxorubicin resistance ATP-binding protein DrrA | |2441 |Daunorubicin/doxorubicin resistance ABC transporter permease protein DrrB | |2443 |Methionine aminotransferase | |2447 |Metal-pseudopaline receptor CntO | |2448 |Phthiocerol synthesis polyketide synthase type I PpsA | |2451 |Narbonolide/10-deoxymethynolide synthase PikA1 | |2452 |modules 1 and 2 | |2453 |3-hydroxy-5-methyl-1-naphthoate 3-O-methyltransferase | |2454 |6-deoxyerythronolide-B synthase EryA1 | |2456 |Phenolphthiocerol synthesis polyketide synthase type I Pks15/1 | |2472 |High-affinity zinc uptake system membrane protein ZnuB | |2474 |Zinc import ATP-binding protein ZnuC | |2475 |High-affinity zinc uptake system binding-protein ZnuA | |2477 |Rqc2 RqcH | |2480 |Peptide chain release factor 3 | |2481 |Delta-aminolevulinic acid dehydratase | |2485 |2-oxoisovalerate dehydrogenase subunit beta | |2486 |Protein translocase subunit SecD | |2487 |Protein translocase subunit SecF | |2489 |Threonylcarbamoyl-AMP synthase | |2490 |Release factor glutamine methyltransferase | |2494 |tRNA N6-adenosine threonylcarbamoyltransferase | |2496 |Photosystem I reaction center subunit IX | |2498 |Guanylate kinase | |2499 |Extracellular matrix regulatory protein A | |2502 |Phospho-N-acetylmuramoyl-pentapeptide-transferase | |2503 |Photosystem I reaction center subunit IV | |2504 |Formamidopyrimidine-DNA glycosylase | |2505 |NAD(P)H-quinone oxidoreductase subunit O | |2506 |Malate dehydrogenase | |2514 |Energy-dependent translational throttle protein EttA | |2517 |Ribosomal silencing factor RsfS | |2518 |tRNA-Val(gac) | |2520 |Phosphate-import permease protein PhnE | |2521 |Tyrosine recombinase XerC | |2522 |Immunogenic protein MPT70 | |2523 |Toluene 1 | |2524 |2-dioxygenase system ferredoxin subunit | |2525 |Ferric uptake regulation protein | |2528 |Lysine 6-dehydrogenase | |2529 |Phytoene desaturase (lycopene-forming) | |2533 |Energy-coupling factor transporter ATP-binding protein EcfA1 | |2540 |GTP pyrophosphokinase | |2548 |5-dichloro-2 | |2549 |5-cyclohexadiene-1 | |2550 |4-diol dehydrogenase | |2553 |Octanoyltransferase LipM | |2554 |Deoxyribodipyrimidine photo-lyase | |2555 |Teichuronic acid biosynthesis protein TuaB | |2564 |4-hydroxybenzoate solanesyltransferase | |2565 |Exopolyphosphatase | |2568 |Acetate kinase | |2570 |3-bisphosphoglycerate-dependent phosphoglycerate mutase | |2574 |Carnitine transport binding protein OpuCC | |2578 |Exodeoxyribonuclease 7 small subunit | |2579 |Exodeoxyribonuclease 7 large subunit | |2580 |Protein RecA | |2582 |Metallothionein | |2585 |Histidine biosynthesis bifunctional protein HisIE | |2587 |Pyrophosphatase PpaX | |2588 |4-hydroxyphenylpyruvate dioxygenase | |2591 |Thiopurine S-methyltransferase | |2596 |Quinolinate synthase A | |2597 |4-hydroxymandelate oxidase | |2601 |Circadian clock protein KaiA | |2603 |Circadian clock protein kinase KaiC | |2607 |Na(+)/H(+)-K(+) antiporter GerN | |2611 |Inner membrane transport permease YadH | |2612 |Esterase EstP | |2616 |Glutaminase 2 | |2619 |Cyanate hydratase | |2620 |Modification methylase PvuII | |2627 |Phycobilisome rod-core linker polypeptide CpcG4 | |2629 |Phycobilisome rod-core linker polypeptide CpcG2 | |2630 |Phycobilisome rod-core linker polypeptide CpcG1 | |2631 |Phycocyanobilin lyase subunit beta | |2632 |Phycocyanobilin lyase subunit alpha | |2633 |Phycobilisome 8.9 kDa linker polypeptide | |2634 |phycocyanin-associated | |2635 |rod | |2636 |Phycobilisome 32.1 kDa linker polypeptide | |2639 |C-phycocyanin alpha chain | |2640 |C-phycocyanin beta chain | |2641 |Bilin biosynthesis protein PecF | |2642 |Bilin biosynthesis protein PecE | |2643 |Phycobilisome 34.5 kDa linker polypeptide | |2644 |phycoerythrocyanin-associated | |2646 |Phycoerythrocyanin alpha chain | |2647 |Phycoerythrocyanin beta chain | |2648 |Ribosomal large subunit pseudouridine synthase D | |2651 |tRNA-His(gtg) | |2652 |putative lipid II flippase MurJ | |2654 |Mannose-1-phosphate guanylyltransferase 1 | |2655 |Ribosomal RNA small subunit methyltransferase B | |2657 |ADP-ribose pyrophosphatase | |2660 |HTH-type transcriptional regulator CymR | |2663 |tRNA-specific 2-thiouridylase MnmA | |2665 |Arsenate reductase | |2667 |Anaerobic nitric oxide reductase transcription regulator NorR | |2668 |putative oxidoreductase ORF5 in fasciation locus | |2669 |Glutathione-regulated potassium-efflux system protein KefC | |2673 |Methionine synthase | |2674 |Arginine–tRNA ligase | |2677 |Heme A synthase | |2683 |Protein archease | |2685 |putative ferredoxin/ferredoxin–NADP reductase | |2689 |Adenosylcobinamide-GDP ribazoletransferase | |2690 |Queuine tRNA-ribosyltransferase | |2691 |Photosystem II reaction center protein K | |2692 |Photosystem II reaction center protein M | |2693 |Heptaprenyl diphosphate synthase component 2 | |2694 |Glutamate racemase | |2696 |Styrene monooxygenase StyA | |2698 |Pentalenene oxygenase | |2700 |50S ribosomal protein L27 | |2701 |Riboflavin biosynthesis protein RibD | |2702 |Cell shape-determining protein MreB | |2703 |Single-stranded DNA-binding protein | |2704 |26 kDa periplasmic immunogenic protein | |2705 |3-oxoacyl-[acyl-carrier-protein] reductase | |2706 |putative undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase | |2707 |60 kDa chaperonin 2 | |2708 |Cobalt/magnesium transport protein CorA | |2719 |Alpha-acetolactate decarboxylase | |2720 |Ribonuclease J1 | |2721 |4-hydroxy-tetrahydrodipicolinate synthase | |2722 |Aspartate-semialdehyde dehydrogenase | |2723 |Trigger factor | |2725 |ATP-dependent Clp protease ATP-binding subunit ClpX | |2727 |Carboxymethylenebutenolidase | |2729 |Endoribonuclease EndoA | |2731 |Phytoene desaturase (neurosporene-forming) | |2732 |putative ribonucleotide transport ATP-binding protein mkl | |2734 |Cyclopentanol dehydrogenase | |2735 |D-glycero-beta-D-manno-heptose-1 | |2736 |7-bisphosphate 7-phosphatase | |2737 |Bifunctional protein HldE | |2738 |ADP-heptose–LPS heptosyltransferase 2 | |2739 |putative metallo-hydrolase | |2740 |GDP-mannose-dependent monoacylated alpha-(1-6)-phosphatidylinositol monomannoside mannosyltransferase | |2741 |Diacylglycerol kinase | |2743 |Thymidylate kinase | |2744 |NADH dehydrogenase | |2751 |Succinate-semialdehyde dehydrogenase [NADP(+)] 1 | |2752 |Acetolactate synthase | |2753 |catabolic | |2755 |HTH-type transcriptional regulatory protein GabR | |2761 |6-deoxy-6-sulfogluconolactonase | |2762 |Putative amidase AmiB2 | |2763 |5’-methylthioadenosine/S-adenosylhomocysteine nucleosidase | |2764 |Alanine–tRNA ligase | |2765 |Ribosome biogenesis GTPase A | |2766 |Putative pyridoxal phosphate-dependent aminotransferase EpsN | |2768 |GTPase Obg | |2772 |4’-diapolycopene oxygenase | |2773 |Foldase protein PrsA | |2775 |Autoinducer 2 sensor kinase/phosphatase LuxQ | |2780 |6-methylpretetramide 4-monooxygenase | |2781 |sn-glycerol-3-phosphate import ATP-binding protein UgpC | |2782 |Cysteine–tRNA ligase | |2783 |Putative metal chaperone YciC | |2786 |Molybdenum cofactor biosynthesis protein B | |2787 |ATP-dependent RNA helicase RhlB | |2788 |Sulfate adenylyltransferase | |2789 |Lysine racemase | |2794 |Lipid II isoglutaminyl synthase (glutamine-hydrolyzing) subunit GatD | |2795 |Peptide chain release factor 2 | |2796 |Endoribonuclease YbeY | |2797 |Undecaprenol kinase | |2798 |CTP synthase | |2805 |Modification methylase BamHI | |2806 |Type-2 restriction enzyme BamHI | |2807 |Putative phosphinothricin acetyltransferase YwnH | |2808 |Xanthine phosphoribosyltransferase | |2809 |Putative glycoside/cation symporter YagG | |2810 |Phycocyanobilin lyase CpcS 1 | |2812 |Cytochrome b6-f complex subunit 4 | |2813 |Serine-protein kinase RsbW | |2814 |transfer-messenger RNA | |2815 |SsrA | |2816 |ATP synthase gamma chain | |2817 |ATP synthase subunit alpha | |2818 |ATP synthase subunit delta | |2819 |ATP synthase subunit b | |2820 |ATP synthase subunit b’ | |2821 |ATP synthase subunit c | |2822 |ATP synthase subunit a | |2826 |Allophycocyanin alpha chain | |2828 |Phycobilisome 7.8 kDa linker polypeptide | |2829 |allophycocyanin-associated | |2830 |core | |2836 |putative multidrug resistance ABC transporter ATP-binding/permease protein YheI | |2837 |Toxin RelK | |2838 |Antitoxin YefM | |2839 |ATP-dependent Clp protease ATP-binding subunit ClpC | |2844 |Galactose-1-phosphate uridylyltransferase | |2848 |Diflavin flavoprotein A 1 | |2850 |Shikimate dehydrogenase (NADP(+)) | |2854 |Putative N-acetylmannosamine-6-phosphate 2-epimerase | |2859 |Glycerol-3-phosphate dehydrogenase [NAD(P)+] | |2860 |Lipoyl synthase | |2861 |tRNA-Pro(cgg) | |2865 |N-acetylmuramoyl-L-alanine amidase LytC | |2868 |NAD(P)H-quinone oxidoreductase subunit M | |2871 |Protein/nucleic acid deglycase 2 | |2876 |UDP-N-acetyl-D-glucosamine 6-dehydrogenase | |2878 |UDP-2-acetamido-3-amino-2 | |2879 |3-dideoxy-D-glucuronate N-acetyltransferase | |2888 |3-diacetamido-2 | |2889 |3-dideoxy-D-glucuronate 2-epimerase | |2906 |Metalloprotease PmbA | |2909 |Formate-dependent phosphoribosylglycinamide formyltransferase | |2914 |TPR repeat-containing protein YrrB | |2917 |Glutamyl-tRNA(Gln) amidotransferase subunit C | |2919 |SOS response-associated protein YedK | |2921 |DNA nickase | |2923 |Putative monooxygenase YdhR | |2926 |Biphenyl dioxygenase ferredoxin subunit | |2930 |Adenylylsulfate reductase subunit alpha | |2934 |putative N-acetyltransferase YafP | |2936 |Alpha-2-macroglobulin | |2938 |Inorganic triphosphatase | |2940 |Membrane-bound lytic murein transglycosylase F | |2941 |UDP-glucose:undecaprenyl-phosphate glucose-1-phosphate transferase | |2945 |3-dehydroquinate dehydratase | |2946 |5 | |2947 |6-dimethylbenzimidazole synthase | |2948 |Putative pre-16S rRNA nuclease | |2951 |4-dihydroxy-2-naphthoyl-CoA synthase | |2953 |tRNA-dihydrouridine(20/20a) synthase | |2954 |RNA polymerase sigma-B factor | |2956 |Sulfate transport system permease protein CysW | |2957 |Sulfate transport system permease protein CysT | |2958 |Sulfate-binding protein | |2959 |PEP-dependent dihydroxyacetone kinase | |2960 |ADP-binding subunit DhaL | |2962 |dihydroxyacetone-binding subunit DhaK | |2963 |Manganese-exporting P-type ATPase | ::: :::

## 14.1 Further analyses

The trees give a nice visual of relationship between the species while comparing their relationships based on genes of interest. With more time, it is necessary to investigate the secondary structure of the 16S - 23S region of these cyanobacteria to identify the hairpin loop structures. Furthermore, although products of JS2 were determined, further investigation of the products needs to be done to better understand the secondary metabolites produced by JS2. Similarly, once the products have been thoroughly investigated, the MSMS should be preformed to determine if there are any produced at the time of extraction.

# 15. Discussion

## 15.1 Summary and Interpretation

For this project, the cleaned data was taken and analyzed using Rstudio to make graphs and plots to help visualize the data. Three questions were posed at the beginning, 1. The individual genes did yield different phylogenetic trees, however, in the majority of trees we see a pattern of JS2 being grouped near F.thermalis, F.major, and F.muscicola, 2. There were toxic and inhibitory genes based on the genome annotations for JS2 and 3. Additional testing will need to be done to determine if these genes are being expressed at the time of extraction.

## 15.2 Strengths and Limitations

This study is to investigate the presence of toxic, antibiotic, and/or inhibitory genes within the whole genome of our novel species. Thus, one huge factor to this experiment will be whether or not the secondary metabolite is being expressed when the MSMS and/or extraction is preformed. Secondary metabolites such as those I am interested are not consistently produced as this would be energetically expensive. Stressing the cyanobacteria out with environmental factors such as temperature, humidity, light, or pH will most likely have little to no effect on the secondary metabolites of interest, however introducing another bacterial species has its own problems. The current struggle is to keep these cultures anexic due to the fact that contaminates will add secondary metabolites not produced by the cyanobacteria, however, they can cause the cyanobacteria to produce secondary metabolites as a response mechanism. Another way to potentially obtain secondary metabolites of interest if they are not expressed, or in high enough concentrations would be to create a vector in another organism and promote the expression in that organism since the cyanobacteria grow so slow already.

## 15.3 Conclusions

To summarize, we found that there is a difference between phylogentic genetic trees, and more specifically, there is a difference between the placement of species between the phylogentic tree based on all genes concatenated verses each individual genes.

# 16. References

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