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



- 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 differentation 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, SAGEtag, 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,

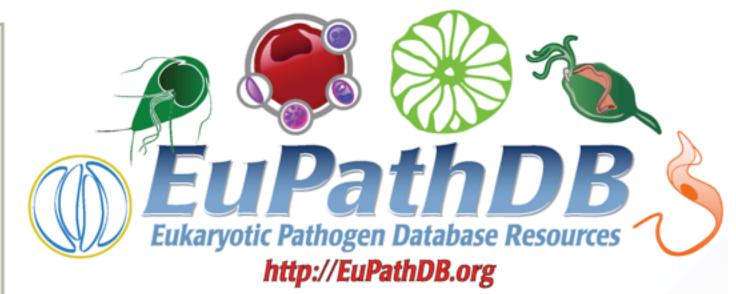
http://PlasmoDB.org, http://ToxoDB.org,

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 Cryptosporidium pathogens 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).

