Resource Summary Report

Generated by NIF on Aug 30, 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: analysis service resource, data access protocol, data analysis service, data or information resource, data repository, database, production service resource, service resource, software resource, storage service resource, web service

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: 20260829T182434+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 1324 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Zhang Y, et al. (2026) Integration of ATAC-seq and RNA-seq reveals temperature-responsive regulatory regions in Plasmodium falciparum asexual stages. Parasites & vectors, 19(1).

Yang W, et al. (2026) PfVPS4, an ESCRT AAA-ATPase, is essential for asexual proliferation and gametocyte sexual conversion in Plasmodium falciparum. Parasites & vectors, 19(1).

Bower-Lepts C, et al. (2026) Double Mutations in Plasmodium falciparum Kelch13 drive resistance to next-generation artemisinin derivatives in malaria parasites. bioRxiv : the preprint server for biology.

Okombo J, et al. (2026) Collateral hypersensitivity between ZY19489 and piperaquine neutralizes PfCRT-mediated drug efflux and Plasmodium falciparum resistance. Nature communications, 17(1).

Seager BA, et al. (2026) PTRAMP, CSS and Ripr form a conserved complex required for merozoite invasion of Plasmodium species into erythrocytes. Nature communications, 17(1), 1780.

Sanchez SG, et al. (2026) A Spinster-like Transporter at the Inner Membrane Complex is critical for Toxoplasma gondii cytokinesis, motility and invasion. PLoS pathogens, 22(1), e1013886.

Michie K, et al. (2026) Antimalarial drug resistance in Plasmodium falciparum isolates from the Pacific Coast of Colombia. Parasitology, 153(4), 1.

Costa CM, et al. (2026) Different clinical forms of Plasmodium vivax infection result in unique T cell epitope-specific immune responses. Journal of immunology (Baltimore, Md. : 1950), 215(4).

Lefebvre MJM, et al. (2026) Genomic Insights Into Host Shifts Between Plasmodium vivax and Plasmodium simium in Latin America. Evolutionary applications, 19(3), e70222.

Ko K, et al. (2026) A common DNA deletion altering the 3'UTR of mdr1 is associated with reduced mefloquine susceptibility in P. vivax parasites from Cambodian patients. Nature communications, 17(1), 1748.

Gujarati S, et al. (2026) Differential expression of mitochondria-associated genes in clinical samples of Plasmodium falciparum showing severe manifestations. BMC genomics, 27(1).

Wirth D, et al. (2026) PfApiAT2 is a proline transporter essential for the transmission of Plasmodium falciparum by the mosquito vector. Research square.

Brown N, et al. (2026) Replication stress increases de novo CNVs across the malaria parasite genome. Nucleic acids research, 54(1).

Brown AS, et al. (2026) Chromatin state dynamics during the Plasmodium falciparum intraerythrocytic development cycle. BMC genomics, 27(1), 142.

Niedermüller K, et al. (2026) An atlas of novel microtubule-associated proteins in the malaria parasite Plasmodium falciparum. mBio, 17(1), e0340725.

Nwankwo I, et al. (2026) Pyrophosphate homeostasis in multiple subcellular compartments is essential in Plasmodium falciparum. mBio, 17(5), e0047526.

Wu J, et al. (2026) RALP1 is essential for schizont maturation and erythrocyte invasion in Plasmodium falciparum. Parasites & vectors, 19(1).

Ndung'u L, et al. (2026) Persistent and Circulating Plasmodium falciparum dhfr and dhps Mutations in Busia County, Western Kenya. Pathogens (Basel, Switzerland), 15(2).

Liu X, et al. (2026) The Plasmodium falciparum PPCS is a unique heteromeric complex with prokaryote-like activity and is a target of pantothenate analogs. Science advances, 12(11), eadx5265.

Guillén-Samander A, et al. (2026) A bridge-like lipid transfer protein is critical for generation of invasive stages in malaria parasites. Nature communications, 17(1).