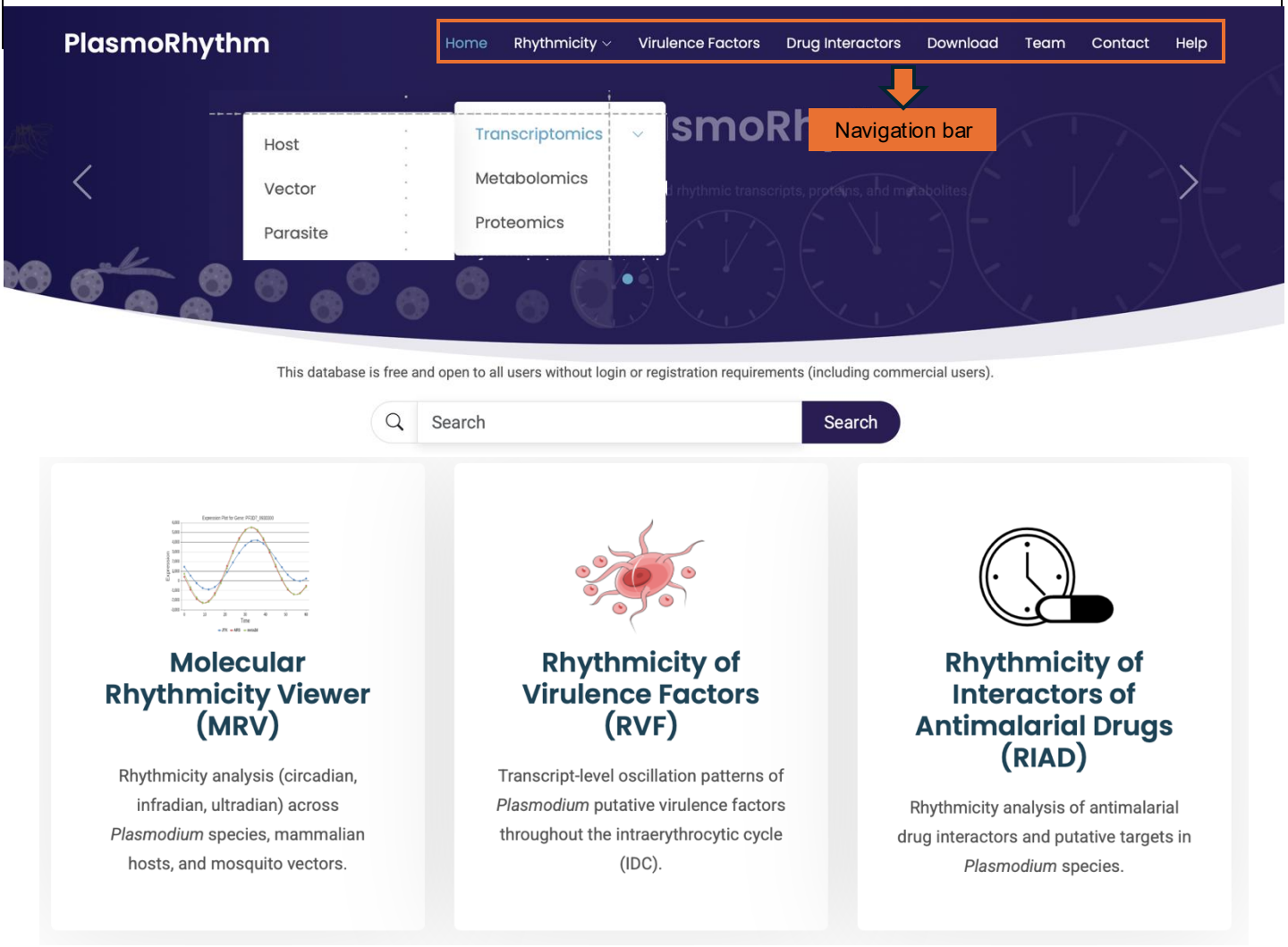
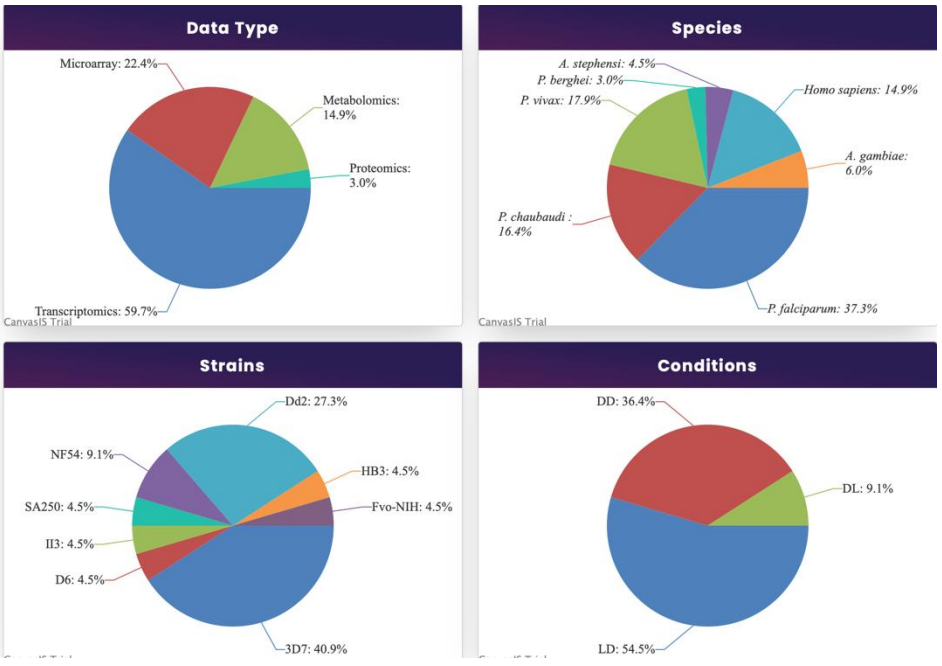
1. **Homepage**:

- The **homepage** features a top navigation bar that links to all major modules: ***Home, Rhythmicity, Virulence Factors, Drug Interactions, Download, Team, Contact, and Help***.
- The Rhythmicity module includes dropdown menus for selecting a biological entity (***Parasite, Host, Vector***) and an omics layer (***Transcriptomics, Proteomics, Metabolomics***), enabling quick access to time-series datasets.



2. **Data Visualization:** The section presents key dataset categories as an interactive pie chart. Users can select any segment to navigate directly to the corresponding dataset, enabling quick and intuitive access to specific data groups.



3. Search bar: A dedicated search panel enables queries by name, ID, or description, returning matched entries with organism details, functional annotation, omics type, and rhythmicity status (significant/nonsignificant). Selecting a result opens the corresponding detailed expression or abundance profile. This feature enhances transparency and usability, ensuring that users can easily navigate and understand the scope of PlasmoRhythm from the very first page.

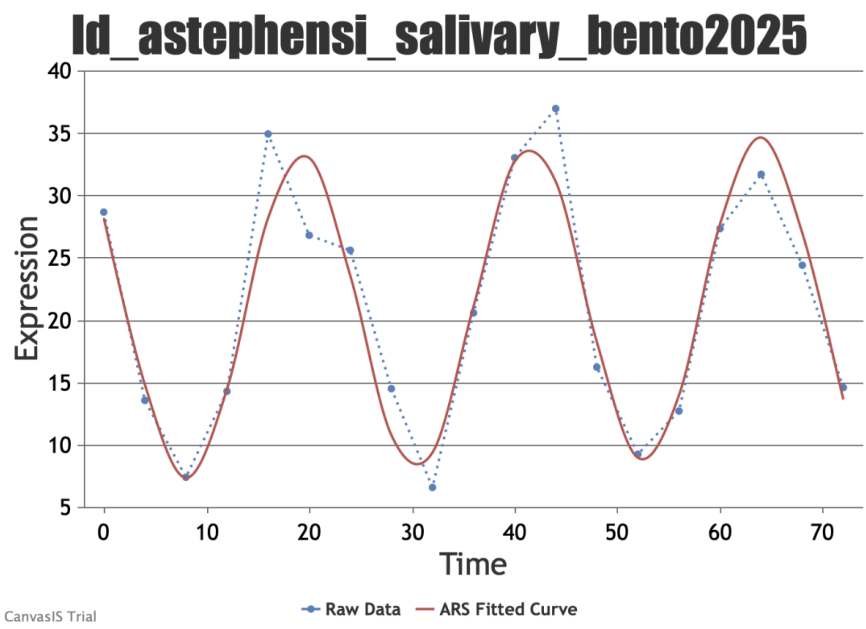
Search gene, protein, or metabolite.

ASTE009868 Search

Searched query: ASTE009868

S.No	CycID	Description	Dataset	Organism	Omics Type	Reference	Rhythmicity
1	ASTE009868	period circadian protein [Source:Projected from Anopheles gambiae (AGAP001856) VB Community Annotation]	dd_astephensi_salivary_bento2025	Anopheles stephensi	RNAseq	Bento et al., Nat Microbiol. 2025, PMID: 40164831	Significant
2	ASTE009868	period circadian protein [Source:Projected from Anopheles gambiae (AGAP001856) VB Community Annotation]	ld_astephensi_salivary_bento2025	Anopheles stephensi	RNAseq	Bento et al., Nat Microbiol. 2025, PMID: 40164831	Significant

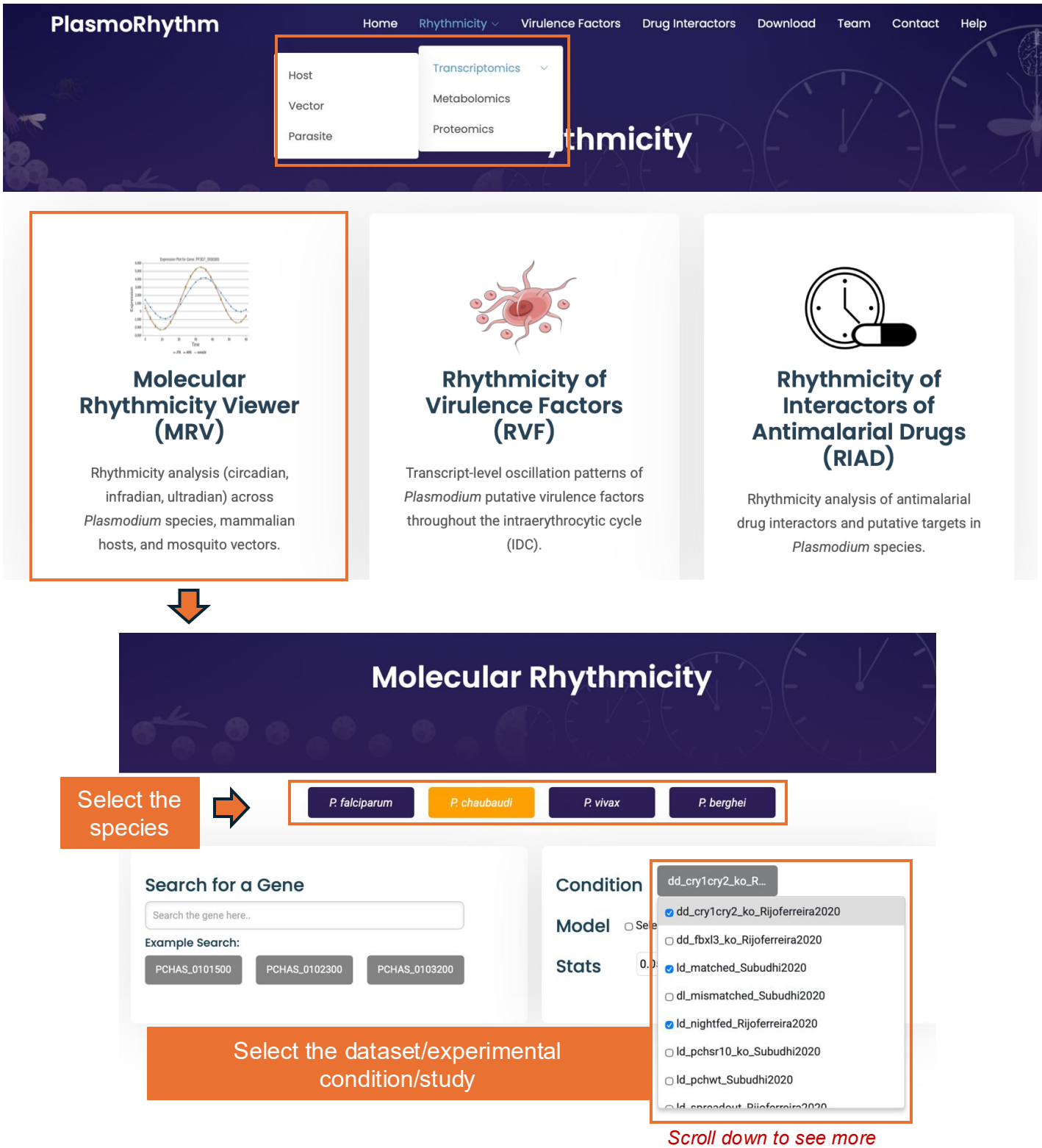
Result



Download CSV Download Time Point Table

CycID	Model	Amplitude	pvalue	qvalue	Period	Phase
ASTE009868	ARS	12.777	0.000	0.000	22.302	19.246
ASTE009868	JTK	10.743	0.000	0.024	24.000	20.000
ASTE009868	LS	22.417	0.005	0.923	22.484	10.094
ASTE009868	meta2d	12.345	0.000	0.000	22.929	17.757

4. Molecular Rhythmicity viewer (MRV): The MRV offers a direct entry point on the homepage/main menu to explore transcript-level time-dependent expression profiles across hosts, *Plasmodium* parasites, and mosquito vectors. All panels share a uniform interface, ensuring a consistent user experience regardless of the selected organism. Users can search and filter genes by PlasmoDB ID, name, species, strain, or experimental condition, and compare results across multiple datasets.



Molecular Rhythmicity

P. falciparum | P. chaubaudi | P. vivax | P. berghei

Search for a Gene

PCHAS_0101500

Example Search:

PCHAS_0101500 | PCHAS_0102300 | PCHAS_0103200

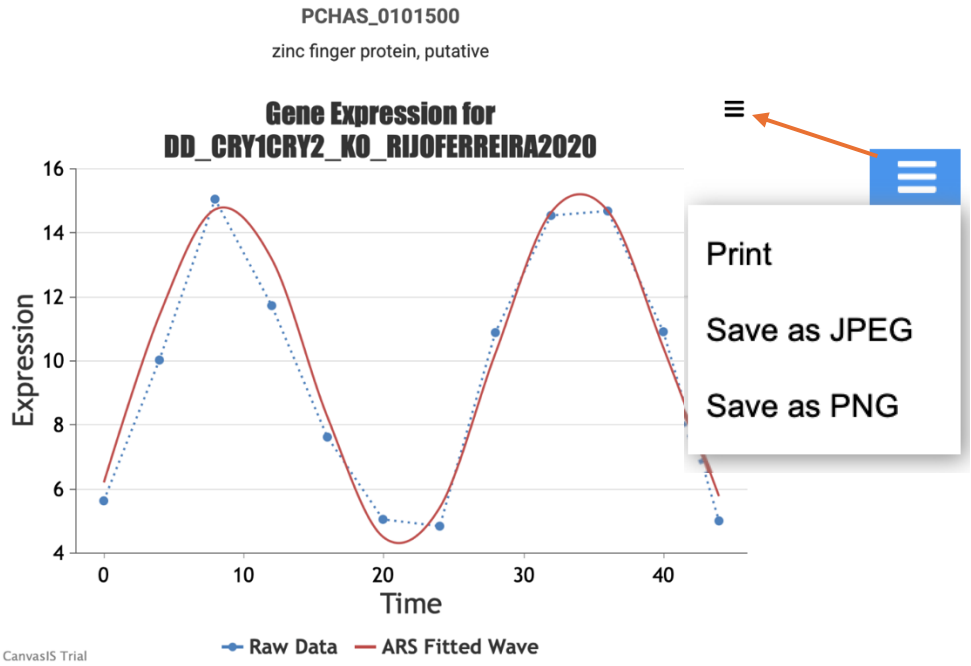
Condition: dd_cry1cry2_ko_R...

Model: Select All | JTK | ARS | LS | META2D

Stats: 0.05 | p-value | q-value

Here, the user can select the desired model and statistical cutoff.

Click here → Submit



Download Result Table | Download Plot Table

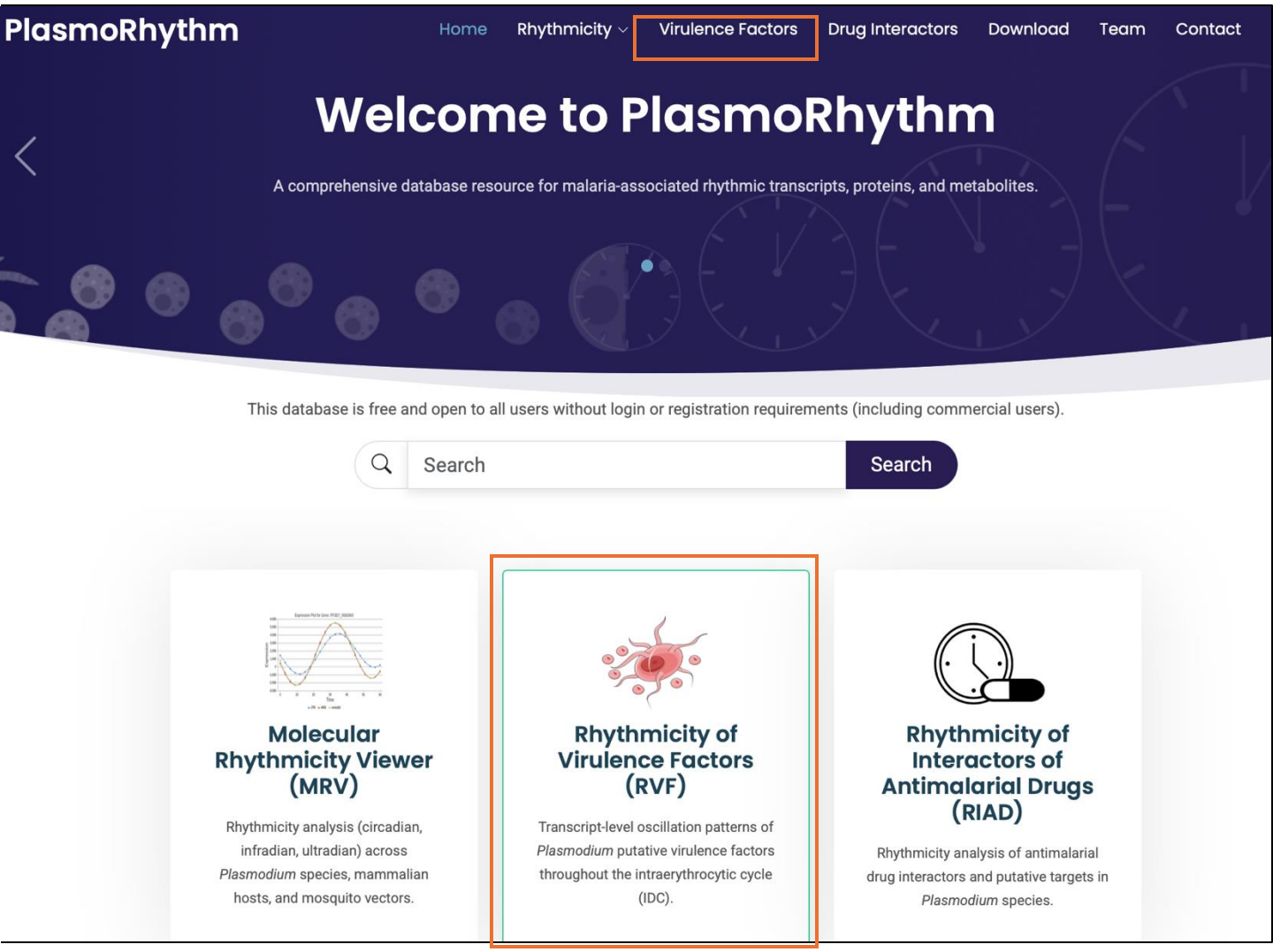
Results Table for DD_CRY1CRY2_KO_RIJOFERREIRA2020

CycID	Model	Amplitude	pvalue	qvalue	Period	Phase
PCHAS_0101500	JTK	4.348	0.00079	0.00705	28.000	8.000
PCHAS_0101500	ARS	5.420	< 0.00001	0.00010	25.266	8.715
PCHAS_0101500	LS	13.194	0.04250	0.37485	25.019	9.191
PCHAS_0101500	meta2d	5.461	< 0.00001	< 0.00001	26.095	8.684

The user can select the model and check the available model fitting using the raw data. Subsequently, the user can scroll down to review the rhythmic profiles and statistical values of the other datasets.

5. Rhythmicity of virulence factor (RVF):

- The RVF module provides access to curated *Plasmodium* virulence gene families, including PfEMP1, RIFIN, STEVOR, MSP, SERA, CLAG, and FIKK kinases. Users can select the species (*P. falciparum or P. vivax*) and browse rhythmic expression profiles of these gene sets.
- The interface displays each gene family as a selectable category; choosing a category retrieves its corresponding time-series expression data and rhythm parameters (period, phase, amplitude).
- Gene Ontology (GO) terms and identifiers linked to each virulence gene are available directly within the module, enabling quick functional interpretation.
- The RVF module supports comparison across datasets and experimental conditions, allowing users to evaluate temporal expression dynamics and identify patterns relevant to invasion, immune evasion, and other virulence-associated processes.



User can either directly select from the homepage or the navigation panel

Rhythmicity of Virulence Factors

Transcript-level oscillation patterns of *Plasmodium* virulence factors throughout the intraerythrocytic cycle (IDC).

P. falciparum *P. vivax*

Analysis of putative virulence factors

PfEMP1 RIFIN STEVOR MSP SERA
RhopH/CLAG FIKK ETRAMP PFMC-2TM Invasion Ligands
PTEX Chaperones & Transporters Proteases & Enzymes Surface Antigens

Click here → Submit

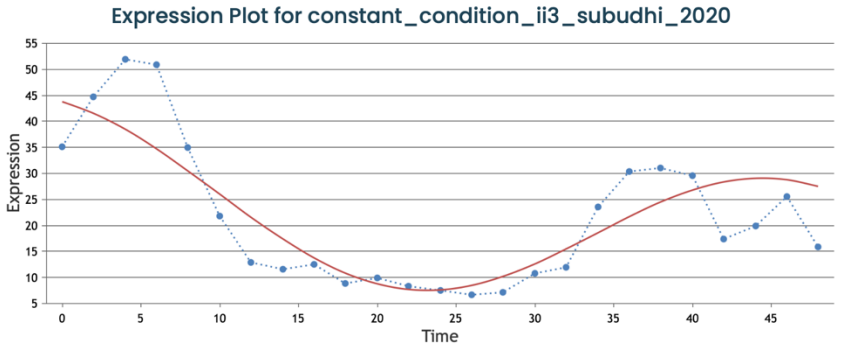
PfEMP1

Major surface antigen family mediating sequestration and immune evasion.

PfEMP1 – erythrocyte membrane protein 1, PfEMP

Gene	Curated GO Component IDs
PF3D7_0100100	GO:0020002;GO:0020030
PF3D7_0100300	N/A
PF3D7_0115700	GO:0020002;GO:0020030
PF3D7_0200100	GO:0020002;GO:0020030
PF3D7_0223500	GO:0020002;GO:0020030
PF3D7_0300100	N/A
PF3D7_0324900	N/A
PF3D7_0400100	GO:0020002;GO:0020030
PF3D7_0400400	GO:0020002;GO:0020030
PF3D7_0412400	GO:0020002;GO:0020030
PF3D7_0412700	GO:0020002;GO:0020030
PF3D7_0412900	GO:0020002;GO:0020030
PF3D7_0413100	GO:0020002;GO:0020030
PF3D7_0420700	GO:0020002;GO:0020030

Scroll down to see more



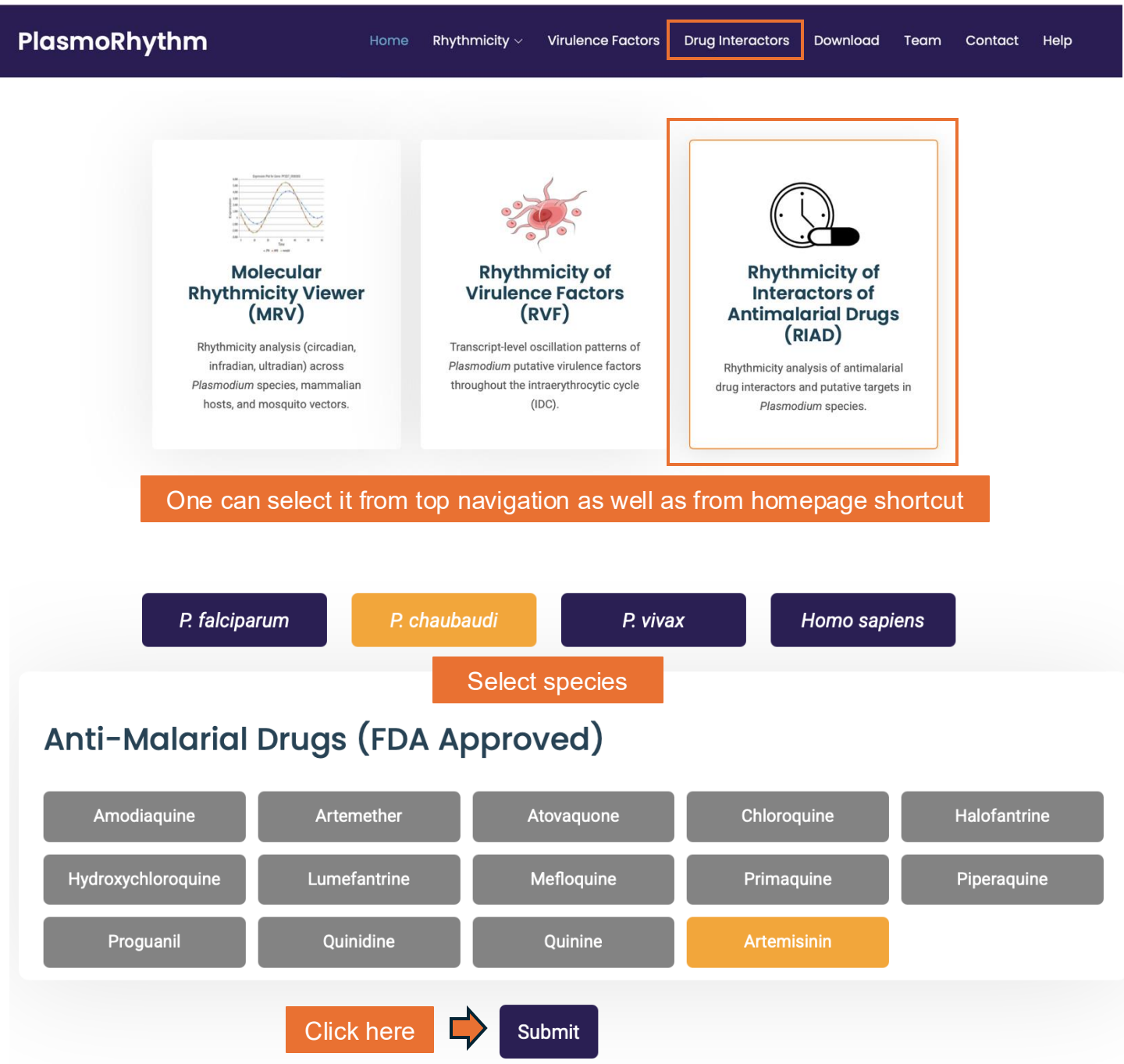
Model	Amplitude	pvalue	qvalue	Period	Phase
ARS	14.611	0.000	0.000	48.000	45.815
JTK	14.791	0.000	0.000	46.000	2.000
LS	23.827	0.028	0.040	46.000	40.966
meta2d	15.330	0.000	0.000	46.667	44.917

Scroll down to see more

A literature-derived set of putative virulence-associated genes from *P. falciparum* and *P. vivax*, compiled from peer-reviewed studies and annotated with functional categories and GO terms from the PlasmoDB database (PlasmoDB). This module presents high-resolution transcriptomic rhythmicity profiles of these factors across the intraerythrocytic cycle. A comprehensive list of curated virulence factors, annotations, GO terms, and references is provided in the **Download** tab

6. Rhythmicity of interactors of antimalarial drug (RIAD):

- Allows users to select a species (*P. falciparum, P. chabaudi, P. vivax, or Homo sapiens*) to explore drug–gene interactions.
- Displays a curated panel of FDA-approved antimalarial drugs, each shown as a clickable button.
- Selecting a drug retrieves the corresponding list of predicted or literature-supported gene interactors for the chosen species.
- Provides interactive time-series expression plots for each interactor, enabling exploration of rhythmic transcriptional patterns.
- Offers downloadable rhythm parameters (period, phase, amplitude, p-value, q-value) for further analysis.



Artemisinin in *P.chaubaudi*

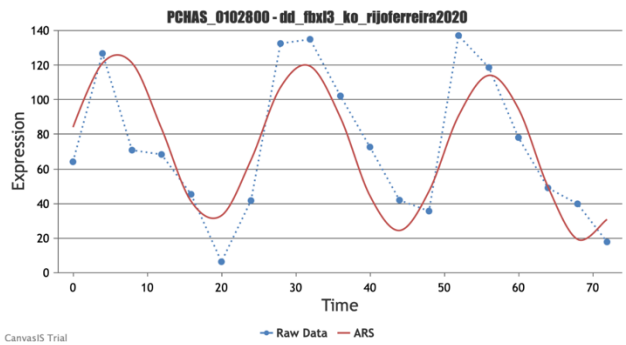
The foundational artemisinin compound; its endoperoxide bridge is activated by heme-iron to generate reactive radicals that damage parasite proteins.

Drug Interactors

Gene	Description
PCHAS_0101000	lysophospholipase, putative
PCHAS_0102800	dihydroorotate dehydrogenase, putative
PCHAS_0105300	elongation of fatty acids protein, putative
PCHAS_0106000	coatomer alpha subunit, putative
PCHAS_0107550	sorting assembly machinery 50 kDa subunit, putative
PCHAS_0107700	proteasome subunit alpha type-2, putative
PCHAS_0107900	T-complex protein 1 subunit zeta, putative

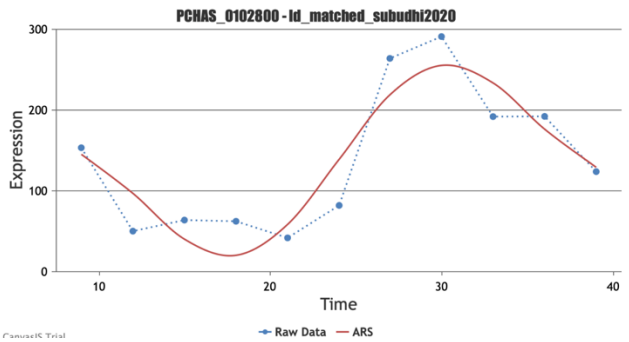
Scroll down to see more

Rhythmic Expression Profile



PCHAS_0102800 (dd_fbxl3_ko_rijoferreira2020)

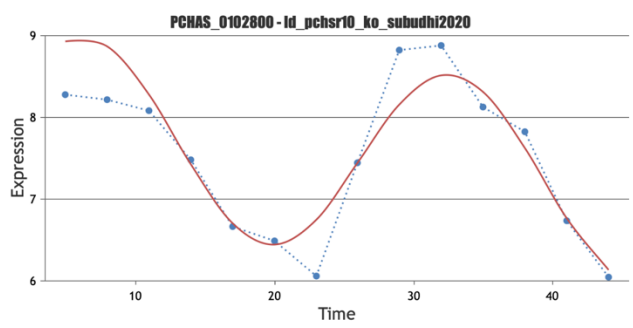
Model	Amplitude	pvalue	qvalue	Period	Phase
ARS	46.447	0.000	0.000	25.107	6.100
JTK	41.012	0.004	0.009	28.000	4.000
LS	91.514	0.024	0.097	25.060	11.669
meta2d	40.807	0.000	0.000	26.056	7.151



PCHAS_0102800 (ld_matched_subudhi2020)

Not significant for JTK, LS

Model	Amplitude	pvalue	qvalue	Period	Phase
ARS	90.814	0.003	0.012	22.855	6.811
JTK	105.115	0.075	0.162	27.000	4.500
LS	260.876	0.108	0.550	27.000	3.561
meta2d	98.398	0.002	0.006	25.618	5.055



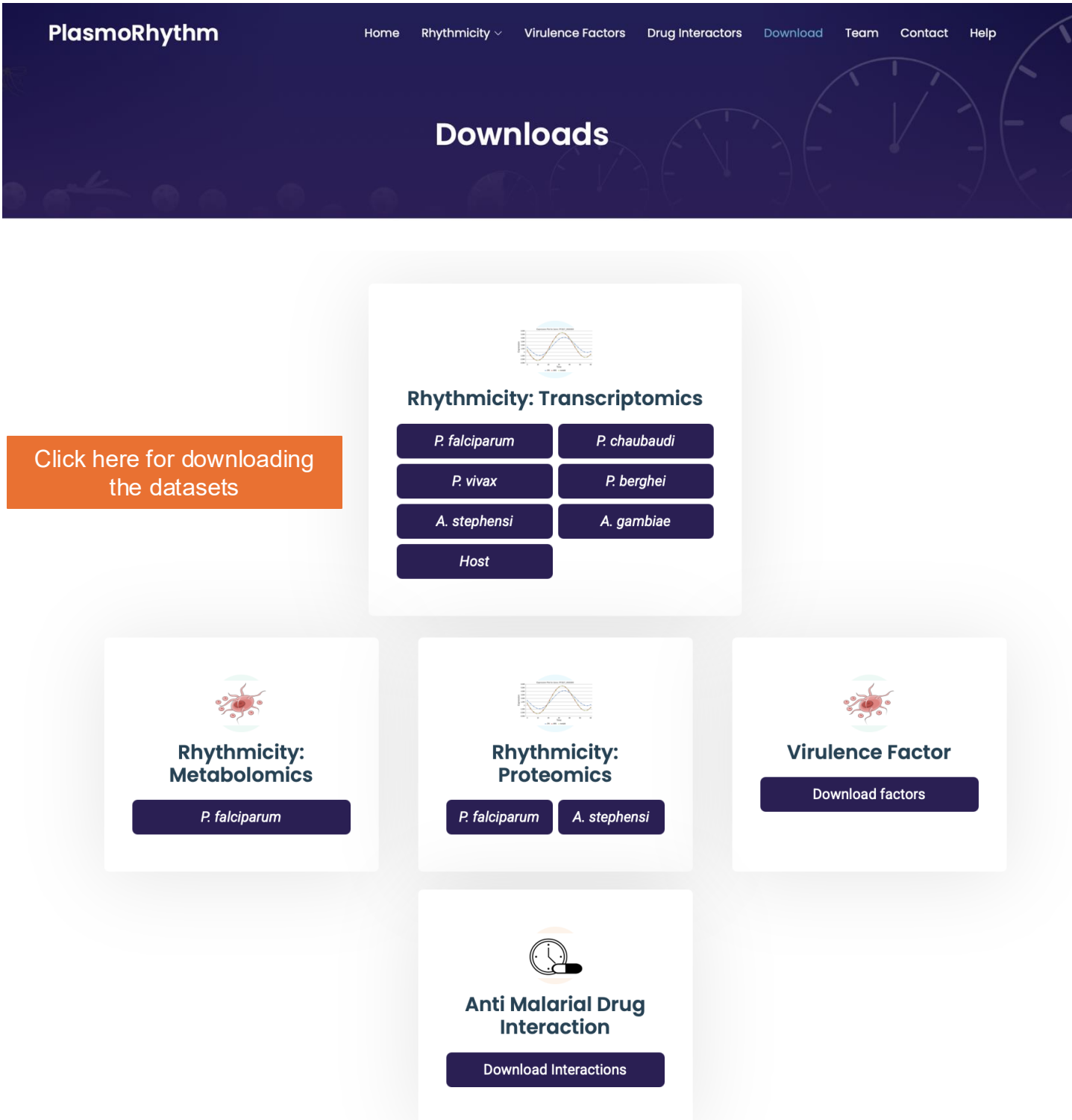
PCHAS_0102800 (ld_pchsr10_ko_subudhi2020)

Model	Amplitude	pvalue	qvalue	Period	Phase
ARS	1.150	0.000	0.001	26.263	6.457
JTK	1.098	0.000	0.001	27.000	6.500
LS	8.538	0.028	0.243	24.344	8.793
meta2d	1.216	0.000	0.000	25.869	7.289

Scroll down to see more

7. Downloads

- The Downloads page provides direct access to all datasets in **PlasmoRhythm.** Users can download rhythmicity outputs for transcriptomics (across parasite, vector, and host species), metabolomics (*P. falciparum*), proteomics (*P. falciparum, A. stephensi*), virulence factors, and curated drug–gene interaction files. Each module is presented as a clickable card, allowing quick retrieval of species-specific datasets for external analysis.



Help

Submit Your File

Name:

Email:

Pubmed Link:

Institute:

Upload File:

Choose File | no file selected

Submit

The **Help** page allows users to submit their own datasets for inclusion in PlasmoRhythm. A simple form is provided to enter contact details (name, email, institute), an optional PubMed link, and to upload a file. After completing the form, users can submit their dataset for review by the PlasmoRhythm team.

Address

Dr. Sandipan Ray, BT 317, Third Floor, Department of Biotechnology, Indian Institute of Technology Hyderabad 502285, India.

Call Us

+91 87903 43903

Email Us

sandipan.ray@bt.iith.ac.in