



PanWSGA Web Server Tutorial

Web-Based Platform for Single Genome Analysis

A Screenshot-Based Guide for Single Genome Analysis to identify unique features of a Bacterium

PanWSGA enables researchers to project a single bacterial genome onto a curated, species-level pangenome reference derived from more than 100,000 high-quality assemblies.

The platform integrates standardized reannotation, and a dedicated visualization module to deliver reproducible gene-category profiles and functional summaries within minutes.

Section- I

 Get Started

 Learn More

Overview of PanWSGA



PanWSGA

Web-Based Platform for Single-Genome Pangenome Analysis

PanWSGA enables researchers to project a single bacterial genome onto a curated, species-level pangenome reference derived from more than 100,000 high-quality assemblies.

The platform integrates standardized **reannotation**, a custom classification engine, and a dedicated visualization module to deliver reproducible gene-category profiles and functional summaries within minutes.

[🚀 Get Started](#)[📘 Learn More](#)

The navigation menu provides access to all major sections of PanWSGA.

Section- II

Species Catalog



Species Catalog

Browse all available species in the database with their gene statistics and genome information

The Catalog section help user to find species specific available pan-genome datasets.

Q Search Species

Sort By

Search by name or scientific name...

Name (A-Z)

Aerococcus viridans

8,393

Total Genes

31

Genomes

164

Core Genes

8,229

Accessory Genes

Added: Dec 6, 2025

Information file

Campylobacter gracilis

3,001

Total Genes

6

Genomes

772

Core Genes

2,229

Accessory Genes

Added: Dec 7, 2025

Information file

Campylobacter lari

11,364

Total Genes

835

Genomes

785

Core Genes

10,579

Accessory Genes

Added: Dec 7, 2025

Information file

Demo Test Chlamydia avium

Demo:

Granulicatella adiacens

Kingella oralis

Section- III

Demo Data

Demo Data helps to understand how users interact with PanWSGA. There is no need for raw data. All data is available in this section



Demo Data

Test our tools quickly with pre-loaded smaller datasets. Perfect for exploring features without uploading large files!



Quick Testing Guide

Pre-loaded demo genomes for quick testing. No upload needed!

1. Browse available demo genomes below
2. Click "Select for Testing" on any genome
3. Go to dashboard and select species/pan-genome
4. Start comparison and test all features!

Pre-loaded Demo Genomes



Treponema paraluisuniculi

GCF_000217655.1

Demo dataset for testing

982 genes

☒ Select for Testing

ID: 995dcf14-f63e-4e68-b068-737fabf45bfc



Mycoplasma genitalium

GCF_040556925.1

Demo dataset for testing

524 genes

☒ Select for Testing

ID: adff532b-5756-4669-81c1-d6d5ba83f56d



Fructilactobacillus florum

GCF_000512295.1

Demo dataset for testing

1,259 genes

☒ Select for Testing

ID: ec5a20fe-c4b2-4958-baae-81320162d76a



Run Pipeline Test

✓ **Selected Genome:** Mycoplasma genitalium
ID: adff532b-5756-4669-81c1-d6d5ba83f56d

****Note:** Raw Assembled Genome is recommended for unique gene identification, Use of CDS sequence may affect the results due to Difference in annotation

Select Species

Demo Test Mycoplasma genitalium

Select Pan-Genome

Demo Mycoplasma genitalium Base Pan-Genome

Input File Type

☐ **CDS (Coding Sequences)**
For files with coding sequences only

☒ **Genomic (Run Prokka)**
For whole genome sequences

Here we only select the input type (Genome) and upload input and identify the unique genes, we did not choose the option to classify them and their visualization

Optional Processing

☐ **Run eggNOG-mapper Annotation** ✗
Functional annotation (takes longer)

☐ **Generate GO Classification Chart** ✗
Create charts showing COG classification distribution (requires eggNOG-mapper)

****Note:** As we only selected the identification of unique genes this process will completed in 2—3 minutes

Run Pipeline Test



Run Pipeline Test

✓ Pipeline Completed! (Time: 0m 17s)

Test Results



855

Total Genes



769

Core Genes



51

Accessory Genes



35

Unique Genes

Gene Distribution



COG chart not generated.

To generate COG classification charts, enable both:

- Run eggNOG-mapper
- Generate GO Classification Chart

Download Results

FASTA Sequences:

↓ Core Genes

↓ Accessory Genes

↓ Unique Genes

Annotations (Excel):

❗ Excel annotations not available. Enable "Run eggNOG-mapper" to generate annotation files.

Visualizations:

❗ COG chart not generated. Enable both options to generate charts.

User can download the fasta sequence of Core, Accessory and Unique Genes



Run Pipeline Test

Selected Genome: Mycoplasma genitalium
ID: adff532b-5756-4669-81c1-d6d5ba83f56d

Select Species

Demo Test Mycoplasma genitalium

Select Pan-Genome

Demo Mycoplasma genitalium Base Pan-Genome

Input File Type

☐ CDS (Coding Sequences)
For files with coding sequences only

☒ Genomic (Run Prokka)
For whole genome sequences

Here we select the input type (Genome) and select all the options unique genes identification, classification and their visualization

Optional Processing

☒ Run eggNOG-mapper Annotation
Functional annotation (takes longer)

☒ Generate GO Classification Chart
Create charts showing COG classification distribution (requires eggNOG-mapper)

Select Chart Types

☒ Pie Chart

☒ Horizontal Bar Chart

☐ Heatmap

☒ Vertical Bar Chart

☐ Radar Chart

Run Pipeline Test

Pipeline Completed! (Time: 13m 27s)

Test Results



Gene Distribution

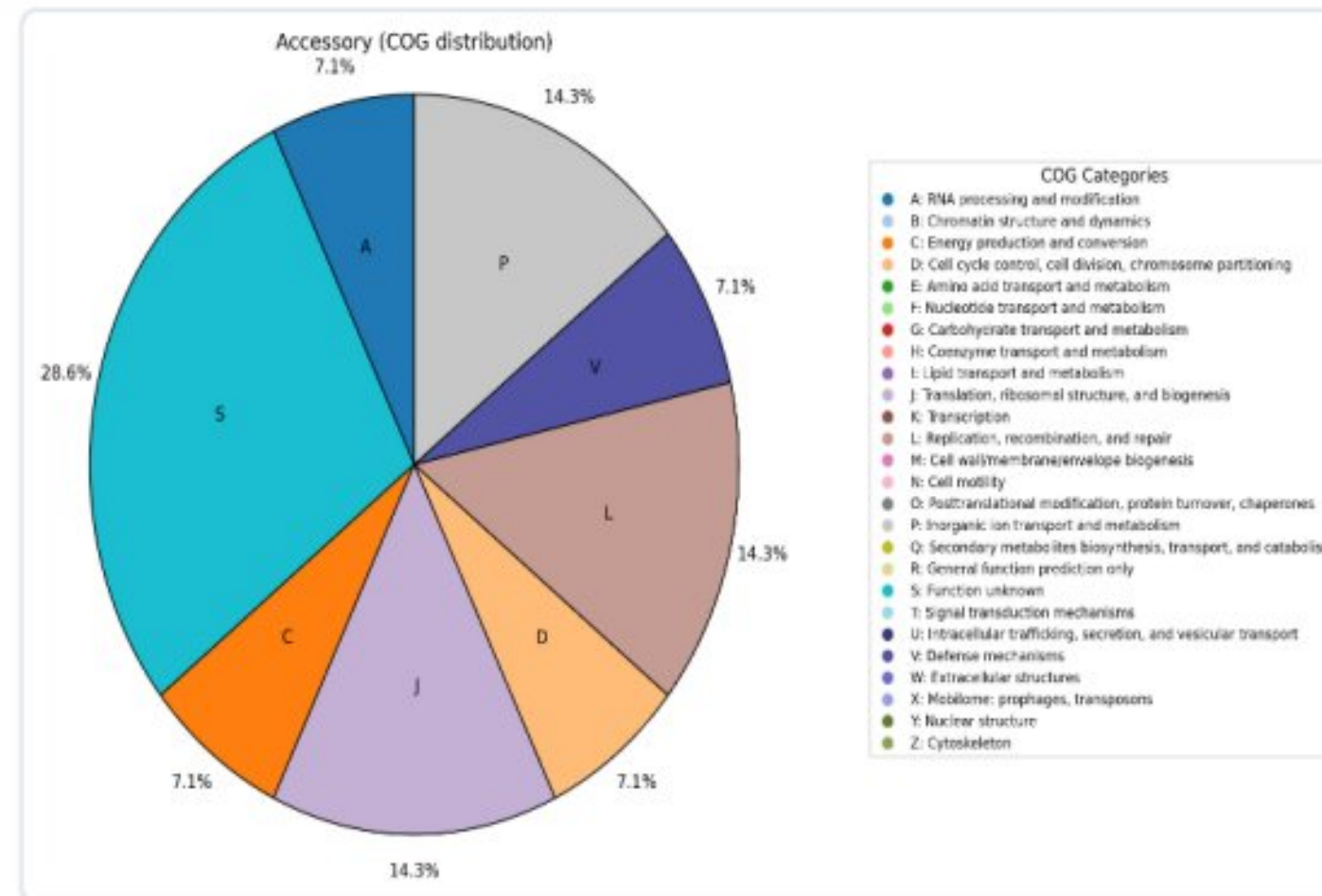




COG Classification Chart

Select Chart Type:

Pie Chart



Download Chart

Download Results

FASTA Sequences:

Core Genes

Accessory Genes

Unique Genes

Annotations (Excel):

Unique Annotations

Visualizations:

COG Chart (PNG)

Section- IV

How to use Unique gene finder in real time data



[Unique Gene Finder](#)

[Unique Gene Search](#)

PanWSGA

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[Get Started](#)

[Learn More](#)



Unique Gene Finder

Primary workflow (upload → compare → annotate)

Runs the core pipeline that classifies genes into core, accessory, and unique buckets using the selected pan-genome reference. Outputs FASTA files, summaries, and download bundles.

- Same Celery comparison job exposed on the dashboard.
- Stores every run under your account for later download.
- Works with all registered pan-genomes.

[Open Workflow](#)

Optional Steps

- ☐ **Include annotation**
Runs eggNOG-mapper after gene classification.
- ☐ **Visualise annotation results**
Adds the visualization script after annotation.

Annotation is skipped (only FASTA outputs).
Visualization remains disabled.

Upload Genome FASTA

Upload your genome sequence file in FASTA format. This will create a genome record that you can use for comparison.

Input File Type

☐ CDS (Coding Sequences) ☒ Genomic (Will run Prokka)

Select CDS if your file contains coding sequences, or Genomic if you want Prokka to generate CDS first

FASTA File

Choose file No file chosen

Accepted formats: fasta, fa, fna (Max: 200MB)

Organism (optional)

e.g., Acinetobacter baumannii

Strain (optional)

e.g., AB5075

Description (optional)

Additional information

Upload query genome here

Upload Genome

Upload to create a genome record

Select Name of your specie

Select Species and Pan-Genome

Choose the species and pan-genome reference database for comparative analysis. Select a species first to see available pan-genomes.

Species

Search and select a species

Loading available species from database...

Pan-Genome

-- Select a species first --

Select pre computed pan genome of your species & run

If you want to annotate the identified unique gene select all these option as describe in demo data

Run Comparison

Start the pan-genome comparison using your uploaded genome and selected pan-genome. This will compare your genome against the reference database and classify genes as core, accessory, or unique.

Optional Processing Steps

- ☐ **Run eggNOG-mapper Annotation**
Annotate genes using eggNOG-mapper for functional classification (takes additional time)
- ☐ **Generate GO Classification Chart**
Create charts showing GO classification distribution (requires eggNOG-mapper)

Start Comparison

Compare uploaded genome with selected pan-genome

Pan-Web Single Genome Analyzer

[Home](#)[Dashboard](#)[About](#)[Tools](#)[Catalog](#)[Demo](#)[Help](#)[FAQs](#)

Upload Genome FASTA

Upload your genome sequence file in FASTA format. This will create a genome record that you can use for comparison.

Input File Type

☐

CDS (Coding Sequences)

☒

Genomic (Will run Prokka)

Select CDS if your file contains coding sequences, or Genomic if you want Prokka to generate CDS first

FASTA File

Choose file

GCF_040556925.1_ASM4055692v1_genomic.fna



Upload Genome

Upload to create a genome record

Accepted formats: .fasta, .fa, .fna (Max: 200MB)

Organism (optional)

Strain (optional)

Description (optional)

e.g., Acinetobacter baumannii

e.g., AB5075

Additional information

GCF_040556925.1_ASM4055692v1_genomic.fna selected (0.56 MB)

Uploaded successfully! Genome ID: b9a912ba-f21b-495e-9119-e6ca28e3bd2e

Select Species and Pan-Genome

Choose the species and pan-genome reference database for comparative analysis. Select a species first to see available pan-genomes.

Species

Pan-Genome

Mycoplasmoides genitalium



Mycoplasmoides genitalium Base Pan-Genome



Loading available species from database...

Run Comparison

Start the pan-genome comparison using your uploaded genome and selected pan-genome. This will compare your genome against the reference database and classify genes as core, accessory, or unique.

Optional Processing Steps

☒Run eggNOG-mapper Annotation

Annotate genes using eggNOG-mapper for functional classification (takes additional time)

☒Generate GO Classification Chart

Create charts showing COG classification distribution (requires eggNOG-mapper)

Select Chart Types

☒Pie Chart

☒Horizontal Bar Chart

☒Heatmap

☒Vertical Bar Chart

☒Radar Chart

Start Comparison

Compare uploaded genome with selected pan-genome

****Note: Here is a real time example with all selected option ,It not only find unique gene but also annotate these gene and classify them**

CS CamScanner

