# Resource Summary Report

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## 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:** data repository, storage service resource, data access protocol, service resource, database, software resource, data or information resource, data analysis service, web service, 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 Agency:** NIAID

**Resource Name:** PlasmoDB

**Resource ID:** SCR_013331

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

## 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 1038 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.


Rios KT, et al. (2024) Global Release of Translational Repression Across Plasmodium's Host-to-Vector Transmission Event. bioRxiv : the preprint server for biology.

de Cesare M, et al. (2024) Flexible and cost-effective genomic surveillance of P. falciparum malaria with targeted nanopore sequencing. Nature communications, 15(1), 1413.

Lopez-Perez M, et al. (2024) Profiling the antibody response of humans protected by immunization with Plasmodium vivax radiation-attenuated sporozoites. Scientific reports, 14(1), 2790.

Niikura M, et al. (2024) Characterization of a nuclear transport factor 2-like domain-containing protein in Plasmodium berghei. Malaria journal, 23(1), 13.

Thawornpan P, et al. (2024) Longitudinal analysis of antibody responses to Plasmodium vivax sporozoite antigens following natural infection. PLoS neglected tropical diseases, 18(1), e0011907.

Castellano CM, et al. (2024) The genetic landscape of origins of replication in P. falciparum. Nucleic acids research, 52(2), 660.

De Meulenaere K, et al. (2024) Selective whole-genome sequencing of Plasmodium parasites directly from blood samples by nanopore adaptive sampling. mBio, 15(1), e0196723.

Kanatani S, et al. (2024) Revisiting the Plasmodium sporozoite inoculum and elucidating the efficiency with which malaria parasites progress through the mosquito. Nature communications, 15(1), 748.

Fraering J, et al. (2024) Infected erythrocytes and plasma proteomics reveal a specific protein signature of severe malaria. EMBO molecular medicine, 16(2), 319.

Cepeda AS, et al. (2024) The Genome of Plasmodium gonderi: Insights into the Evolution of Human Malaria Parasites. Genome biology and evolution, 16(2).

Alvarez-Jarreta J, et al. (2024) VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center in 2023. Nucleic acids research, 52(D1), D808.

Nguyen TK, et al. (2024) Enhancing malaria detection in resource-limited areas: A high-performance colorimetric LAMP assay for Plasmodium falciparum screening. PloS one, 19(2), e0298087.

Higgins M, et al. (2024) New reference genomes to distinguish the sympatric malaria parasites, Plasmodium ovale curtisi and Plasmodium ovale wallikeri. Scientific reports, 14(1), 3843.

Kimenyi KM, et al. (2024) Distinct transcriptomic signatures define febrile malaria depending on initial infective states, asymptomatic or uninfected. BMC infectious diseases, 24(1), 140.

Xie SC, et al. (2024) Reaction hijacking inhibition of Plasmodium falciparum asparagine tRNA synthetase. Nature communications, 15(1), 937.

Lenz T, et al. (2024) Chromatin structure and var2csa - a tango in regulation of var gene expression in the human malaria parasite, Plasmodium falciparum? bioRxiv : the preprint server for biology.

Xu R, et al. (2024) Deaggregation of mutant Plasmodium yoelii de-ubiquitinase UBP1 alters MDR1 localization to confer multidrug resistance. Nature communications, 15(1), 1774.

Crispim M, et al. (2024) Beyond the MEP Pathway: A novel kinase required for prenol utilization by malaria parasites. PLoS pathogens, 20(1), e1011557.

Bennett JM, et al. (2024) Mixed Alkyl/Aryl Phosphonates Identify Metabolic Serine Hydrolases as Antimalarial Targets. bioRxiv : the preprint server for biology.

Hollin T, et al. (2024) Proteome-Wide Identification of RNA-dependent proteins and an emerging role for RNAs in Plasmodium falciparum protein complexes. Nature communications, 15(1), 1365.