



VEuPathDB

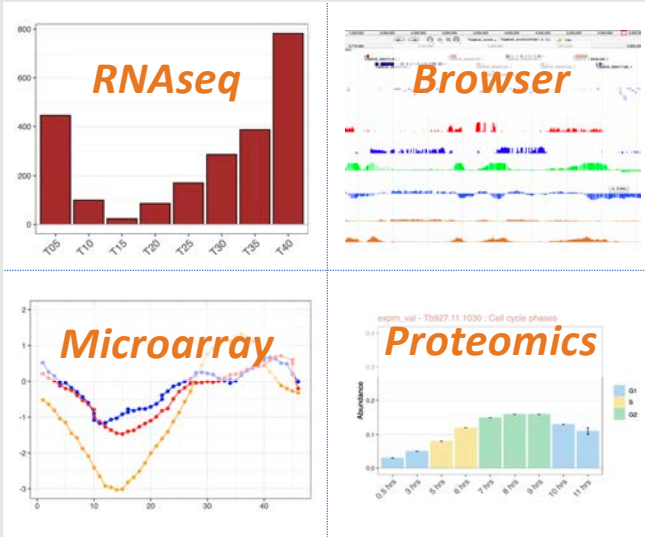
Eukaryotic Pathogen, Vector & Host Informatics Resources

Free online bioinformatic resource center providing tools for data exploration, visualization and analysis

<http://VEuPathDB.org>

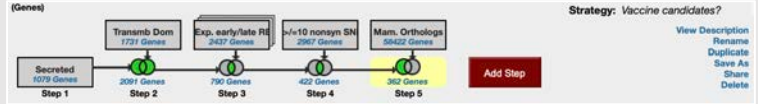
Explore & Visualize:

VEuPathDB integrates diverse datatypes and provides mechanisms to explore and visualize results from many published and unpublished experiments.



Data Mining:

Use custom searches to identify biologically meaningful results relevant to your research. Develop testable hypotheses using the search strategy system.



Search Strategy System

For the Experiment: P. berghei transcriptome during return (protein coding) 4 Genes that are up or down regulated 2 Genes with a Fold change >= 2

between each gene's (average 2) expression value (or a Floor of (10 reads / 22 FPKM) 2) and its (average 2) expression value (or the Floor selected above)

In the following Reference Samples: Control Asexual 0hr, Control Asexual 12hr, Control Asexual 18hr, Control Asexual 24hr, Induced Asexual 0hr

In the following Comparison Samples: Induced Gametes 0hr, Induced Gametes 12hr, Induced Gametes 18hr, Induced Gametes 24hr, Induced Gametes 30hr

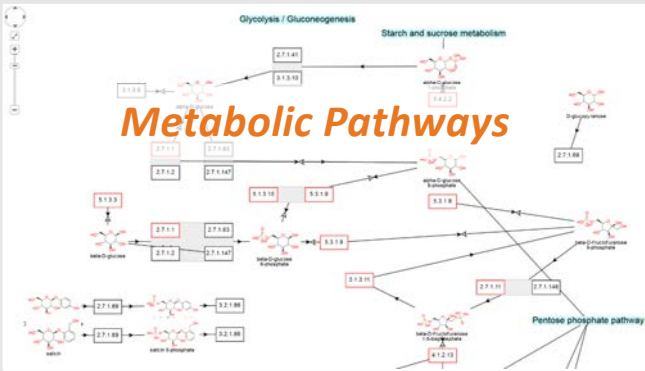
Configurable Searches

Up or down regulated

fold change_{up} = average expression level in comparison / average expression level in reference

fold change_{down} = average expression level in reference / average expression level in comparison

and returns genes when fold change_{up} >= 2 or fold change_{down} >= 2.



Annotated Transcripts (UTRs in gray when available)

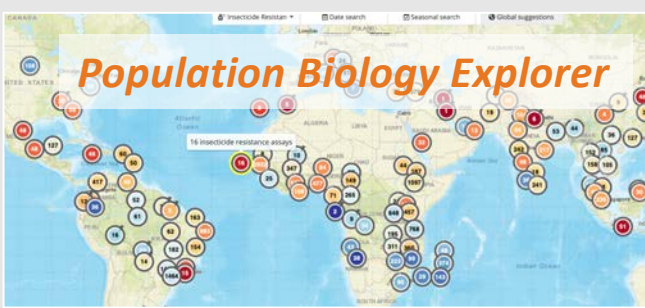
Sequence/GC Content (zoom to <130 nt for sequence)

3 of 171 selected

Geographic Location is Camb...

Geographic Location

Geographic Location	Matching Strains	All Strains	Distribution
Brant	2	2	100%
Subantarctic	1	1	100%
India	1	1	100%
Madagascar	3	3	100%
Mauritania	1	1	100%
North Korea	1	1	100%
Papua New Guinea	1	1	100%
Unknown	2	2	100%



Analyze Your Data

EuPathDB Analyze Data

Workflow: GC-v5.4

History: anaxial vs male, 119: D5462 plots on data 109, data 107, and others, 117: D5462 result file on data 109, data 107, and o others, 115: BAM to BigWig on collection 9, 112: heatmap on collection 9, 111: heatmap on collection 9 (no feature), 104: heatmap on collection 8, 103: heatmap on collection 8 (no feature), 96: BAM to BigWig on collection 8, 92: HAT2 on collection 83

Contact and Funding:

VEuPathDB is one of two nationally funded bioinformatic resource centers – NIH 75N93019C00077
Contact us: help@veupathdb.org

Who we are:

The Eukaryotic Pathogen, host and vector informatic resources (VEuPathDB, <http://VEuPathDB.org>) is a family of free, online data mining resources that facilitate the discovery of meaningful biological and clinical relationships from large volumes of genomic and epidemiological data and is designed for scientists with no bioinformatics training.

Organisms Supported:

VEuPathDB supports over 230 species including pathogenic and non-pathogenic protists (*Amoebae*, *Cryptosporidium*, *Giardia*, *Leishmania*, *Plasmodium*, *Trypanosoma*, etc), fungi (*Aspergillus*, *Cryptococcus*, *Candida*, etc) and invertebrate vectors of human pathogens (Mosquitoes, Ticks, Sand flies, Kissing Bugs, Tsetse flies et.).

- amoebadb.org *Acanthamoeba*, *Entamoeba*, *Naegleria*
- cryptodb.org *Cryptosporidium*, *Gregarina*, *Chromerida*
- eupathdb.org all organisms
- fungidb.org *Oomycetes*, *Fungi*
- giardiadb.org *Giardia*, *Monocercomonoides*, *Spironucleus*
- microsporidiadb.org *Microsporidia*
- piroplasmadb.org *Babesia*, *Cytauxzoon*, *Theileria*
- plasmodb.org *Plasmodium*
- toxodb.org *Toxoplasma*, *Neospora*, *Eimeria*, *Hammondia*, *Sarcocystis*, *Cyclospora*, *Cystoisospora*
- trichdb.org *Trichomonas*
- tritrypdb.org *Crithidia*, *Endotrypanum*, *Leishmania*, *Leptomonas*, *Trypanosoma*, *Blechromonas*, *Bodo*, *Paratrypanosoma*
- Vectorbase.org Invertebrate vectors including mosquitoes, ticks, Tsetse flies et.
Aedes, *Anopheles*, *Culex*, *Glossina*, *Ixodes*, *Leptotrombidium*, *Lutzomyia*, *Musca*, *Ornithodoros*, *Pediculus*, *Phlebotomus*, *Rhodnius*, *Rhipicephalus*, *Sarcoptes*, *Simulium*, *Stomoxys*, *Triatoma*
- orthomcl.org identify phylogenetically conserved or unique proteins across all branches of life
- hostdb.org host responses to pathogen infection

Data Integrated:

VEuPathDB integrates a wide range of data including genome sequence and annotation, transcriptomics, proteomics, epigenomics, metabolomics, population resequencing clinical and field isolates, and data that inform host-pathogen interactions. Data are analyzed using standard workflows and an in-house analysis pipeline generates data including domain predictions, orthology profiles across all genomes and GO term associations.

Data Mining Opportunities

Several general mechanisms permit data exploration and interrogation, including:

- direct examination of record pages representing genes, pathways, study subjects, etc,
- dynamic visualization of sequence-based data aligned to the genome,
- analyses such as functional enrichment and Galaxy workflows,
- a sophisticated Search Strategy system offering pre-configured searches associating diverse evidence with specific hypotheses.
- tools for visualization, search and analysis of a wide range of population data, including genotypes, insecticide resistance and other phenotypes, and field collection sample information.

Advantages:

This comprehensive platform places the power of bioinformatics analysis in the hands of the scientific community, supporting hypothesis-driven discovery using guided queries, a graphical web-interface, and powerful tools for data mapping and analysis. VEuPathDB sites make it easy to interrogate biological questions relating to stage-specific expression, gene model integrity or alternative splice variants, etc, and to compile lists of genes that share multiple biological characteristics (e.g at a particular time, where they may affect host responses).