

Highlights

All Sites

- Perform searches using a graphical strategy builder
- Attach comments to genes and sequences
- Easier access to queries from the home page and tool bar on all pages
- Save the results of your searches for later retrieval

E EuPathDB

- Gene, genome, EST & ORF queries spanning all component databases
- Ortholog relationships and metabolic pathway maps spanning all supported organisms
- BLAST against all genomes in EuPathDB, including *Theileria* genomes and ESTs from multiple species
- Access to additional relevant sites, including GeneDB and NCBI apicomplexan resources



CryptoDB

- Genes and genomes for *C. parvum*, *C. hominis* and *C. muris*
- Genome alignments and synteny maps
- Gene expression evidence from EST and proteomic analysis
- Isolate data based on criteria such as geographic location



GiardiaDB

- Genes and annotation for three *G. lamblia* genomes
- Phylogenetic trees with conserved proteins
- Gene expression evidence from EST alignment, SAGE tag, microarray and proteomics experiments



PlasmoDB

- Genes and genomes for six *Plasmodium* species
- SNP and CGH polymorphism data for multiple *P. falciparum* strains; comparison with *P. reichenowi*
- Experimental and predicted protein-protein interactions
- Cross-species genome synteny and orthologous proteins
- EST for multiple species; Microarray expression and/or proteomics data for *P. falciparum* and rodent malarial parasites



ToxoDB

- Complete annotation and gene predictions for representative type I, II and III strains (GT1, ME49, VEG) and *Neospora caninum*
- Sequence alignment and synteny maps of *T. gondii* strains and *N. caninum*
- EST, microarray and proteomics data supporting gene expression
- Whole-genome analysis of chromatin marks



TrichDB

- Genes and annotation for the *T. vaginalis* genome
- Identification of repetitive genes
- More than 90,000 ESTs aligned to genome provide expression evidence and validate gene models



TriTrypDB

- Genes and genomes from *L. braziliensis*, *L. infantum*, *L. major*, *L. tarentolae*, *T. brucei* and *T. cruzi*
- Alignments between all available genome sequences, permitting comparative genomic analysis of synteny
- *T. cruzi* scaffolds assembled into virtual chromosomes
- EST and proteomics evidence for *L. infantum*, *T. brucei* and *T. cruzi*
- Phenotypic information for *T. brucei*
- Microarray differentiation evidence for *L. donovani*
- RNA-seq data for *T. brucei*

Help extend the value of your community database ... contribute comments and experimental data to EuPathDB.

Add value to your large-scale genome analyses by placing them in context with others. We currently support genomic, microarray, proteomic, EST, SAGE-tag, SNP and metabolic pathway data sets for *Cryptosporidium*, *Giardia*, *Plasmodium*, *Toxoplasma*, *Trichomonas*, *Leishmania* and *Trypanosoma* species. We will work with you to integrate your data. Please contact your representative database at the email address below to begin the submission process.

Share comments on individual genes with others. If you have a confirmation or suggested change to a gene structure, its expression or its function, please visit the relevant Gene Page and submit a comment. Your comments will be displayed on the Gene pages in the Annotation section and forwarded to genome curators if changes in annotation are required.

Information on annual EuPathDB training workshops can be found at:

<http://eupathdb.org/workshop/>

Examples of questions that can be addressed using EuPathDB can be found at:

<http://eupathdb.org/workshop/2009/>

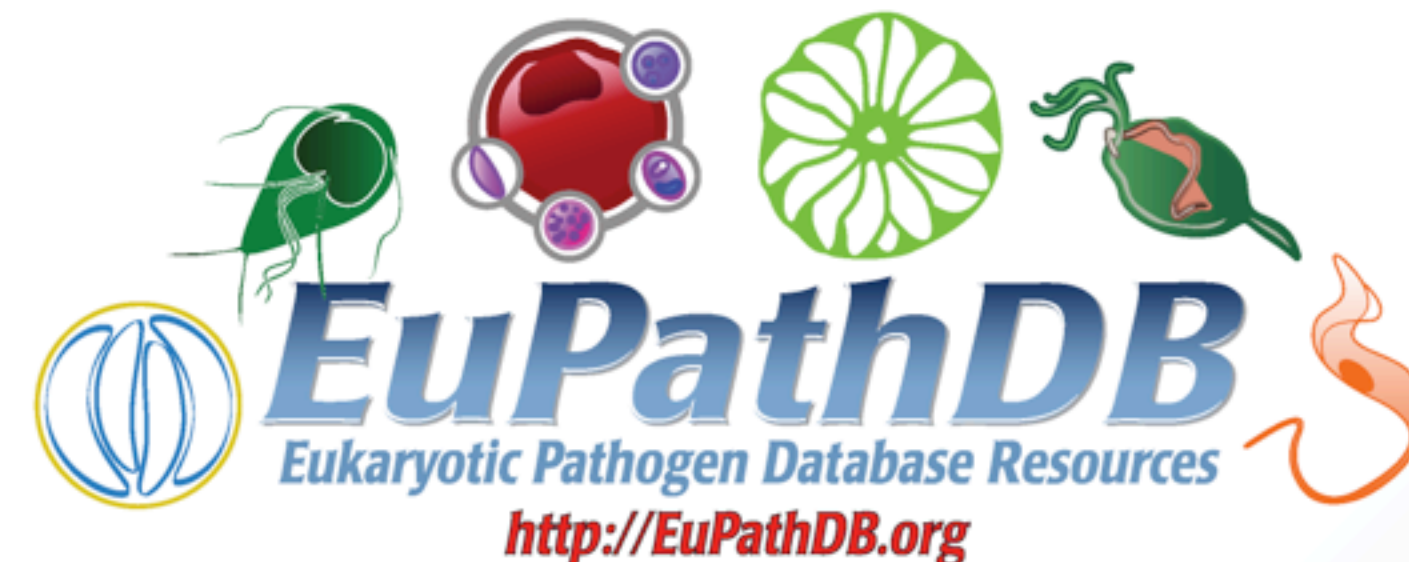
The component databases can be accessed directly at:

<http://CryptoDB.org>, <http://GiardiaDB.org>,
<http://PlasmoDB.org>, <http://ToxoDB.org>,
<http://TrichDB.org> or <http://TriTrypDB.org>

The EuPathDB team can be contacted by clicking on the “contact us” link in each website or by sending an e-mail to:

help@EuPathDB.org

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Trypanosoma brucei
Trypanosoma cruzi
Leishmania spp
Trichomonas
Giardia

Cryptosporidium
Plasmodium spp
Toxoplasma
Neospora

Coming in 2010:

Entamoeba
Microsporidia
Babesia

Acanthamoeba
Cyclospora

EuPathDB provides a unified entry point for the Eukaryotic Pathogen Bioinformatics Resource Center integrating CryptoDB.org, GiardiaDB.org, PlasmoDB.org, ToxoDB.org, TrichDB.org and TriTrypDB.org.

EuPathDB encompass eukaryotic pathogens including *Plasmodium* (malaria), *Giardia*, *Trichomonas*, *Leishmania* (kala-azar), *Trypanosoma* (African sleeping sickness and Chagas disease), and the AIDS-related pathogens *Cryptosporidium* and *Toxoplasma*.

Using the **EuPathDB** site, scientists may explore the genomes and genomic-scale datasets available for these species, formulate complex biological queries and link to additional resources.

EuPathDB is an NIH/NIAID-funded project. TriTrypDB is a joint endeavor between EuPathDB and GeneDB. Funding for the EuPathDB portion of TriTrypDB is provided by the Bill and Melinda Gates Foundation.

Tool bar provides access to all searches, to your search history, download files and community resources from all EuPathDB Web pages.

Side bar components contain expandable sections for release notes, community resources, tutorials and help (new items are highlighted with a yellow alert).

The screenshot shows the EuPathDB homepage with a navigation bar (Home, New Search, My Searches: 0, Tools, Data Sources, Downloads, Community) and a sidebar with News, Community Resources, and Web Tutorials. The main content area features a banner for the Bioinformatics Resource Center and sections for identifying genes and other data types, along with a tools section including BLAST, PubMed and Entrez, and ApiCyc.

Interactive Banner

- Quick Search Windows
- Register and Log in
- Contact us with your Questions and Comments

Quick access to your favorite organism's Web page

Access Tools

Retrieve upstream and downstream sequence

BLAST your sequence against EuPathDB genomes

The screenshot shows the BLAST search interface with fields for Target Data Type, BLAST Program, Target Organism, Input Sequence, Expectation value, Maximum alignments, and a Download Type selection.

The Gene Page

Access and download gene-level data

Synteny map between species

The synteny map shows gene order across different species, with a color-coded legend for different gene types.

Transcriptomic and Proteomic data

The screenshot displays a line graph of gene expression levels over time, with a legend for different gene types.

Orthology

The orthology graph shows relationships between genes from different species, with a legend for different gene types.

Add a comment on a gene -- even upload images !!!

The screenshot shows a form for adding a comment to a gene page, with fields for text and image upload.

Combine results from diverse data types, such as expression data (proteomics and transcriptomics), InterPro domains, text searches, phylogenetic profile and more using the graphical strategy system

Start new strategies **Open strategies** **Browse all strategies in your history** **Import sample strategies into your workspace** **Access strategy help pages**

The screenshot shows the graphical strategy system interface with a workflow of steps (All Genes, Kinases, Phosphatases, Predicted Signal Peptide, No Ortho Mamm) and a table of results.

Expanded steps include other searches without the need to re-run the entire strategy

Results are summarized in clickable tables

Generate tailored downloads of your results

Add new columns to your results table