Download data from VEuPathDB

https://VEuPathDB.org

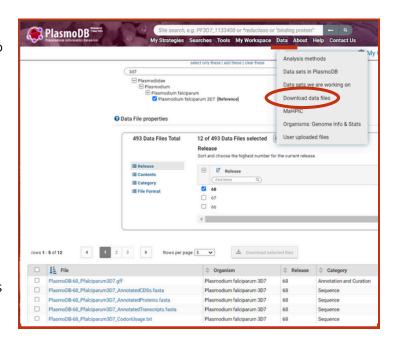
help@VEuPathDB.org



DOWNLOAD GENOME DATA FILES

VEuPathDB genomes (assemblies and annotation) are easily downloaded. If your studies are based on a previous release, use >Data File Properties >Release to choose your desired version.

- GFF gene structure in general feature format
- CDSs.fasta multifasta
- Proteins.fasta multifasta
- Transcripts.fasta multifasta
- CodonUsage.txt occurrence of each codon
- Curated_GO.gaf Gene ontology terms assigned by curators
- GO.gaf Gene ontology terms assigned by electronic prediction or transferred by orthology
- GeneAliases.txt previous IDs for current genes
- Genome.fasta chromosomes contigs or scaffolds
- NCBILinkout Nucleotide.xml
- NCBILinkout_Protein.xml
- Orf50.gff

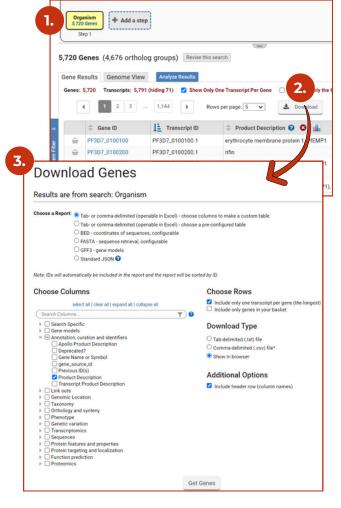


DOWNLOAD DATA FOR MULTIPLE GENES

Data such as expression values, gene metrics, domains, etc. are available for bulk download as custom or preconfigured tables for any list of genes, including a whole genome. This download tool works similarly for lists of other records such as SNPs or metabolic pathways.

1. Retrieve your list of genes as a search result

- a. For all genes in a genome use
 - >Genes >Taxonomy >Organism
- b.To enter a list of your favorite genes use >Genes >Annotation >List of IDs
- 2. Open the Download tool from the search result.
- 3. Configure the Download tool
 - a.custom table one row per gene, choose from all data columns
 - b.pre-configured tables single data type data table that can contain multiple rows per gene
 - c. BED coordinates of sequences, configurable
 - d. FASTA sequence retrieval, configurable
 - e. GFF3 gene models
 - f. Standard JSON compatible with web services.



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DOWNLOAD DATA VIA WEB SERVICES

Data download using Web Services is a programmatic alternative to the **DOWNLOAD DATA FOR MULTIPLE GENES** process described above. Web Services creates a URL that performs a search and retrieves the data to your browser or to a file. Each search contains a link to a wizard that helps create the URL. URLs can be used in scripts to programmatically access VEuPathDB data.



DOWNLOAD A SINGLE GENE

The download link at the top of gene record pages implements the download tool where text, bed, fasta and GFF3 files can be retrieved. Similar download options are available from other record pages such as SNP and metabolic pathway records.

- Text choose from columns and/or tables
- BED coordinates of sequences, configurable
- FASTA sequence retrieval, configurable
- GFF3: Gene models and optional sequences



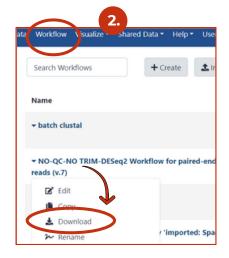
DOWNLOAD GALAXY DATA

Files and workflows can be downloaded from VEuPathDB Galaxy and subsequently uploaded to a different server.

- 1.To download files (1.), open the tile in the history panel and choose Download.

 Histories need be downloaded one file at a time.
- 2.To download a workflow (2.), go to the Workflow tab, choose the workflow name and click Download





Download data from VEuPathDB

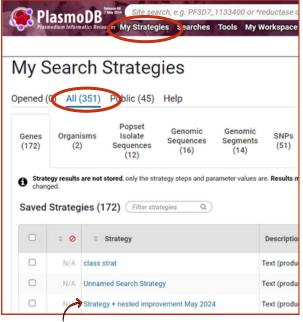
https://VEuPathDB.org

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DOWNLOAD SAVED STRATEGIES

Your VEuPathDB saved strategies are stored in the **All tab** of the **My Strategies** page. Saved searches need to be rerun before the results can be downloaded. Click the strategy name to rerun and then follow the instructions for **DOWNLOAD DATA FOR MULTIPLE GENES**. To download only IDs, choose to download a custom table with no columns checked (Clear All columns).



Click the name to rerun the saved strategy

DOWNLOAD JBROWSE TRACK DATA

JBrowse track data can be downloaded using the Save Track Data feature. Open the dropdown menu associated with the track name and choose the Save Track Data tool. Options to configure the Regions and data format are offered.

