

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

Eukaryotic Pathogen Database Resources

RRID:SCR_004512

Type: Tool

Proper Citation

Eukaryotic Pathogen Database Resources (RRID:SCR_004512)

Resource Information

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

Proper Citation: Eukaryotic Pathogen Database Resources (RRID:SCR_004512)

Description: EuPathDB integrates numerous database resources and multiple data types. The phylum Apicomplexa comprises veterinary and medically important parasitic protozoa including human pathogenic species of genera *Cryptosporidium*, *Plasmodium* and *Toxoplasma*. ApiDB serves not only as database but unifies access to three major existing individual organism databases, PlasmoDB.org, ToxoDB.org and CryptoDB.org, and integrates these databases with data available from additional sources. Through ApiDB site, users may pose queries and search all available apicomplexan data and tools, or they may visit individual component organism databases. EuPathDB Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Diseases is a portal for accessing genomic-scale datasets associated with eukaryotic pathogens.

Abbreviations: EuPathDB, ApiDB

Synonyms: EuPath, Apicomplexan Database Resources, Eukaryotic Pathogen Genome Database, EuPathDB, Eukaryotic Pathogen Database Resources, ApiDB, Apicomplexan Database

Resource Type: service resource, data repository, data access protocol, software resource, web service, portal, topical portal, data or information resource, database, storage service resource

Defining Citation: [PMID:19914931](#), [PMID:17098930](#)

Keywords: Data, Apicomplexa, parasitic, protozoa, *Cryptosporidium*, *Plasmodium*, *Toxoplasma*, database, pathogen, dataset, FASEB list

Related Condition: malaria, kala-azar, african sleeping sickness, chagas disease, aids-related, aids

Funding: NIAID ;
Bill and Melinda Gates Foundation ;
Wellcome Trust

Resource Name: Eukaryotic Pathogen Database Resources

Resource ID: SCR_004512

Alternate IDs: nlx_49652, r3d100011557

Alternate URLs: <http://ApiDB.org>, <https://doi.org/10.17616/R3X06F>

License URLs:

<https://eupathdb.org/eupathdb/wdkCustomization/jsp/questions/XmlQuestions.AboutAll.jsp#download>
http://eupathdb.org/EuPathDB_datasubm_SOP.pdf

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260731T042700+0000

Ratings and Alerts

No rating or validation information has been found for Eukaryotic Pathogen Database Resources.

No alerts have been found for Eukaryotic Pathogen Database Resources.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Moty?ková A, et al. (2023) Adaptation of the late ISC pathway in the anaerobic mitochondrial organelles of *Giardia intestinalis*. *PLoS pathogens*, 19(10), e1010773.

Mayol GF, et al. (2020) Evidence of nuclear transport mechanisms in the protozoan parasite *Giardia lamblia*. *Biochimica et biophysica acta. Molecular cell research*, 1867(1), 118566.

Mack EA, et al. (2019) Knockout of *Babesia bovis* rad51 ortholog and its complementation by expression from the BbACc3 artificial chromosome platform. *PloS one*, 14(8), e0215882.

Li B, et al. (2019) The SNARE protein FoIVam7 mediates intracellular trafficking to regulate conidiogenesis and pathogenicity in *Fusarium oxysporum* f. sp. *lycopersici*.

Environmental microbiology, 21(8), 2696.

Li B, et al. (2019) FoLVps9, a Guanine Nucleotide Exchange Factor for FoLVps21, Is Essential for Fungal Development and Pathogenicity in *Fusarium oxysporum* f. sp. *lycopersici*. *Frontiers in microbiology*, 10, 2658.

Lu J, et al. (2018) Removing contaminants from databases of draft genomes. *PLoS computational biology*, 14(6), e1006277.

Mangul S, et al. (2018) ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. *Genome biology*, 19(1), 36.

Pyrihová E, et al. (2018) A Single Tim Translocase in the Mitosomes of *Giardia intestinalis* Illustrates Convergence of Protein Import Machines in Anaerobic Eukaryotes. *Genome biology and evolution*, 10(10), 2813.

Otarigho B, et al. (2018) Identification and characterization of sodium and chloride-dependent gamma-aminobutyric acid (GABA) transporters from eukaryotic pathogens as a potential drug target. *Bioinformation*, 14(1), 21.

Cova M, et al. (2018) The Apicomplexa-specific glucosamine-6-phosphate N-acetyltransferase gene family encodes a key enzyme for glycoconjugate synthesis with potential as therapeutic target. *Scientific reports*, 8(1), 4005.

Marzano V, et al. (2017) "Omic" investigations of protozoa and worms for a deeper understanding of the human gut "parasitome". *PLoS neglected tropical diseases*, 11(11), e0005916.

Gentekaki E, et al. (2017) Extreme genome diversity in the hyper-prevalent parasitic eukaryote *Blastocystis*. *PLoS biology*, 15(9), e2003769.

Santos JM, et al. (2017) Malaria parasite LIMP protein regulates sporozoite gliding motility and infectivity in mosquito and mammalian hosts. *eLife*, 6.

Liu S, et al. (2016) Comparative genomics reveals *Cyclospora cayetanensis* possesses coccidia-like metabolism and invasion components but unique surface antigens. *BMC genomics*, 17, 316.

Liu S, et al. (2016) Evolution of mitosome metabolism and invasion-related proteins in *Cryptosporidium*. *BMC genomics*, 17(1), 1006.

Fort P, et al. (2015) Evolution of proteasome regulators in eukaryotes. *Genome biology and evolution*, 7(5), 1363.

El-Ashram S, et al. (2015) From the Macro to the Micro: Gel Mapping to Differentiate between Sporozoites of Two Immunologically Distinct Strains of *Eimeria maxima* (Strains M6 and Guelph). *PloS one*, 10(12), e0143232.

Murungi E, et al. (2014) A comparative analysis of trypanosomatid SNARE proteins. *Parasitology international*, 63(2), 341.

DeBarry JD, et al. (2014) A survey of innovation through duplication in the reduced genomes of twelve parasites. *PloS one*, 9(6), e99213.

Ghouila A, et al. (2014) Identification of divergent protein domains by combining HMM-HMM comparisons and co-occurrence detection. PloS one, 9(6), e95275.