Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

PlasmoDB

RRID:SCR_013331
Type: Tool

Proper Citation

PlasmoDB (RRID:SCR_013331)

Resource Information

URL: http://PlasmoDB.org

Proper Citation: PlasmoDB (RRID:SCR_013331)

Description: Functional genomic database for malaria parasites. Database for Plasmodium spp. Provides resource for data analysis and visualization in gene-by-gene or genome-wide scale. PlasmoDB 5.5 contains annotated genomes, evidence of transcription, proteomics evidence, protein function evidence, population biology and evolution data. Data can be queried by selecting from query grid or drop down menus. Results can be combined with each other on query history page. Search results can be downloaded with associated functional data and registered users can store their query history for future retrieval or analysis.Key community database for malaria researchers, intersecting many types of laboratory and computational data, aggregated by gene.

Synonyms: PlasmoDB, Plasmodium Genomics Resource, PlasmoDB 5.5, Plasmodium genome-resource

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

Defining Citation: PMID:18957442

Keywords: Functional, genomic, database, malaria, parasite, data, analysis, visualization, gene, genome, annotation, transcription, proteomics, protein, evolution, FASEB list

Related Condition: malaria

Funding: NIAID

Resource Name: PlasmoDB

Resource ID: SCR_013331

Alternate IDs: nif-0000-03314, SCR_017665, r3d100011569

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260731T042854+0000

Ratings and Alerts

No rating or validation information has been found for PlasmoDB.

No alerts have been found for PlasmoDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1239 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Ellis VA, et al. (2025) A generalist vector-transmitted parasite exhibits population genetic structure among host genera. Parasitology, 152(1), 82.

D Sa J, et al. (2025) Stabilized designs of the malaria adhesin protein PvRBP2b for use as a potential diagnostic for Plasmodium vivax. The Journal of biological chemistry, 301(3), 108290.

Ceesay S, et al. (2025) Plasmodium falciparum expresses fewer var genes at lower levels during asymptomatic dry season infections than clinical malaria cases. PLoS pathogens, 21(6), e1013210.

Li Q, et al. (2025) Malaria: past, present, and future. Signal transduction and targeted therapy, 10(1), 188.

Emmanuel J, et al. (2025) An optimized deep-forest algorithm using a modified differential evolution optimization algorithm: A case of host-pathogen protein-protein interaction prediction. Computational and structural biotechnology journal, 27, 595.

Jonsdottir TK, et al. (2025) A scalable CRISPR-Cas9 gene editing system facilitates CRISPR screens in the malaria parasite Plasmodium berghei. Nucleic acids research, 53(2).

Lawton JG, et al. (2025) Diamonds in the rif: Alignment-free comparative genomics analysis reveals strain-transcendent Plasmodium falciparum antigens amidst extensive genetic diversity. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 129, 105725.

Kiboi D, et al. (2025) Isolation and characterization of Plasmodium falciparum blood-stage persisters by improved selection protocols using dihydroartemisinin alone. Antimicrobial agents and chemotherapy, 69(3), e0005324.

Probst AS, et al. (2025) In vivo screen of Plasmodium targets for mosquito-based malaria control. Nature, 643(8072), 785.

Smith C, et al. (2025) Activity-based protein profiling reveals both canonical and novel ubiquitin pathway enzymes in Plasmodium. PLoS pathogens, 21(4), e1013032.

Rawat A, et al. (2025) PfPPM2 signalling regulates asexual division and sexual conversion of human malaria parasite Plasmodium falciparum. Nature communications, 16(1), 4790.

Okafor A, et al. (2025) Transcriptome analysis reveals a de novo DNA element that may interact with chromatin-associated proteins in Plasmodium berghei during erythrocytic development. Scientific reports, 15(1), 18621.

de Fátima Ferreira-da-Cruz M, et al. (2025) Diagnosing P. simium zoonotic malaria infection in the Rio de Janeiro Atlantic forest, Brazil. Scientific reports, 15(1), 23695.

Anton L, et al. (2025) Integrated structural biology of the native malarial translation machinery and its inhibition by an antimalarial drug. Nature structural & molecular biology, 32(11), 2158.

Gao J, et al. (2025) The Plasmodium berghei merozoite protein PbGAC is critically involved in erythrocyte binding during invasion. Parasites & vectors, 18(1), 432.

Salomane N, et al. (2025) The impact of Iso-mukaadial acetate on Plasmodium falciparum transcriptional gene regulation. Scientific reports, 15(1), 42381.

Muzenda FL, et al. (2025) Characterization and Inhibition of the Chaperone Function of Plasmodium falciparum Glucose-Regulated Protein 94 kDa (Pf Grp94). Proteins, 93(5), 957.

Acevedo GR, et al. (2025) Liver stage P. falciparum antigens highly targeted by CD4+ T cells in malaria-exposed Ugandan children. PLoS pathogens, 21(2), e1012943.

Kisambale AJ, et al. (2025) Genetic diversity of Plasmodium falciparum reticulocyte binding protein homologue-5, which is a potential malaria vaccine candidate: baseline data from areas of varying malaria endemicity in Mainland Tanzania. Malaria journal, 24(1), 29.

Tan MH, et al. (2025) A paradoxical population structure of var DBL? types in Africa. PLoS pathogens, 21(2), e1012813.