# Table 1 (required, fixed format)

Table 1a: Classification of *Genus species* strain designation(required)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| GenomeID | Domain | Phylum | Class | Order | Family | Genus |
| TH00953 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Unclassified |
| TE02167 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Methylotenera |
| TH02902 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Unclassified |
| ME03080 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Methylotenera |
| ME00068 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Unclassified |
| AAA028K02 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Unclassified |
| TH00545 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Methylotenera |
| TE00913 | Bacteria | Proteo-bacteria | Betaproteo-bacteria | Methylophilales | Methylophilaceae | Unclassified |

Table 1b: Origin of *Genus species* strain designation(required)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GenomeID | Habitat | Salinity | Geographic Location | Sample Collection Date | Latitude | Longitude | Altitude |
|  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |

Table 1c: (Optional -isolates) General features of *Genus species* strain designation

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genome ID | Gram Stain | Cell Shape | Motility | Sporulation | Temperature Range; Optimum | pH Range; Optimum |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

Table 1d: (Optional -isolates) General features of *Genus species* strain designation (con’t)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genome ID | Carbon Source | Oxygen Requirement | Biotic relationship | Pathogenicity |
|  |  |  |  |  |
|  |  |  |  |  |
|  |  |  |  |  |

# Table 2 (required, fixed format)

**Table 2a.** Project information.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genome ID | Genome Type | Finishing Quality | Libraries used | Sequencing platforms | Fold Coverage | Assemblers |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

**Table 2b.** Project information. (con’t)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genome ID | Binning Method  (if MAGs) | Gene calling method | Locus Tag | Genbank ID | Genbank Date of Release |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

**Table 2c.** Project information. (con’t)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genome ID | GOLD ID | BIOPROJECT | Source Material Identifier | Project Relevance |
|  |  |  |  |  |
|  |  |  |  |  |
|  |  |  |  |  |

# Table 3

Genome statistics, listed in base pairs and percent of total. Genome size, DNA coding, and DNA G+C should be reported as the actual size, not as estimates for a complete genome. Estimates should be listed under corresponding columns

**Table 3a**. Genome statistics.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genome ID | Genome Size (bp) | DNA coding (bp) | DNA G+C (bp) | DNA scaffolds | Estimated Completeness (%) | Estimated Genome Size  (bp) |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

**Table 3b**. Gene statistics.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genome ID | Total Genes | Protein coding genes | RNA genes | Pseduo genes | CRISPR repeats |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

**Table 3c**. Annotation statistics.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genome ID | Genes with Internal Clusters | Genes with function prediction | Genes assigned to COGs | Genes with Pfam domains | Genes with signal peptides | Genes with transmembrane helices |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

# Table 5 or 4 if optional table is not used (required, fixed format)

Number of genes associated with general COG functional categories.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Genome ID | Translation, ribosomal structure and biogenesis | RNA processing and modification | Transcription | Replication, recombination and repair | Chromatin structure and dynamics | Cell cycle control, Cell division, chromosome partitioning | Defense mechanisms | Signal transduction mechanisms | Cell wall/membrane biogenesis | Cell motility | Intracellular trafficking and secretion | Posttranslational modification, protein turnover, chaperones | Energy production and conversion | Carbohydrate transport and metabolism | Amino acid transport and metabolism | Nucleotide transport and metabolism | Coenzyme transport and metabolism | Lipid transport and metabolism | Inorganic ion transport and metabolism | Secondary metabolites biosynthesis, transport and catabolism | General function prediction only | Function unknown | Not in COGs |
|  | J | A | K | L | B | D | V | T | M | N | U | O | C | G | E | F | H | I | P | Q | R | S | - |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |