

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

GeneDB Pfalciparum

RRID:SCR_006567

Type: Tool

Proper Citation

GeneDB Pfalciparum (RRID:SCR_006567)

Resource Information

URL: <http://www.genedb.org/Homepage/Pfalciparum>

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Description: Database of the most recent sequence updates and annotations for the *P. falciparum* genome. New annotations are constantly being added to keep up with published manuscripts and feedback from the Plasmodium research community. You may search by Protein Length, Molecular Mass, Gene Type, Date, Location, Protein Targeting, Transmembrane Helices, Product, GO, EC, Pfam ID, Curation and Comments, and Dbxrefs. BLAST and other tools are available. The *P. falciparum* 3D7 nuclear genome is 23.3 Mb in size, with a karyotype of 14 chromosomes. The G+C content is approximately 19%. The *P. falciparum* genome is undergoing re-annotation. This process started in October 2007 with a weeklong workshop co-organized by staff from the Wellcome Trust Sanger Institute and the EuPathDB team. Ongoing curation and sequence checking is being carried out by the Pathogen Genomics group. Plasmodium falciparum is the most deadly of the five Plasmodium species that cause human malaria. Malaria has a massive impact on human health; it is the world's second biggest killer after tuberculosis. Around 300 million clinical cases occur each year resulting in between 1.5 - 2.7 million deaths annually, the majority in sub-Saharan Africa. It is estimated that 3,000 children under the age of five years fall victim to malaria each day. Around 40% of the world's population are at risk. In collaboration with EuPathDB, genomic sequence data and annotations are regularly deposited on PlasmoDB where they can be integrated with other datasets and queried using customized queries.

Abbreviations: GeneDB_Pfalciparum, GeneDB Pfalciparum, GeneDB *P. falciparum*

Synonyms: Plasmodium falciparum homepage on GeneDB, Plasmodium falciparum 3D7 on GeneDB

Resource Type: data or information resource, database

Defining Citation: [PMID:12368864](#)

Funding: Wellcome Trust

Resource Name: GeneDB Pfalciparum

Resource ID: SCR_006567

Alternate IDs: nlx_13809

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260905T133135+0000

Ratings and Alerts

No rating or validation information has been found for GeneDB Pfalciparum.

No alerts have been found for GeneDB Pfalciparum.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Witmer K, et al. (2021) Using scRNA-seq to Identify Transcriptional Variation in the Malaria Parasite Ookinete Stage. *Frontiers in cellular and infection microbiology*, 11, 604129.

Szuster-Ciesielska A, et al. (2019) Immunogenic Evaluation of Ribosomal P-Protein Antigen P0, P1, and P2 and Pentameric Protein Complex P0-(P1-P2)₂ of Plasmodium falciparum in a Mouse Model. *Journal of immunology research*, 2019, 9264217.

Reid AJ, et al. (2018) Single-cell RNA-seq reveals hidden transcriptional variation in malaria parasites. *eLife*, 7.

Claessens A, et al. (2017) Culture adaptation of malaria parasites selects for convergent loss-of-function mutants. *Scientific reports*, 7, 41303.

Wawerka L, et al. (2015) In vivo formation of Plasmodium falciparum ribosomal stalk - a unique mode of assembly without stable heterodimeric intermediates. *Biochimica et biophysica acta*, 1850(1), 150.

Pradhan A, et al. (2015) Chemogenomic profiling of Plasmodium falciparum as a tool to aid antimalarial drug discovery. *Scientific reports*, 5, 15930.