

Comprehensive Genome Analysis

Easier way to submit and analyze new genomes in PATRIC

Comprehensive Genome Analysis provides:

- Assembly
- Annotation
- Indication of genome quality
- Antimicrobial resistance phenotype predictions
- Genes of interest
 - Antimicrobial resistance and virulence factor genes
- Functional categorization using Subsystems
- Quick phylogenetic tree

Comprehensive Genome Analysis provides:

- Assembly
- Annotation
- Indication of taxonomic affiliation
- Antimicrobial resistance
- Genes of interest
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- Functional categorization using Subsystems
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And an AWESOME report

Service accepts reads or contigs

Reads

Start With: ⓘ

☒ Read File ☐ Assembled Contigs

Input File ⓘ

PAIRED READ LIBRARY

SINGLE READ LIBRARY

SRA RUN ACCESSION

Selected libraries ⓘ

Place read files here using the arrow buttons.

Parameters ⓘ

ASSEMBLY PARAMETERS

STRATEGY

TRIM READS BEFORE ASSEMBLY

RACON ITERATIONS PILON ITERATIONS

MIN. CONTIG LENGTH MIN. CONTIG COVERAGE

ANNOTATION PARAMETERS

DOMAIN

TAXONOMY NAME ⓘ

TAXONOMY ID

MY LABEL

GENETIC CODE

OUTPUT FOLDER

OUTPUT NAME

Contigs

Start With: ⓘ

☐ Read File ☒ Assembled Contigs

Input File ⓘ

CONTIGS

Parameters ⓘ

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