

## Pangenome - RhizobiaWiki

This tool is designed to gain evolutionary insights into specific group of rhizobia and close-related strains through pan-genome analysis. This tool allows users to run pangenome analysis using own genomes and strains in RhizobiaWiki.

Two modes are now applied in this tool:

- (1) specific genomes in RhizobiaWiki;
- (2) genomes in RhizobiaWiki + user uploaded genome.

Upload genome type:

- ☒ Upload genome only from database  
☐ Upload your own genome

Upload Genome file:

Upload genome id file **strain\_list.txt**

Submit

### ✓ Successful Submission!

Dear User:

We have received your task and assigned a **Job ID** for your task, you can get the analysis results with the **Job ID**. Please record your **Job ID** and the **Job ID Link**, it's the only way to get the results. The task takes some moment, and the analysis results will be retained for **24 hours**.

Job ID	1751446308510in_pan
Job ID Link	<a href="https://rhizobiawiki.com/pangenome_results?jobid=1751446308510in_pan">https://rhizobiawiki.com/pangenome_results?jobid=1751446308510in_pan</a>
Submission Time	7/2/2025, 16:51:48

The user only need to upload a text file containing all NCBI accessions of strains and click the submit button to submit your task.

Once you submit your task, a new text will be displayed at the bottom of the website. Please save the Job ID or Link of your job, the result can be traced by job ID.

### Pangenome Results

Job ID: 1751446308510in\_pan

#### Statistical results

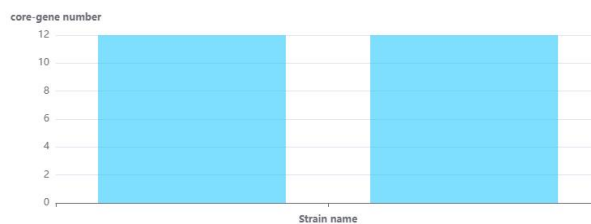
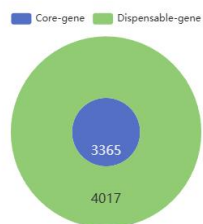
##### Basic Information:

Number of Species: 2    Number of genes: 13168    Number of genes in orthogroups: 11453  
Number of unassigned genes: 1715    Number of orthogroups: 4421    Number of species-specific orthogroups: 194  
Number of genes in species-specific orthogroups: 643

Download result compressed file

Search in tree:  

● GCA\_000009265  
● GCA\_000020265



**The users can view basic pangenome statistics of strains. In additions, all results files can be downloaded for downstream analysis.**