



# VEuPathDB

## Eukaryotic Pathogen, Vector & Host Informatics Resources

Research

### Bioinformatics Resource Centers

The Bioinformatics Resource Centers (BRCs) for Infectious Diseases program was initiated in 2004 with the main objective of providing public access to computational platforms and analysis tools that enable collecting, archiving, updating, and integrating a variety of genomics and related research data relevant to infectious diseases, and pathogens and their interaction with hosts

<https://www.niaid.nih.gov/research/bioinformatics-resource-centers>

What's in it for you?

# Enable researchers to ask their own questions



## ORGANISMS

Pathogens and  
related species  
Disease causing

<https://veupathdb.org/veupathdb/app/search/organism/GenomeDataTypes/result>

## DATA

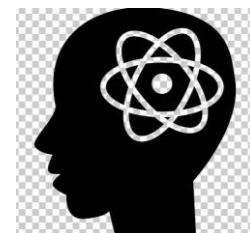
Genomes, Functional  
genomics, Metadata

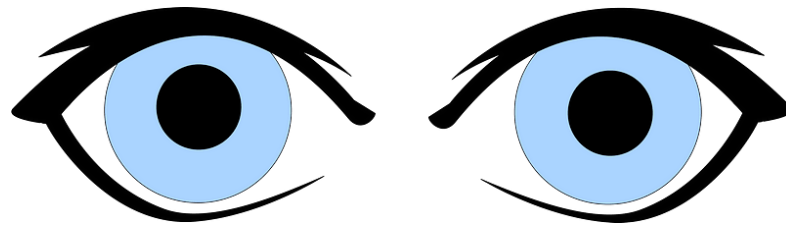
**Analyze with standard  
workflows**

**Results** integrated into one  
DB for comparing within  
and across data sets

## MINE & VISUALIZE

Web based graphical  
interface to mine,  
visualize and search  
the data





# MINE and VISUALIZE

(Basic Functions for integrated data)

## **Record Pages**

Compile all data for entity

## **Dynamic visualization**

Genome Browsing, Network viewing

## **Search strategy**

Genome scale questions that merge evidence

## **Galaxy Workspace**

Primary analysis

# VALUE ADDED



- Public data assembled into **one place**
- **Pre-analyzed.** We show our results. **No need for computational skills**
- **Many data types** from many organisms
- Same workflows so **compare across data sets**
- Orthology so **compare across organisms**
- Standard visualizations and data presentations

# THE DATA

What is it and where does it come from

- genome sequence and annotation,
  - domain predictions
  - orthology profiles across all organisms (OMCL)
- transcriptomics,
- proteomics,
- epigenomics,
- metabolomics,
- population resequencing,
- clinical data,
- surveillance data,
- host-pathogen interactions,





### Functional Characterization of Proteins

- classify proteins into families
- predicting domains and important sites
- predictive models, (signatures)
- several different databases that are members of the InterPro consortium.

<http://www.ebi.ac.uk/interpro/>