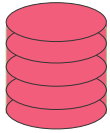


Analysis

Input



Curated plasmids
in fasta format

Basic features

Basic

Quast

Length
GC content
Data source

Quast

Host



Eukaryotes
Prokaryotes

Text minning

Topology



Circular
Linear
Direct terminal repeat
Inverted terminal repeat

Text minning

Completeness



Complete
Incomplete

Text minning

Mobility



Mobilizable
Non-mobilizable
Conjugative

MOB suite

Clustering



cluster

MOB suite

Gene prediction

Prokka

Prokka

Function annotation

eggNOG

Clusters of
Orthologous Genes
(COG)

+

Gene Ontology
Database
(GO)

+

Kyoto Encyclopedia of
Genes and Genomes
(KEGG)

Protein Family
(Pfam)

+

Carbohydrate-Active
Enzyme Database
(CAZy)

+

Biochemical Genetic
and Genomic Knowledgebase
(BiGG)

RGI



Comprehensive Antibiotic
Resistance Database

Antibiotic resistance genes

Diamond



Virulence Factor
Database

Virulence factors

antiSMASH

Secondary metabolites

SignalP

Singal peptides

TMHMM

Transmembrane proteins

Aragorn

tRNA & tmRNA

CRISPR-CAS prediction

CRISPRCasTyper → CRISPR-Cas system

Protein structure prediction

ESMFold → Protein structure



Software/methods



Databases



Output