# Resource Summary Report

Generated by ASWG on May 3, 2025

# Malaria Parasite Metabolic Pathways

RRID:SCR_007072
Type: Tool

## Proper Citation

Malaria Parasite Metabolic Pathways (RRID:SCR_007072)

## Resource Information

**URL:** http://sites.huji.ac.il/malaria/

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**Description:** Data set of metabolic pathways for the malaria parasite based on the present knowledge of parasite biochemistry and on pathways known to occur in other unicellular eukaryotes. This site extracted the pertinent information from the universal sites and presented them in an educative and informative format. The site also includes, cell-cell interactions (cytoadherence and rosetting), invasion of the erythrocyte by the parasite and transport functions. It also contains an artistic impression of the ultrastructural morphology of the interaerythrocytic cycle stages and some details about the morphology of mitochondria and the apicoplast. Most pathways are relevant to the erythrocytic phase of the parasite cycle. All maps were checked for the presence of enzyme-coding genes as they are officially annotated in the Plasmodium genome (http://plasmodb.org/). The site is constructed in a hierarchical pattern that permits logical deepening: * Grouped pathways of major chemical components or biological process ** Specific pathways or specific process *** Chemical structures of substrates and products or process **** Names of enzymes and their genes or components of process Each map is linked to other maps thus enabling to verify the origin of a substrate or the fate of a product. Clicking on the EC number that appears next to each enzyme, connects the site to BRENDA, SWISSPROT ExPASy ENZYME, PlasmoDB and to IUBMB reaction scheme. Clicking of the name of a metabolite, connects the site to KEGG thus providing its chemical structure and formula. Next to each enzyme there is a pie that depicts the stage-dependent transcription of the enzyme''s coding gene. The pie is constructed as a clock of the 48 hours of the parasite cycle, where red signifies over-transcription and green, under-transcription. Clicking on the pie links to the DeRisi/UCSF transcriptome database.

**Abbreviations:** Malaria Parasite Metabolic Pathways

**Resource Type:** image collection, data or information resource, data set

**Keywords:** enzyme, gene, genome, map, metabolic, mosquito, parasite, pathway, plasmodium falciparum, protein, reaction, sequence, metabolic pathway, chemical structure, cell-cell interaction, transport, morphology, mitochondria, apicoplast

**Related Condition:** Malaria

**Funding:** UNDP/World Bank/WHO Special Programme ;
NIAID ;
European Union ;
6th FP- BioMalPar Network of Excellence on Biology and Pathology of the Malaria Parasite

**Resource Name:** Malaria Parasite Metabolic Pathways

**Resource ID:** SCR_007072

**Alternate IDs:** nif-0000-21249

**Record Creation Time:** 20220129T080239+0000

**Record Last Update:** 20250502T055655+0000

## Ratings and Alerts

No rating or validation information has been found for Malaria Parasite Metabolic Pathways.

No alerts have been found for Malaria Parasite Metabolic Pathways.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Wang D, et al. (2018) Identification of Nutritional Components in Black Sesame Determined by Widely Targeted Metabolomics and Traditional Chinese Medicines. Molecules (Basel, Switzerland), 23(5).

Kim YJ, et al. (2017) Integration of Traditional and Metabolomics Biomarkers Identifies Prognostic Metabolites for Predicting Responsiveness to Nutritional Intervention against Oxidative Stress and Inflammation. Nutrients, 9(3).

Xu J, et al. (2016) Genetic Diversity and Molecular Evolution of a Violaxanthin De-epoxidase Gene in Maize. Frontiers in genetics, 7, 131.

Skorokhod OA, et al. (2015) Oxidative stress-mediated antimalarial activity of plakortin, a natural endoperoxide from the tropical sponge Plakortis simplex. Free radical biology & medicine, 89, 624.

Dorin-Semblat D, et al. (2015) Malaria Parasite-Infected Erythrocytes Secrete PfCK1, the Plasmodium Homologue of the Pleiotropic Protein Kinase Casein Kinase 1. PloS one, 10(12), e0139591.

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

Penarete-Vargas DM, et al. (2014) A chemical proteomics approach for the search of pharmacological targets of the antimalarial clinical candidate albitiazolium in Plasmodium falciparum using photocrosslinking and click chemistry. PloS one, 9(12), e113918.

Walter V, et al. (2013) Molecular subtypes in head and neck cancer exhibit distinct patterns of chromosomal gain and loss of canonical cancer genes. PloS one, 8(2), e56823.

Singh VK, et al. (2013) Methylerythritol phosphate pathway to isoprenoids: kinetic modeling and in silico enzyme inhibitions in Plasmodium falciparum. FEBS letters, 587(17), 2806.

Dastidar EG, et al. (2012) Involvement of Plasmodium falciparum protein kinase CK2 in the chromatin assembly pathway. BMC biology, 10, 5.

Cancino-Rodezno A, et al. (2012) Comparative proteomic analysis of Aedes aegypti larval midgut after intoxication with Cry11Aa toxin from Bacillus thuringiensis. PloS one, 7(5), e37034.

Kaplan F, et al. (2012) Transcriptional and metabolic insights into the differential physiological responses of arabidopsis to optimal and supraoptimal atmospheric CO2. PloS one, 7(8), e43583.

Huthmacher C, et al. (2010) Antimalarial drug targets in Plasmodium falciparum predicted by stage-specific metabolic network analysis. BMC systems biology, 4, 120.

Plata G, et al. (2010) Reconstruction and flux-balance analysis of the Plasmodium falciparum metabolic network. Molecular systems biology, 6, 408.

Briolant S, et al. (2010) Plasmodium falciparum proteome changes in response to doxycycline treatment. Malaria journal, 9, 141.

Rowe JA, et al. (2009) Adhesion of Plasmodium falciparum-infected erythrocytes to human cells: molecular mechanisms and therapeutic implications. Expert reviews in molecular medicine, 11, e16.

Morris PF, et al. (2009) Multiple horizontal gene transfer events and domain fusions have created novel regulatory and metabolic networks in the oomycete genome. PloS one, 4(7), e6133.

Jiménez-Marín Á, et al. (2009) Biological pathway analysis by ArrayUnlock and Ingenuity Pathway Analysis. BMC proceedings, 3 Suppl 4(Suppl 4), S6.

Gunasekera AM, et al. (2007) Regulatory motifs uncovered among gene expression clusters in Plasmodium falciparum. Molecular and biochemical parasitology, 153(1), 19.

Gunasekera AM, et al. (2004) Widespread distribution of antisense transcripts in the Plasmodium falciparum genome. Molecular and biochemical parasitology, 136(1), 35.