



VEuPathDB

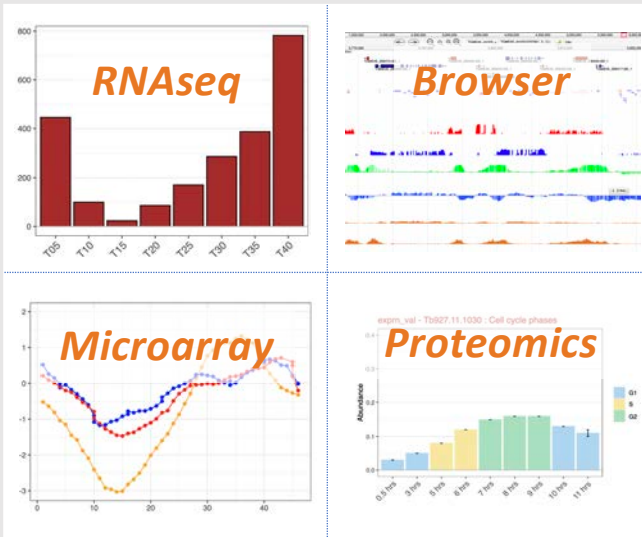
Eukaryotic Pathogen, Vector & Host Informatics Resources

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

<http://VEuPathDB.org>

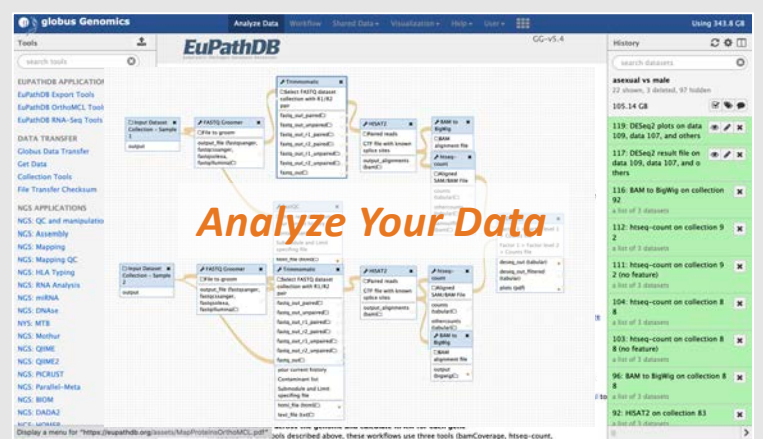
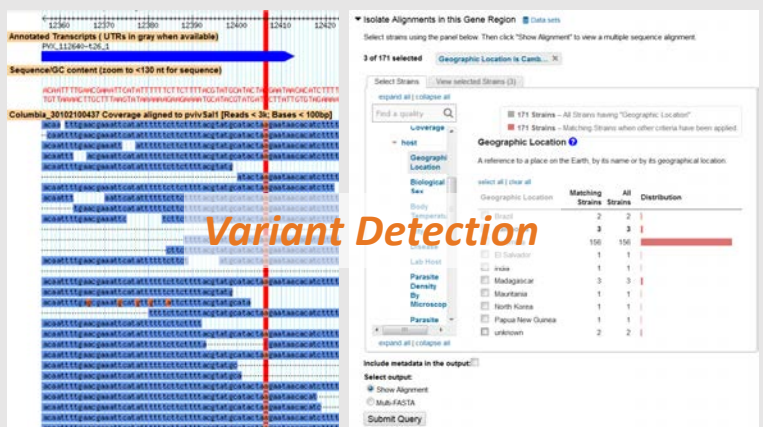
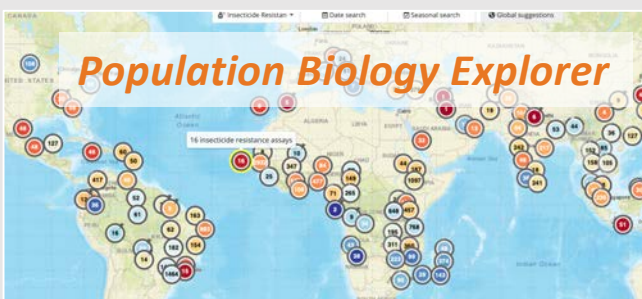
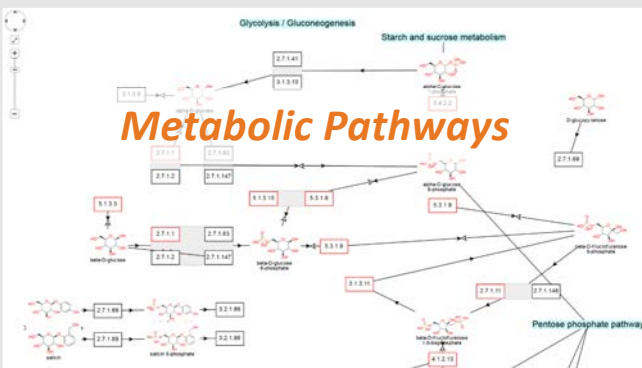
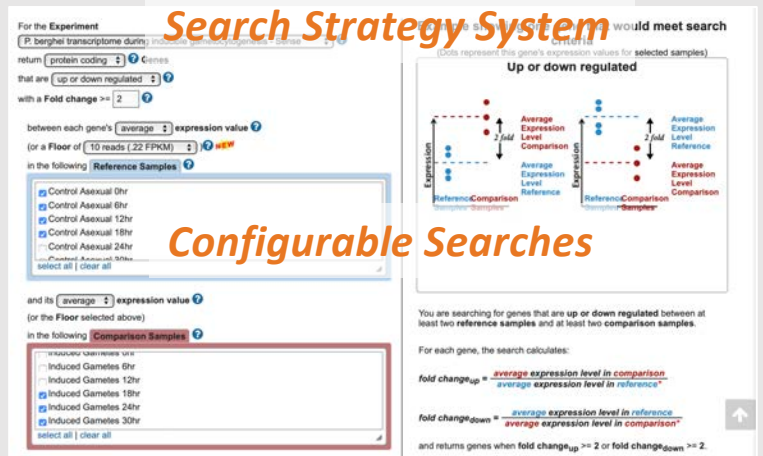
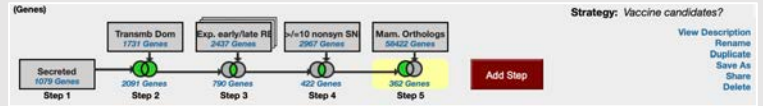
Explore & Visualize:

VEuPathDB integrates diverse datatypes and provides mechanisms to explore and visualize results from many published and unpublished experiments.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



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.).

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|-----------------------|---|
| • amoebadb.org | <i>Acanthamoeba</i> , <i>Entamoeba</i> , <i>Naegleria</i> |
| • cryptodb.org | <i>Cryptosporidium</i> , <i>Gregarina</i> , <i>Chromerida</i> |
| • eupathdb.org | all organisms |
| • fungidb.org | <i>Oomycetes</i> , <i>Fungi</i> |
| • giardiadb.org | <i>Giardia</i> , <i>Monocercomonoides</i> , <i>Spironucleus</i> |
| • microsporidiadb.org | <i>Microsporidia</i> |
| • piroplasmadb.org | <i>Babesia</i> , <i>Cytauxzoon</i> , <i>Theileria</i> |
| • plasmodb.org | <i>Plasmodium</i> |
| • toxodb.org | <i>Toxoplasma</i> , <i>Neospora</i> , <i>Eimeria</i> , <i>Hammondia</i> , <i>Sarcocystis</i> , <i>Cyclospora</i> , <i>Cystoisospora</i> |
| • trichdb.org | <i>Trichomonas</i> |
| • tritrypdb.org | <i>Crithidia</i> , <i>Endotrypanum</i> , <i>Leishmania</i> , <i>Leptomonas</i> , <i>Trypanosoma</i> , <i>Blechnomonas</i> , <i>Bodo</i> , <i>Paratrypanosoma</i> |
| • Vectorbase.org | Invertebrate vectors including mosquitoes, ticks, Tsetse flies et. <i>Aedes</i> , <i>Anopheles</i> , <i>Culex</i> , <i>Glossina</i> , <i>Ixodes</i> , <i>Leptotrombidium</i> , <i>Lutzomyia</i> , <i>Musca</i> , <i>Ornithodoros</i> , <i>Pediculus</i> , <i>Phlebotomus</i> , <i>Rhodnius</i> , <i>Rhipicephalus</i> , <i>Sarcoptes</i> , <i>Simulium</i> , <i>Stomoxys</i> , <i>Triatoma</i> |
| • 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).