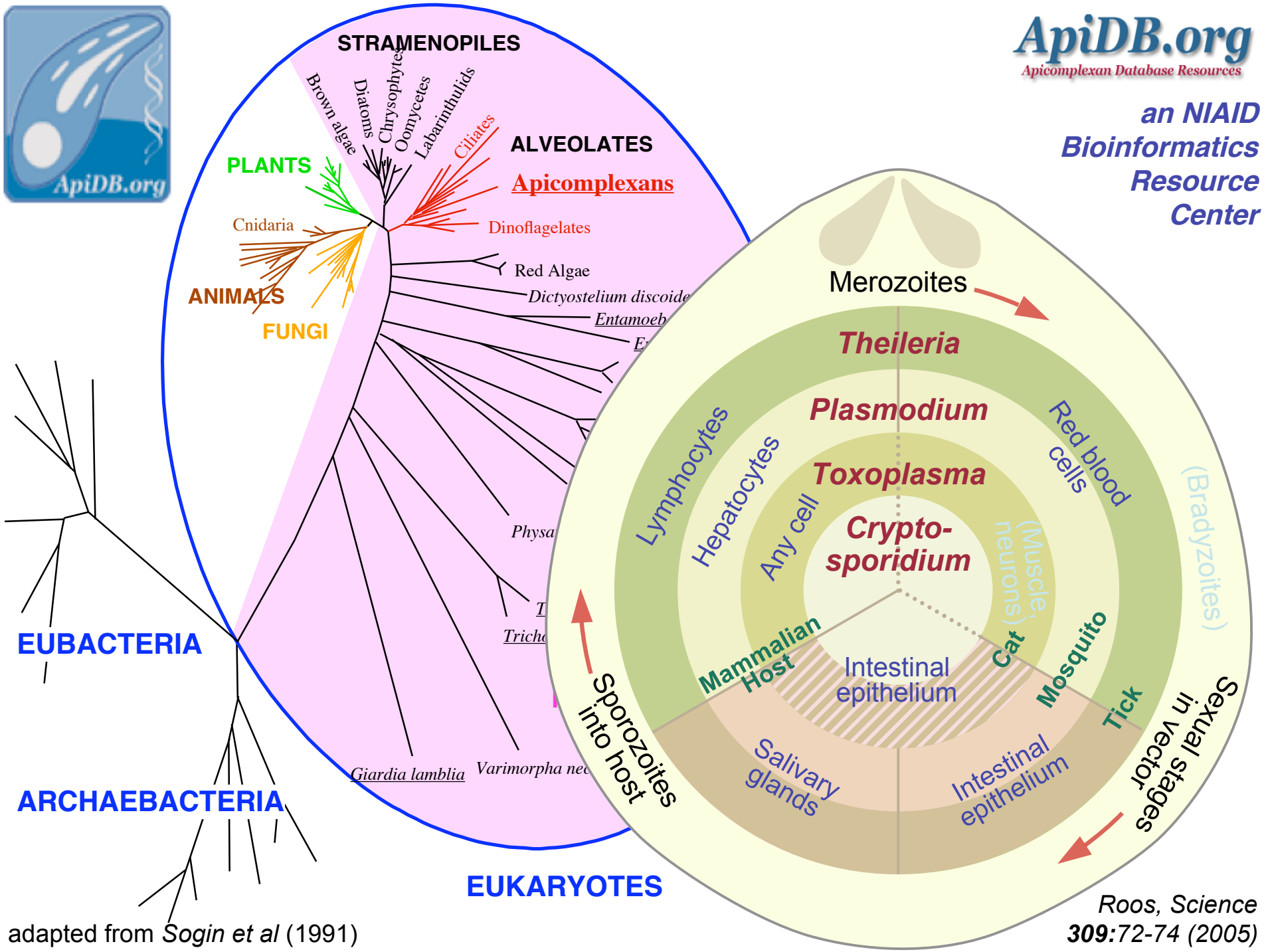


adapted from *Sogin et al* (1991)

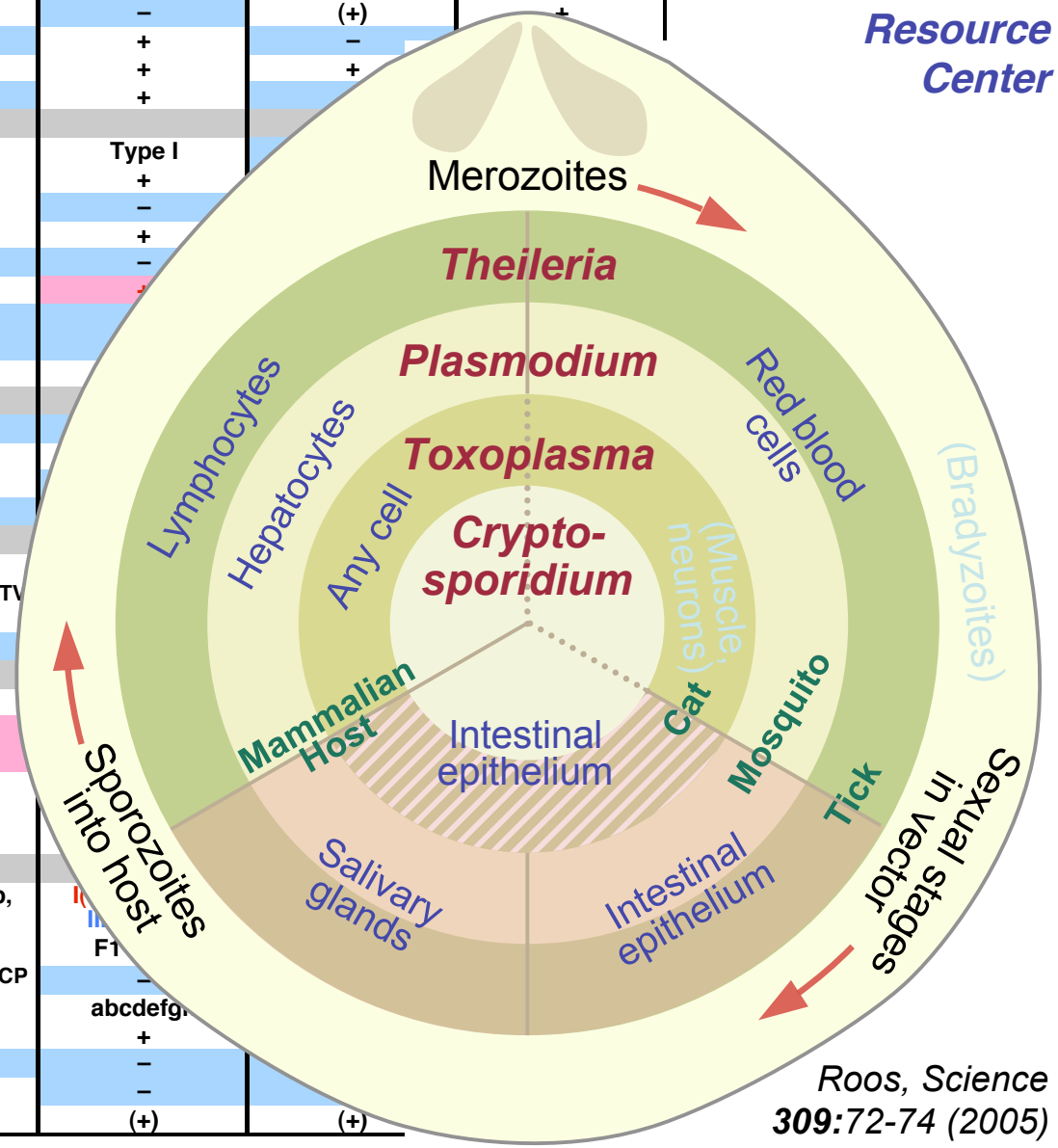
Roos, Science ***309:****72-74 (2005)*

Metabolic Pathway Comparisons

Pathways	Toxoplasma	Plasmodium	Cryptosporidium	Theileria	Human
Carbohydrates					
glycolysis	+	+	+	+	+
gluconeogensis	+	–	–	–	+
TCA cycle	+	+	–	+	+
PDH complex	+	+	+	–	+
pentose phosphate pathway	+	+	–	(+)	+
methyl-glyoxal detoxification	+	+	–	(+)	+
polysaccharide metabolism	+	–	+	–	
N-glycosylation	+	+	+	+	
O-glycosylation	+	–	+		
Lipids					
FA biosynthesis	Type I & II	Type II	Type I		
elongation	+	+	+		
isoprenoid biosynthesis	DoxP	DoxP	–		
farnesylation	+	+	+		
sterol biosynthesis	–	–	–		
polyketide synthesis	+	–	+		
beta oxidation	+	–			
propionate metabolism	Me–citrate	–			
glycerolipid metabolism	+	+			
Nucleic acids					
purine synthesis	–	–			
purine salvage	+	+			
pyrimidine biosynthesis	+	+			
pyrimidine salvage	+	–			
Amino acids					
biosynthesis	ACDEGKNPQSY	DEGNQ ACFHIKLMPRSTV WY			
essential AAs	FHILMRTVW				
degradation	IVL	–			
Cofactors					
lipoate	+	+			
folate	+	+			
pyridoxine	+	+			
pantothenate	+	–			
riboflavin, nicotinate, biotin	–	–			
cofactor interconversion	+	+			
Other					
oxidative phosphorylation complex	I(typeII),II,Ub, III,IV	I(typeII),II,Ub, III,IV	I(II		
mitochondrial ATP synthase	F1 – αβγδε F0 - abcdeg/OSCP	F1 – αβγδε F0 - abcdeg/OSCP	F1 –		
vacuolar ATPase	abcdefgh	abcdefgh	abcdefg		
polyamine biosynthesis	–	+	+		
urea cycle	–	–	–		
heme biosynthesis	(+)	(+)	–		
redox metabolism	+	(+)	(+)	(+)	

ApiDB.org
Apicomplexan Database Resources

an NIAID Bioinformatics Resource Center

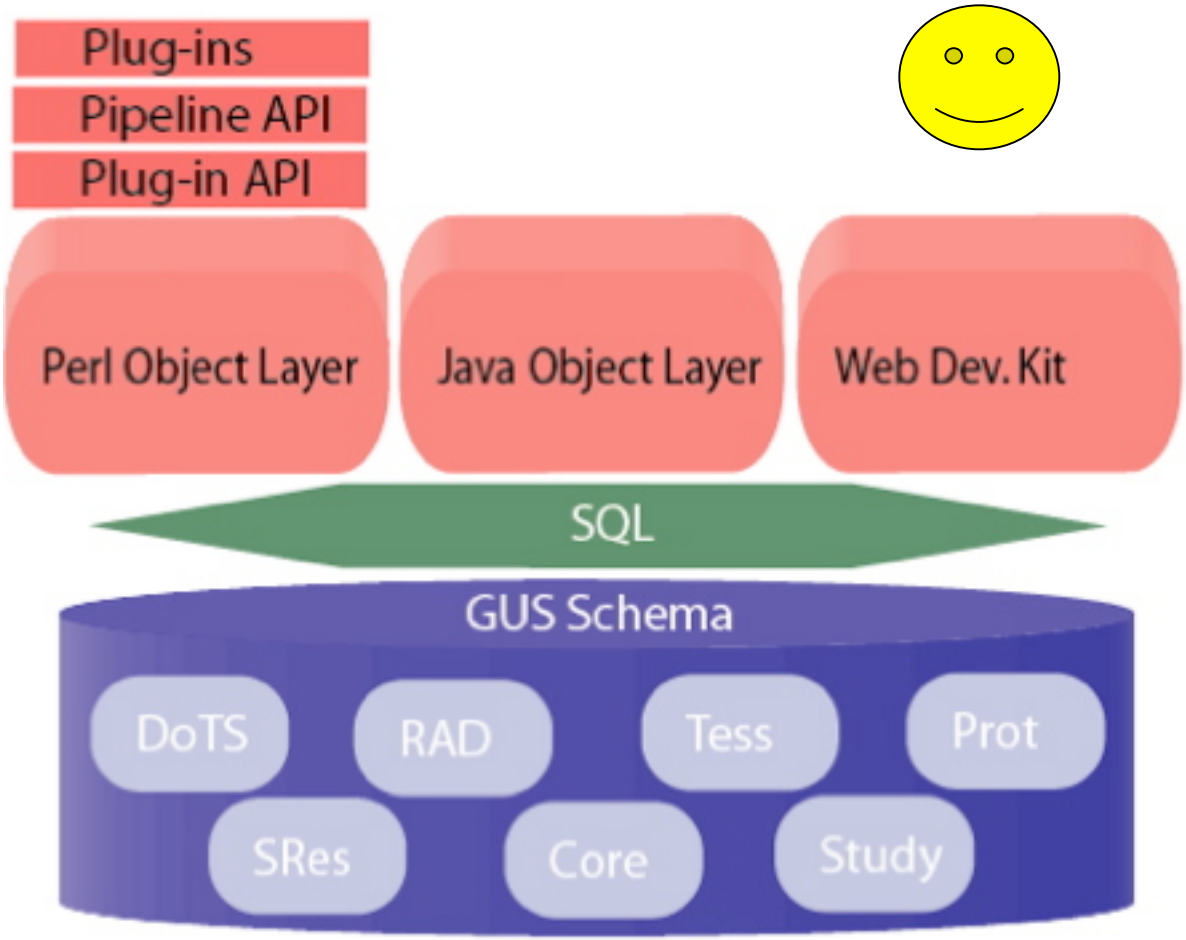


Roos, Science ***309:****72-74 (2005)*

What's New Highlights

- Infrastructure and features
  - New Architecture continues to improve.
    - User registration and persistent history
    - Count of items in history
  - Reorganized query presentation
  - Tutorials
- Key New Data
  - Proteomics (C, T soon)
  - Gene expression (T, P)
  - Polymorphism (P, T)
- ApiDB
  - Many additional queries
  - Identify orthologs between the apicomplexans
  - Cyc tools for all component databases
  - Moving to web services for federation

Architecture



ApiDB Personnel

- UGA
  - Jessica Kissinger
  - John Miller
  - Eileen Kraemer
  - Mark Heiges
  - Cristina Aurrecoechea
  - Cary Pennington
  - Haiming Wang
  - Kathy Couch
  - Shanshan Ding
  - Alan Gingle
  - Pablo Mendes
  - Kelly Storm
  - Rui Wang
  - Zhiming Wang
  - Yunzhou Wu
- Upenn
  - David Roos
  - Chris Stoeckert
  - Brian Brunk
  - Steve Fischer
  - Bindu Gajria
  - Debbie Pinney
  - John Iodice
  - Jennifer Dommer
  - Praveen Chakravarti
  - Jerric Gao
  - John Brestelli
  - Jonathan Schug
  - Greg Grant
  - Trish Whetzel

CryptoDB PlasmoDB ToxoDB

ApiDB.org

Apicomplexan Database Resources

Release 2.1
November 17,2006

ApiDB: A Bioinformatics Resource Center for Biodefense and Emerging/Re-emerging Infectious Diseases.
It comprises four member Websites: ApiDB.org, CryptoDB.org, PlasmoDB.org and ToxoDB.org.
ApiDB.org is the portal that offers Gene, Genome, EST & ORF queries spanning all component databases.

My Queries: 5

As part of our ongoing education efforts we are proud to announce the second of four, annual, apicomplexan database workshops, next June. Please click here for further information and to register. The registration deadline is January 19, 2007.

Home | Queries and Tools | Query History | Data Sources | Downloads | News | Help

ApiDB.org Release 2.1

- New login system to keep all your queries between sessions
- Ortholog relationships spanning all supported organisms
- New support page for you to send us feedback
- More ApiDB.org News

My ApiDB Account

Email: brunkb@pcbi.u
Password: ••••••••
Login
Forgot Password? Register/Subscribe

ApiDB Outreach

- Events with ApiDB Presence
- ApiDB Workshops
- ApiDB Publications

Community Resources

- BRC Central
- OrthoMCL

Tools

BLAST: BLAST search of all available apicomplexan sequences
This search returns a NCBI-like BLAST report. This report is more taxonomically extensive than the one you can obtain under "Queries" (see below), but will not be included in your "Query History". ▸go!

KEGG Maps: View "painting" of KEGG metabolic pathway maps with apicomplexan enzymes ▸go!

Queries

The BLAST queries below contain only Crypto, Plasmo and Toxo species, but results will be saved in your "Query History" and can be combined with other queries.

Identify Genes Based On:

Gene ID: PFI0735c ▸go!
(Examples: cgd1_1090, PFI0735c, 83.m00004. You can use a wildcard *)

Keyword Text (search product name) ▸go!
Species ▸go!
Orthologs and Paralogs ▸go!
Orthology Profile ▸go!
Type (e.g. rRNA, tRNA) ▸go!
EC Number ▸go!
GO Term ▸go!
InterPro/Pfam Domain ▸go!
Protein Motif ▸go!
Signal Peptide ▸go!
Transmembrane Domain ▸go!
Molecular Weight ▸go!
BLAST Similarity ▸go!
Chromosomal Location ▸go!
Exon/Intron Structure ▸go!

Release 2.1

Availability: A = ApiDB C = CryptoDB P = PlasmoDB T = ToxoDB

Identify Genes Based On:

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- Chromosomal Location A C P T
- Proximity to Centromeres P
- Proximity to Telomeres P
- Non-nuclear Genomes P

Gene Attributes
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- Exon/Intron Structure A C P T

Population Biology
- SNPs P T
- Microsatellites

Transcript Expression
- EST Evidence C P T
- SAGE Tag Evidence
- Microarray Evidence P

Similarity/Pattern
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- Interpro/Pfam Domain A C P T
- BLAST similarity A C P T

Protein Expression
- Mass Spec. Evidence C P

Predicted Proteins
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- Isoelectric Point P T
- Secondary Structure P
- Crystal Structure P
- Predicted 3D Structure P

Putative Function
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- EC Number A C P T
- Metabolic Pathway C P T
- Y2H Interaction P
- Predicted Interaction P

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- Exported to Host P

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- Homology Profile P

Other Attributes
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- ID A C P T
- Species A C P
- Available Reagents P

Identify Genomic Sequences Based On:

- BLAST Similarity A C P T
- DNA Sequence Motif
- ID A C P T
- Species A P

Identify ESTs Based On:

- Chromosomal Location P T
- Extent of Gene Overlap C P T
- BLAST Similarity A C P T
- EST Sequence Motif
- Library C P T
- Species

Identify ORFs Based On:

- Chromosomal Location P T
- BLAST Similarity A C P T
- ORF Sequence Motif A C
- Mass Spec. Evidence C
- Species

Identify SNPs Based On:

- Chromosomal Location P T
- Gene ID P T
- AlleleFrequency P

PlasmoDB : The Plasmodium genome resource

PlasmoDB

The Plasmodium Genome Resource

Release 5.2

Welcome to PlasmoDB! PlasmoDB.org hosts genomic, proteomic and accessory data for different species of the parasitic eukaryote Plasmodium, the causative agent of the disease Malaria. Publications exploiting PlasmoDB should provide appropriate acknowledgement to the database developers and those scientists who have made their data available on this site. PlasmoDB is part of an NIH/NIAID funded Bioinformatics Resource Center to provide Apicomplexan Database Resources.

Why the new look and feel? PlasmoDB 5.1 employs a new architecture designed to accommodate new data types and facilitate frequent updates to the database. For further details click here. Features not yet available in PlasmoDB 5.1 may still be accessed via PlasmoDB 4.4, and the results of PlasmoDB 4.4 queries may be exported to PlasmoDB 5.1 (see PlasmoDB 4.4 Query History).

Home | Queries & Tools | Data Sources | Downloads | My Query History (no queries) | About PlasmoDB | Support | Coming soon...

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Did you know?

Did you know you can hide or show some sections of the Gene page by enabling cookie in your browser?

Read all the 'Did you knows'

Featured data source

Transcriptome: HB3 erythrocytic series from the DeRisi lab

See all data sources

Access the latest PlasmoCD

Related Sites:

- ApiDB
- ToxoDB
- CryptoDB
- OrthoMCL-DB
- Recent *Plasmodium* publications

News

- **16 August 2006** PlasmoDB 5.1 is released
- **25 May 2006** PlasmoDB 5.0 is fully released (PlasmoDB 4.4 still available)
- **04 April 2006** P. berghei and P. chabaudi genomes added
- **04 April 2006** PlasmoMAP data included
- All PlasmoDB News

PlasmoDB Events | Release Notes

Quick Tools [Genome browser | BLAST Genes | BLAST Genome | Sequence Retrieval]

Search Genes

PlasmoDB Gene ID — Gene ID: PF11_0344 ›go!

Text (search product name, notes, etc.) — Text term: membrane ›go!

Gene Type — Gene type: protein coding ›go!

Search Genomic Sequences

Genomic Sequence ID — Sequence ID: MAL4 ›go!

All available queries:

Search genes — Chromosomal Location ›go!

Search genomic sequences — Genomic Sequence ID ›go!

Find ESTs by — Chromosomal Location ›go!

Find ORFs by — Chromosomal Location ›go!

Find SNPs by — SNPs by Gene ID ›go!

PlasmoDB 4.4 queries/tools not yet in 5.1 >> ›go!

PlasmoDB.org is a member of ApiDB.org

For help, please visit the PlasmoDB Support page

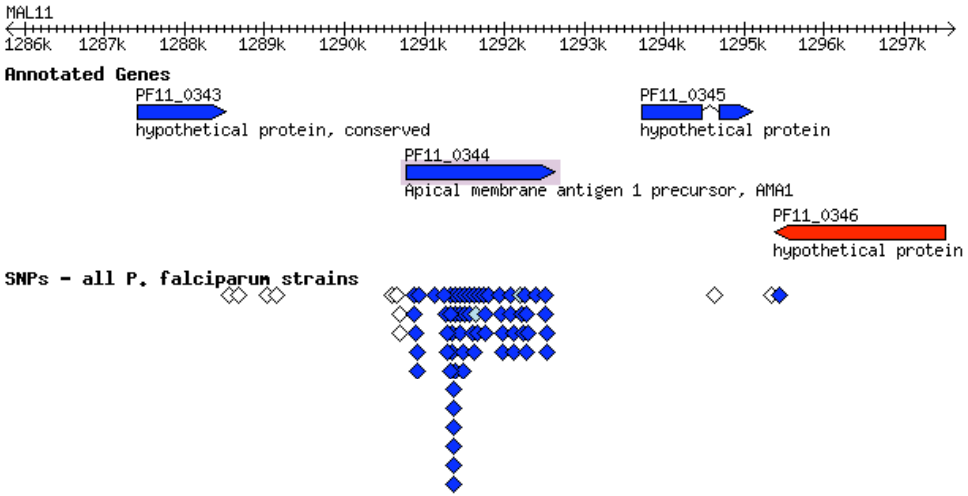
PF11_0344
Apical membrane antigen 1 precursor, AMA1

P. falciparum 3D7 protein coding gene on MAL11 from 1290767 to 1292635 (1868 bp) **Release 5.2**

Annotation ▸ Protein ▸ Expression ▸ Sequence ▸ PF11_0344 in PlasmoDB 4.4 ▸

Genomic Context Hide

[Data Sources]



View this sequence in the genome browser
(use right click or ctrl-click to open in a new window)

SNPs Summary Hide

[Data Sources]

Strains	CDS SNP Density	Non-synonymous	Synonymous	Nonsense	Non-coding	Total
3D7 vs 7G8	17.66	31	2	0	0	33
3D7 vs GHANA1	16.59	30	1	0	0	31
GHANA1 vs HB3	16.05	30	0	0	0	30
3D7 vs HB3	15.52	28	1	0	0	29
7G8 vs D10	14.98	27	1	0	0	28
D10 vs HB3	14.98	28	0	0	0	28
3D7 vs Dd2	14.98	27	1	0	0	28
Dd2 vs HB3	14.45	27	0	0	0	27

PF11_0344
Apical membrane antigen 1 precursor, AMA1

Annotation

back to top

Paralogs and Plasmodium Orthologs Hide [Data Sources]

Find PF11_0344 in the OrthoMCL database

Gene	Species	Product
PB000821.01.0	Plasmodium berghei	apical membrane antigen 1 precursor, putative
PC300445.00.0	Plasmodium chabaudi	hypothetical protein
PC301665.00.0	Plasmodium chabaudi	apical membrane antigen 1 precursor, putative
Pv092275	Plasmodium vivax Sal-1	apical merozoite antigen 1
PY01581	Plasmodium yoelii yoelii str. 17XNL	apical membrane antigen-1

EC Number *none* [Data Sources]

GO Terms Hide [Data Sources]

Is Not	Ontology	GO ID	GO Term Name	Source	Evidence Code
	Biological Process	GO:0009405	pathogenesis	Interpro	IEA
	Biological Process	GO:0030260	entry into host cell	Annotation Center	TAS
	Cellular Component	GO:0016020	membrane	Interpro	IEA
	Cellular Component	GO:0016020	membrane	Annotation Center	IEA
	Cellular Component	GO:0020007	apical complex	Annotation Center	TAS

Aliases Hide [Data Sources]

Alias
1399.t00180

Notes Show [Data Sources]

Publications View

Metabolic Pathways Show [Data Sources]

PlasmoCyc View

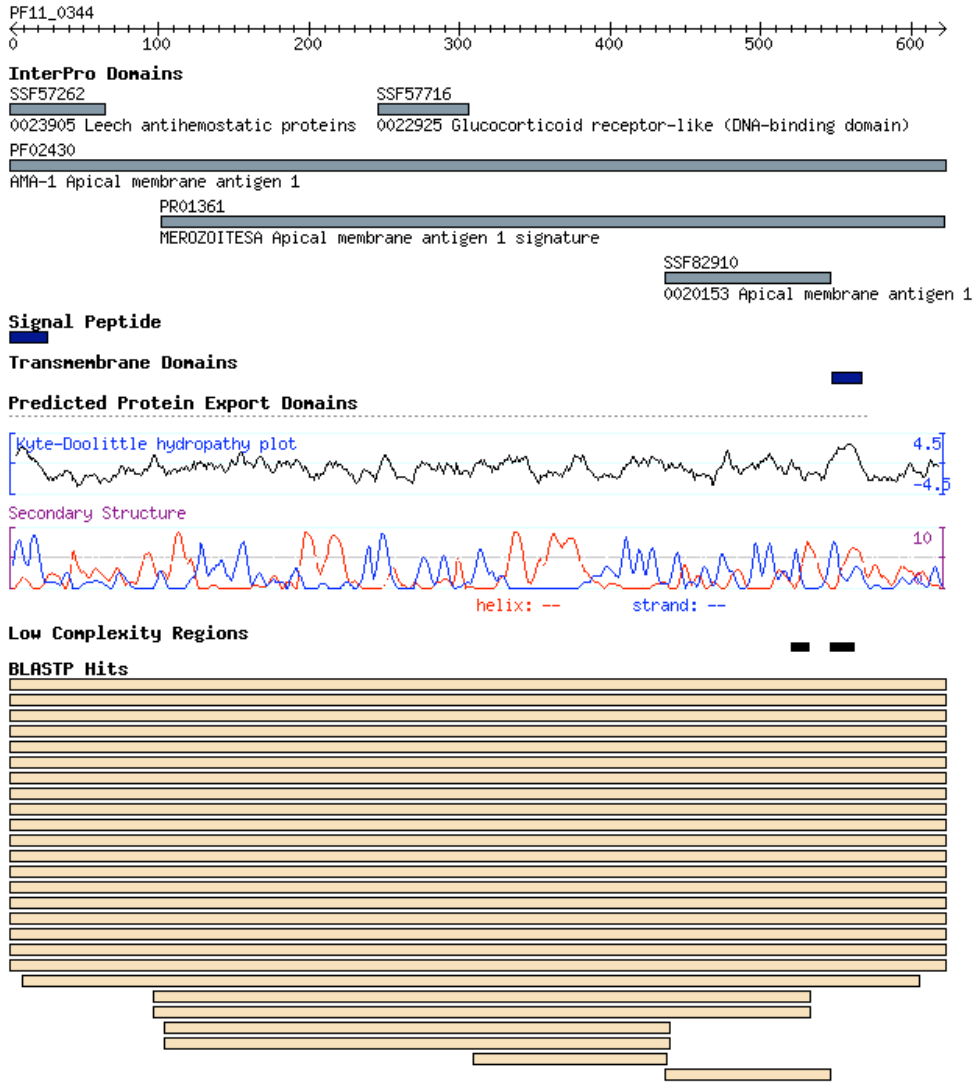
MR4 Reagents Show [Data Sources]

User Comments Hide

PF11_0344
Apical membrane antigen 1 precursor, AMA1

Protein back to top

Protein Features Hide [Data Sources]



Y2H Interactions *none* [Data Sources]

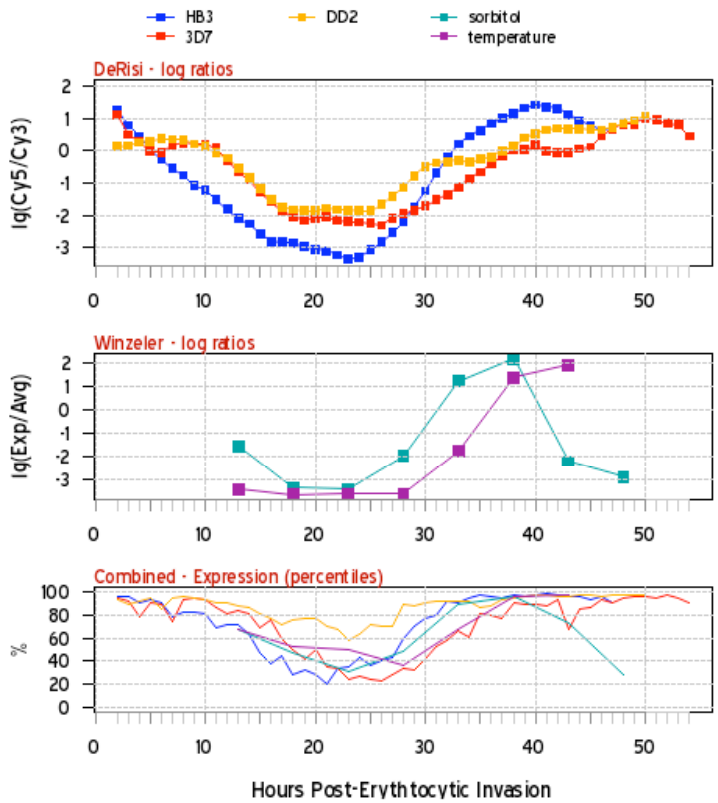
PF11_0344
Apical membrane antigen 1 precursor, AMA1

Expression

back to top

Mapped Array Elements Show [Data Sources]

Overlay of Intraerythrocytic Expression Profiles Hide [Data Sources]



Studies by the Derisi Lab of *P. falciparum* strains HB3, 3D7, and Dd2 used glass slide arrays.

Studies by the Winzeler Lab of Sorbitol- and Temperature-synchronized parasites (of the same three strains) used Affymetrix oligonucleotide arrays.

More on mapping time points between time courses

Intraerythrocytic 3D7 (photolithographic oligo array) Show [Data Sources]

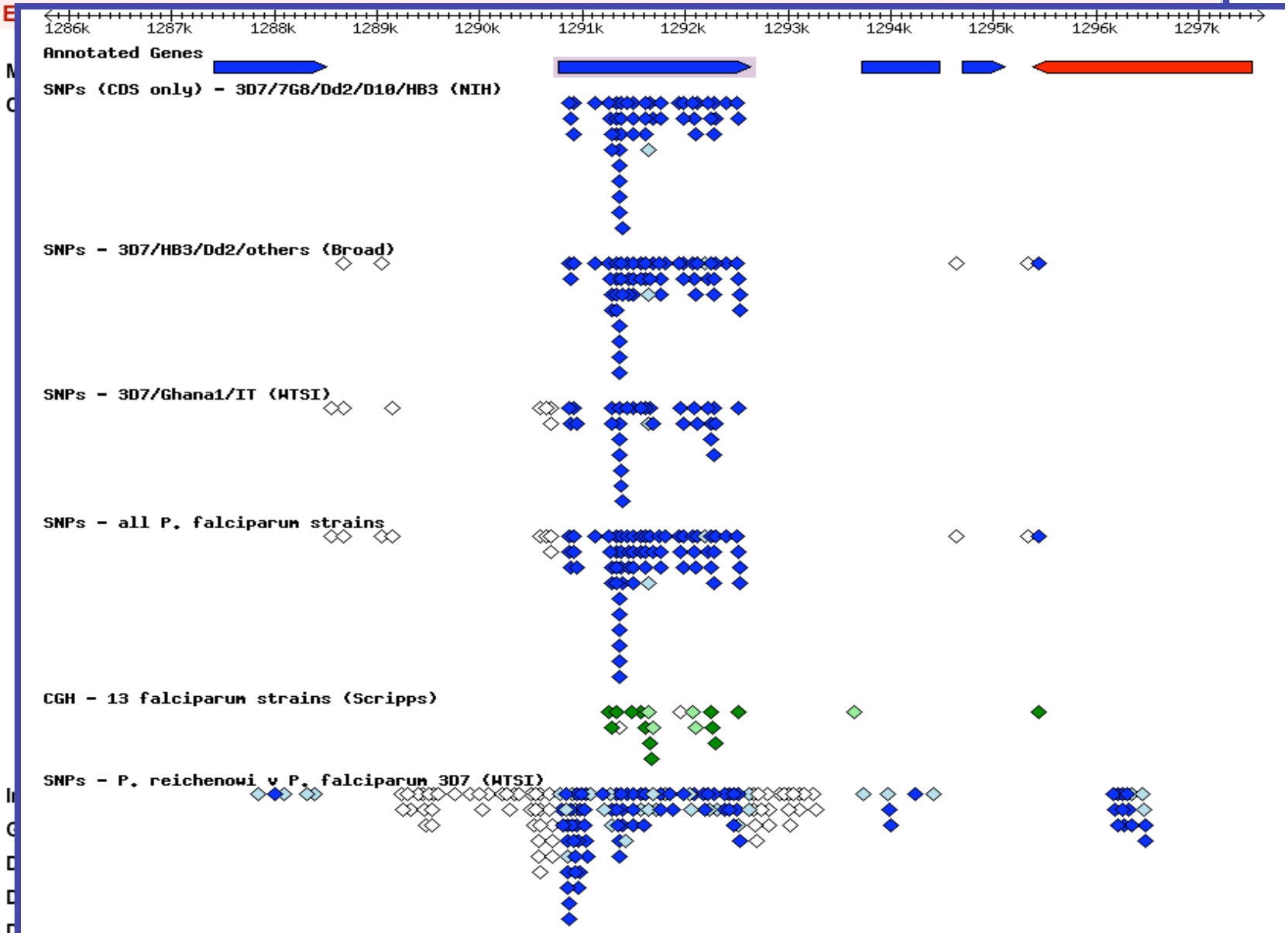
Gametocyte 3D7/NF54 (photolithographic oligo array) Show [Data Sources]

Developmental series 3D7 (glass slide oligo array) Show [Data Sources]

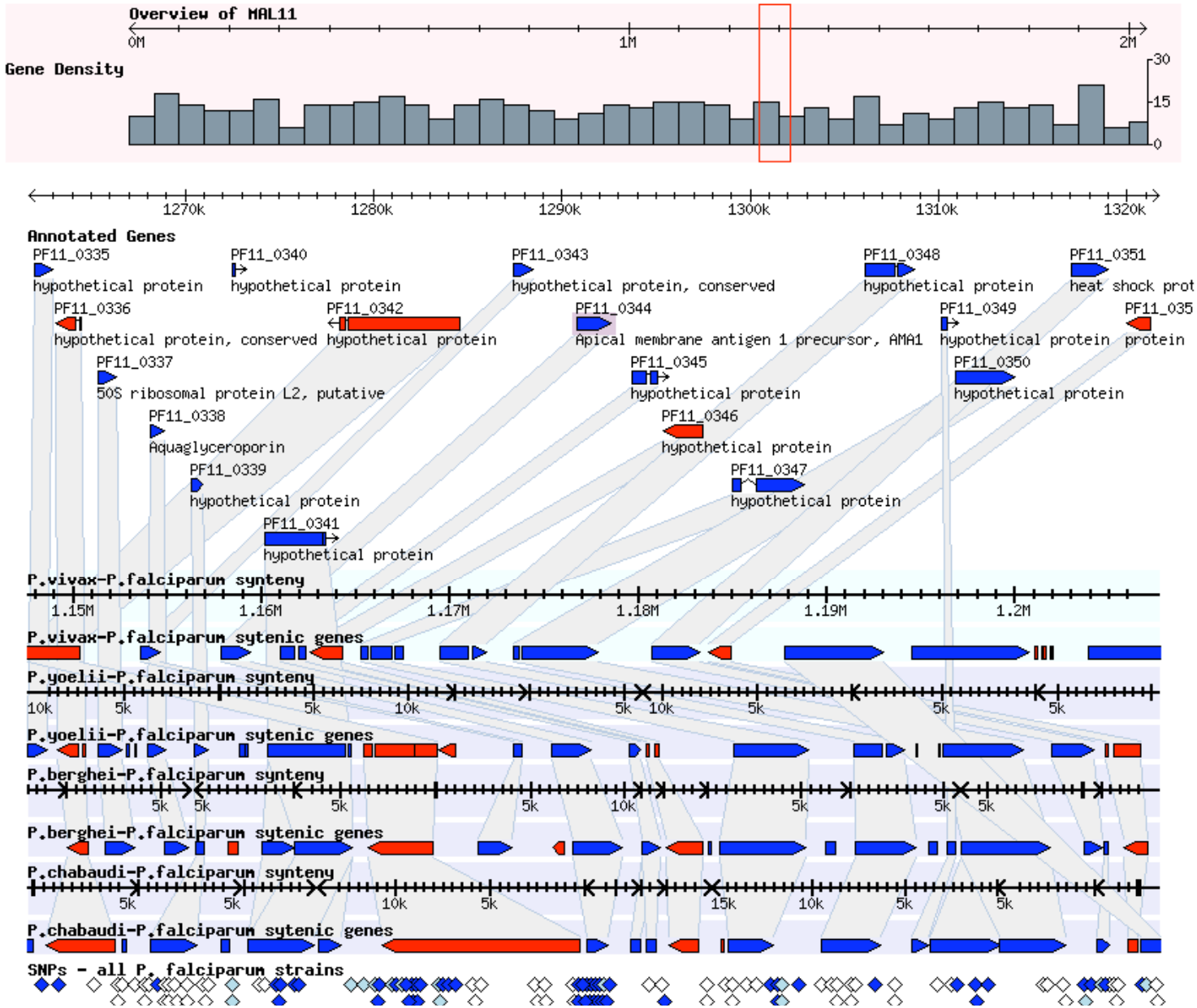
Developmental series Dd2 (glass slide oligo array) Show [Data Sources]

Developmental series HB3 (glass slide oligo array) Show [Data Sources]

PF11_0344
Apical membrane antigen 1 precursor, AMA1



PF11_0344
Apical membrane antigen 1 precursor, AMA1



PlasmoDB : The Plasmodium genome resource

PlasmoDB

The Plasmodium Genome Resource

Release 5.2

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- ToxoDB
- CryptoDB
- OrthoMCL-DB
- Recent *Plasmodium* publications

News
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- **16 August 2006** PlasmoDB 5.1 is released
- **25 May 2006** PlasmoDB 5.0 is fully released (PlasmoDB 4.4 still available)
- **04 April 2006** P. berghei and P. chabaudi genomes added
- All PlasmoDB News

PlasmoDB Events | Release Notes

Quick Tools [Genome browser | BLAST Genes | BLAST Genome | Sequence Retrieval]

Search Genes

PlasmoDB Gene ID — Gene ID: PF11_0344 ›go!

Keyword (search product name, notes, etc.) — Text term: membrane ›go!

Gene Type — Gene type: protein coding ›go!

Search Genomic Sequences

Genomic Sequence ID — Sequence ID: MAL4 ›go!

All available queries:

Search genes — All Categories | Chromosomal Location ›go!

Search genomic sequences — Genomic Sequence ID ›go!

Find ESTs by — Genomic Location ›go!

Find ORFs by — Genomic Location ›go!

Find SNPs by — Gene ID ›go!

PlasmoDB 4.4 queries/tools not yet in 5.1 >> ›go!

Surface antigens

Vaccine Target Identification

PlasmoDB : Queries & Tools

PlasmoDB Queries and Tools

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Featured data source

Organellar: P.falciparum (NF54) mitochondrial DNA sequence and annotation

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Queries

Availability: A = ApiDB C = CryptoDB P = PlasmoDB T = ToxoDB

Identify Genes Based On:

Genomic Position
- Chromosomal Location A C P T
- Proximity to Centromeres P
- Proximity to Telomeres P
- Non-nuclear Genomes

Gene Attributes
- Type (e.g. rRNA, tRNA) A C P T
- Exon/Intron Structure A C P T

Population Biology
- SNPs P T
- Microsatellites

Transcript Expression
- EST Evidence C P T
- SAGE Tag Evidence
- Microarray Evidence P

Similarity/Pattern
- Protein Motif A C P T
- Interpro/Pfam Domain A C P T
- BLAST similarity A C P T

Protein Expression
- Mass Spec. Evidence C P

Predicted Proteins
- Molecular Weight A C P T
- Isoelectric Point P T
- Secondary Structure P
- Crystal Structure P
- Predicted 3D Structure P

Putative Function
- GO Term A C P T
- EC Number A C P T
- Metabolic Pathway C P T
- Y2H Interaction P
- Predicted Interaction P

Cellular Location
- Signal Peptide A C P T
- Transmembrane Domain A C P T
- Organellar Compartment P
- Exported to Host P

Evolution
- Orthologs/Paralogs A P
- Orthology Profile A C P T
- Homology Profile P

Other Attributes
- Keyword A C P T
- ID A C P T
- Species A C P
- Available Reagents P

Identify Genomic Sequences Based On:

- BLAST Similarity A C P T
- DNA Sequence Motif
- ID A C P T
- Species A P

Identify ESTs Based On:

- Chromosomal Location P T
- Extent of Gene Overlap C P T
- BLAST Similarity A C P T
- EST Sequence Motif
- Library C P T
- Species

Surface antigens

Vaccine Target Identifi-cation

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Identify Genes based on Predicted Signal Peptide

Release 5.2

Plasmodium species

- [x] *Plasmodium falciparum*
- [ ] *Plasmodium vivax*
- [ ] *Plasmodium yoelii*
- [ ] *Plasmodium berghei*
- [ ] *Plasmodium chabaudi*

select all | clear all

Get Answer

›help

Query description: Find genes that are predicted to encode a signal peptide.

The predictions are made with the SignalP program.

• Predicted 3D Structure • Predicted Interaction

Identify Genes based on Transmembrane Domain Count

Release 5.2

Minimum Number of Transmembrane Domains 1 ›help

Plasmodium species

- [x] *Plasmodium falciparum*
- [ ] *Plasmodium vivax*
- [ ] *Plasmodium yoelii*
- [ ] *Plasmodium berghei*
- [ ] *Plasmodium chabaudi*

select all | clear all

Get Answer

›help

Query description: Find genes with at least a given number of transmembrane domains.

Transmembrane domains were predicted using TMHMM2.

Vaccine Target Identifi-cation

PlasmoDB : Queries & Tools

PlasmoDB Queries and Tools

Surface antigens

Identify Genes based on Predicted Signal Peptide

Gene Results

Release 5.2

Query: SP+ & 1+TM Rename

Details: Hide

INTERSECT

Predicted Signal Peptide
Plasmodium species = Plasmodium falciparum

Transmembrane Domain Count
Minimum Number of Transmembrane Domains = 1
Plasmodium species = Plasmodium falciparum

Results: 537 (showing 1 to 20)

Download | Combine with other results | Orthologs

First 1 2 3 4 5 6 7 8 9 10 Next Last Go to page: 1 [1 ... 27] page size: 20 GO

Gene	Organism	Product	Number of Transmembrane Domains
MAL13P1.106	P. falciparum 3D7	hypothetical protein	1
MAL13P1.121	P. falciparum 3D7	hypothetical protein	1
MAL13P1.154	P. falciparum 3D7	hypothetical protein	1
MAL13P1.160	P. falciparum 3D7	unknown	1
MAL13P1.161	P. falciparum 3D7	unknown	1
MAL13P1.171	P. falciparum 3D7	transmembrane protein Tmp21 homologue, putative	2
MAL13P1.174	P. falciparum 3D7	MSP7-like protein	1
MAL13P1.186	P. falciparum 3D7	1-deoxy-D-xylulose 5-phosphate synthase	1
MAL13P1.193	P. falciparum 3D7	hypothetical protein	1

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PlasmoDB : Queries & Tools

PlasmoDB Queries and Tools

Release 5.2

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- ID A C P T
- Species A C P
- Available Reagents P

Identify Genomic Sequences Based On:

- BLAST Similarity A C P T
- DNA Sequence Motif
- ID A C P T
- Species A P

Identify ESTs Based On:

- Chromosomal Location P T
- Extent of Gene Overlap C P T
- BLAST Similarity A C P T
- EST Sequence Motif
- Library C P T
- Species

Expressed in schizonts

Vaccine Target Identifi-cation

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Identify Genes based on Expression Timing (P.f)

Release 5.2

Microarray time course(s) to query	Any of the time courses	help
Query based on	Timing of maximal expression	help
Timing of maximal expression	40 hours	help
Maximal expression time plus or minus	8 hours	help
Timing of minimum expression	1 hour	help
Minimum expression time plus or minus	1 hour	help
Induction ratio cut-off	>= 2 fold induction	help
Maximum percentile cut-off	>= 80th percentile	help

Get Answer

Query description: Find genes with peaks or troughs occuring within specified intervals during the intraerythrocytic infection cycle. Five intraerythrocytic time courses may be queried in turn (and results may be combined using the query history). The five time courses are those provided by the Winzeler Lab and the DeRisi Lab -- the first two time courses rely on photolithographic (Affy) arrays and employ sorbitol and temperature synchronizations, while the other three time courses rely on a glass slide array and analyze HB3, 3D7, and Dd2 parasites.

Identify Genomic Sequences Based On:

- BLAST Similarity
- ID
- DNA Sequence Motif
- Species

Identify ESTs Based On:

- Chromosomal Location
- BLAST Similarity
- Library
- Extent of Gene Overlap
- EST Sequence Motif
- Species

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Identify Genes based on Expression Timing (P.f)

Gene Results

Release 5.2

Query: Expression Timing (P.f): Microarray time course(s) to query = Any of the time courses, Query based on = Timing of maximal expression, Timing of maximal expression = 40 hours, Maximal expression time plus or minus = 8 hours, Timing of minimum expression = 1 hour, Minimum expression time plus or minus = 1 hour, Induction ratio cut-off = >= 2 fold induction, Maximum percentile cut-off = >= 80th percentile

Rename

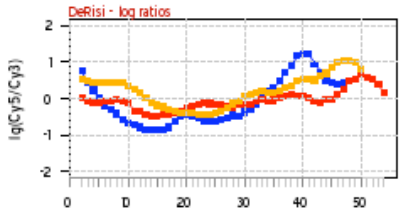
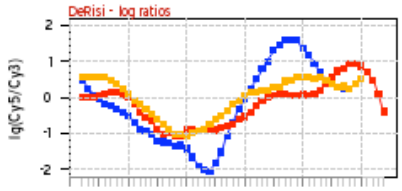
Details: Hide

Query : Expression Timing (P.f)
Microarray time course(s) to query : Any of the time courses
Query based on : Timing of maximal expression
Timing of maximal expression : 40 hours
Maximal expression time plus or minus : 8 hours
Timing of minimum expression : 1 hour
Minimum expression time plus or minus : 1 hour
Induction ratio cut-off : >= 2 fold induction
Maximum percentile cut-off : >= 80th percentile

Results: 1120 (showing 1 to 20)

Download | Combine with other results | Orthologs | Revise query

First 1 2 3 4 5 6 7 8 9 10 Next Last Go to page: 1 [1 ... 56] page size: 20 GO

Gene	Organism	Product	Expression Levels
MAL13P1.102	P. falciparum 3D7	hypothetical protein	
MAL13P1.114	P. falciparum 3D7	hypothetical protein	

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Identify Genes based on Orthology Phylogenetic Profile

Release 5.2

Orthology Phylogenetic Profile

Query description: Find genes that have a specified orthology-based phylogenetic profile. The phylogenetic profile of a gene is a series of 65 "present" or "absent" calls, reflecting the presence or absence of a putative ortholog in 65 genomes.

An OrthoMCL analysis of the proteins of 65 species, including Plasmodia, placed each protein in an ortholog group. From a Plasmodium gene perspective, the other species that are included in that gene's ortholog group can be thought of as a phylogenetic profile.

Use this query to define a pattern across those ortholog groups, and find genes that match that pattern. The pattern is a specification, for each species, of "include", "exclude", or "don't care." Click on the radio button next to a species to toggle through the three states. (A ✔ means "include", an ✖ means "exclude" and ● means "don't care".)

For example, to find genes that are present in Apicomplexa but not in humans, click on Apicomplexa until you see a ✔ and click on *Homo sapiens* until you see an ✖.

Note that this query can take some time because of the large number of combinations of possible presence/absence calls (2^{65} possible combinations, of which 2487 are associated with a total of 30739 genes).

Show results from species: Plasmodium falciparum | Get Answer

- **All Organisms**
  - ***Archaea***
    - *Halobacterium sp. NRC-1* (hal)
    - *Methanococcus jannaschii DSSM 2661* (mja)
    - *Sulfolobus solfataricus P2* (sso)
    - *Nanoarchaeum equitans Kin4-M* (neq)
  - ***Bacteria***
    - ***Proteobacteria***
      - *Wolinella succinogenes DSM 1740* (wsu)
      - *Geobacter sulfurreducens PCA* (gsu)
      - *Agrobacterium tumefaciens C58 Uwash* (atu)
      - *Ralstonia solanacearum GMI1000* (rso)

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Identify Genes based on Orthology Phylogenetic Profile

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Orthology Phylogenetic Profile

- ***Eukaryota***
  - ***Plants/Algae***
    - *Cyanodioschyzon merolae 10D* (cme)
    - *Thalassiosira pseudonana* (tps)
    - *Arabidopsis thaliana* (ath)
    - *Oryza sativa* (osa)
  - ***Alveolates***
    - ***Apicomplexa***
      - ***Coccidia***
        - *Toxoplasma gondii* (tgo)
        - *Cryptosporidium parvum Iowa (Type2)* (cpa)
        - *Cryptosporidium hominis TU502 (Type 1)* (cho)
      - ***Haemosporida***
        - ✔ *Plasmodium falciparum 3D7* (pfa)
        - ✔ *Plasmodium vivax* (pvi)
        - *Plasmodium yoelii 17XNL* (pyo)
        - *Plasmodium berghei* (pbe)
        - *Plasmodium chabaudi* (pch)
        - *Plasmodium knowlesi* (pkn)
      - ***Other Apicomplexa***
        - *Theileria parva* (the)
  - ***Fungi***
    - *Saccharomyces cerevisiae S288C* (sce)
    - *Schizosaccharomyces pombe* (spo)
    - *Yarrowia lipolytica CLIB99* (yli)
    - *Kluyveromyces lactis CLIB210* (kla)
- ***Metazoa***
  - ***Arthropoda***
    - *Drosophila melanogaster* (dme)
    - *Anopheles gambiae PEST* (aga)
  - ***Deuterostomia***
    - ***Bony Fish***
      - *Fugu rubripes* (fru)
      - *Tetraodon nigroviridis* (tni)
      - *Danio rerio* (dre)
    - ***Tetrapoda***
      - ✖ ***Mammals***
        - ✖ ***Primates***
          - ✖ *Homo sapiens* (hsa)
        - ✖ ***Other Mammals***
          - ✖ *Mus musculus* (mmu)
          - ✖ *Rattus norvegicus* (rno)
      - ***Other Tetrapoda***
        - *Gallus gallus* (gga)
    - ***Other Deuterostomia***
      - *Ciona intestinalis* (cin)
  - ***Other Metazoa***
    - *Caenorhabditis elegans* (cel)
    - *Caenorhabditis briggsae* (cbr)
- ***Other Eukaryota***
  - *Entamoeba histolytica* (ehi)
  - *Dictyostelium discoideum* (ddi)

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Gene Results

Release 5.2

Query: Orthology Phylogenetic Profile: Profile Pattern = %hsa:N%mmu:N%pfa:Y%pvi:Y%rno:N%, Included Species = pfa, pvi, Excluded Species = Mammals, phyletic_indent_map = Archaea, phyletic_term_map = rno, Plasmodium species = Plasmodium falciparum

Rename

Details: Hide

Query : Orthology Phylogenetic Profile
Included Species : pfa, pvi
Excluded Species : Mammals
Plasmodium species : Plasmodium falciparum

Results: 2812 (showing 1 to 20)

Download | Combine with other results | Orthologs | Revise query

First 1 2 3 4 5 6 7 8 9 10 Next Last Go to page: 1 [1 ... 141] page size: 20 GO

Gene	Product
MAL13P1.100	hypothetical protein
MAL13P1.102	hypothetical protein
MAL13P1.103	hypothetical protein
MAL13P1.107	hypothetical protein
MAL13P1.11	hypothetical protein
MAL13P1.111	hypothetical protein
MAL13P1.112	hypothetical protein,conserved
MAL13P1.113	hypothetical protein
MAL13P1.114	hypothetical protein
MAL13P1.115	hypothetical protein, conserved
MAL13P1.116	hypothetical protein

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Diversifying selection

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Identify Genes based on Snp Characteristics

Release 5.2

Reference	Pf-3D7	help
Comparator	Pf-GHANA1	help
SNP Class	Non-Synonymous	help
Number of SNPs of above class >=	5	help
Number of SNPs of above class <=	1000	help
Non-synonymous / synonymous SNP ratio >=	0	help
Non-synonymous / synonymous SNP ratio <=	100	help
SNPs per KB (CDS) >=	0	help
Sort by	All SNPs	help
Sort direction	Descending	help

Get Answer

Query description: Search for P. *falciparum* genes by SNP density, the number of SNPs of different classes, ratio of non-synonymous to synonymous, etc. Note that if you don't care about one of the parameters, don't change the defaults on that parameter and you will get all genes irrespective of that parameter. For example, running this query to compare 3D7 and Dd2 using default parameters returns 2577 genes. Among the top 20 on the list are CLAG, AMA1, chloroquine resistance marker and multiple PfEMP1 and SURFIN genes.

Note: Due to the extreme codon bias in the falciparum genome, the ratio of non-synonymous to synonymous snps per gene is much higher than expected so this should be considered when creating queries. We are intending to calculate more reliable normalized Dn/Ds or Ka/Ks ratios in subsequent releases of PlasmoDB.

SNP data was provided by Broad, NIH and WTSI.

Vaccine Target Identification

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Diversifying selection

Identify Genes based on Snp Characteristics

Gene Results

Release 5.2

Query: Snp Characteristics: Reference = Pf-3D7, Comparator = Pf-GHANA1, SNP Class = Non-Synonymous, Number of SNPs of above class >= = 5, Number of SNPs of above class = = 0, Non-synonymous / synonymous SNP ratio = = 0, Sort by = All SNPs, Sort direction = Descending

Rename

Details: Hide

Query : Snp Characteristics
Reference : Pf-3D7
Comparator : Pf-GHANA1
SNP Class : Non-Synonymous
Number of SNPs of above class >= : 5
Number of SNPs of above class <= : 1000
Non-synonymous / synonymous SNP ratio >= : 0
Non-synonymous / synonymous SNP ratio <= : 100
SNPs per KB (CDS) >= : 0
Sort by : All SNPs
Sort direction : Descending

Results: 391 (showing 1 to 20)

Download | Combine with other results | Orthologs | Revise query

First 1 2 3 4 5 6 7 8 9 10 Next Last Go to page: 1 [1 ... 20] page size: 20 GO

Gene	Product	CDS length	SNPs per Kb (CDS)	Non-synonymous / synonymous SNP ratio	Non-synonymous SNPs	Synonymous SNPs	Nonsense SNPs	Non-coding SNPs
PFL0030c	erythrocyte membrane protein 1 (PfEMP1)	9171	67.17	3.19	469	147	5	0
PFE1640w	erythrocyte membrane protein 1 (PfEMP1), truncated	9495	22.12	3.04	158	52	2	0
PF10_0374	gene 11-1 protein precursor	31770	5.41	1.07	89	83	1	1

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Gene query history

ID		Query	Size	
7	Rename	(1 or 2) and 4 and 5 and 6	32	orthologs view download revise delete
6	Rename	Pfa & Pvi not mammals	2812	orthologs view download revise delete
5	Rename	max in Schizonts (40+/- 8 hr, 2x induced, >80%)	1120	orthologs view download revise delete
3	Rename	SP+ & 1+TM	537	orthologs view download revise delete
4	Rename	3D7 vs Ghana1, >5 NS SNPs	391	orthologs view download revise delete
2	Rename	TM	1711	orthologs view download revise delete
1	Rename	SP	835	orthologs view download revise delete

Combine results: (1 or 2) and 4 and 5 and 6 Get Combined Result [eg: 1 or ((4 and 3) not 2)]

Delete All Queries

Be careful: This will delete all your queries on PlasmoDB.

Understanding AND, OR and NOT:

1 and 2 Genes that 1 and 2 have in common. You can also use "1 intersect 2".
1 or 2 Genes present in 1 or 2, or both. You can also use "1 union 2".
1 not 2 Genes in 1 but not in 2. You can also use "1 minus 2".

* If you want to delete a query, you must first delete all other boolean queries that uses this one as a component.

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Create and download a report

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Generate a tab delimited report of your query result. Select columns to include in the report. Optionally include a first line with column names

Combined Answer: 1 and 2 and 3 and 4

Columns: ☐ Default (same as in result), or...

- ☑ Gene ID
- ☑ Product
- ☐ End Location
- ☐ Strand
- ☐ Number of Transmembrane Domains
- ☐ External DB Name
- ☐ Predicted Protein Sequence
- ☐ Predicted RNA/mRNA Sequence (introns spliced out)
- ☐ Anticodon
- ☐ Isoelectric Point
- ☐ Max Molecular Wt
- ☐ Aromaticity
- ☐ Gene Type
- ☐ Start Location
- ☐ Length
- ☐ Genomic Sequence ID
- ☐ Organism
- ☐ External DB Version
- ☐ Molecular Weight
- ☐ Coding Sequence
- ☐ Number of Exons
- ☐ Min Molecular Wt
- ☐ Hydropathicity Gravy Score

select all | clear all

Column names: ◉ include ○ exclude

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Generate a tab delimited report of
with column names

Combined Answer: 1 and 2 and 3

Columns:

- [ ] Default (same
- [x] Gene ID
- [x] Product
- [ ] End Location
- [ ] Strand
- [ ] Number of Tra
- [ ] External DB Na
- [ ] Predicted Prote
- [ ] Predicted RNA
- [ ] Anticodon
- [ ] Isoelectric Poi
- [ ] Max Molecular
- [ ] Aromaticity

Column names: (•) include ( ) exclu

Get Report

#Gene ID	Product
MAL13P1.114	hypothetical protein
MAL13P1.380	chloroquine resistance marker protein, putative
MAL13P1.39	hypothetical protein
MAL7P1.17	hypothetical protein
MAL7P1.176	erythrocyte binding antigen
MAL8P1.144	hypothetical protein
PF07_0061	hypothetical protein
PF10_0045	hypothetical protein
PF10_0082	hypothetical protein
PF10_0177	erythrocyte membrane-associated antigen
PF10_0189	hypothetical protein
PF10_0211	hypothetical protein
PF11_0344	Apical membrane antigen 1 precursor, AMA1
PF14_0363	metacaspase-like protein
PF14_0495	hypothetical protein
PF14_0690	histone deactylase, putative
PFA0215w	hypothetical protein
PFB0190c	hypothetical protein
PFB0935w	cytoadherence linked asexual protein 2
PFC0425w	hypothetical protein
PFC0470w	valine -- tRNA ligase, putative
PFD0105c	SURFIN, surface-associated interspersed gene
PFD0495c	hypothetical protein
PFD1155w	erythrocyte binding antigen, putative
PFE0340c	hypothetical protein, conserved
PFI1180w	hypothetical protein
PFI1475w	merozoite surface protein 1, precursor
PFL0300c	phosphoesterase, putative
PFL0800c	hypothetical protein
PFL1395c	hypothetical protein
PFL1410c	hypothetical protein
PFL2520w	reticulocyte-binding protein, putative

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Generate a tab delimited report of
with column names

Combined Answer: 1 and 2 and 3

Columns:
- [ ] Default (same
- [x] Gene ID
- [x] Product
- [ ] End Location
- [ ] Strand
- [ ] Number of Tra
- [ ] External DB Na
- [ ] Predicted Prote
- [ ] Predicted RNA
- [ ] Anticodon
- [ ] Isoelectric Poi
- [ ] Max Molecular
- [ ] Aromaticity

Column names: (•) include ( ) exclu

Get Report

#Gene ID	Product
MAL13P1.114	hypothetical protein
MAL13P1.380	chloroquine resistance marker protein, putative
MAL13P1.39	hypothetical protein
MAL7P1.17	hypothetical protein
MAL7P1.176	erythrocyte binding antigen
MAL8P1.144	hypothetical protein
PF07_0061	hypothetical protein
PF10_0045	hypothetical protein
PF10_0082	hypothetical protein
PF10_0177	erythrocyte membrane-associated antigen
PF10_0189	hypothetical protein
PF10_0211	hypothetical protein
PF11_0344	Apical membrane antigen 1 precursor, AMA1
PF14_0363	metacaspase-like protein
PF14_0495	hypothetical protein
PF14_0690	histone deactylase, putative
PFA0215w	hypothetical protein
PFB0190c	hypothetical protein
PFB0935w	cytoadherence linked asexual protein 2
PFC0425w	hypothetical protein
PFC0470w	valine -- tRNA ligase, putative
PFD0105c	SURFIN, surface-associated interspersed gene
PFD0495c	hypothetical protein
PFD1155w	erythrocyte binding antigen, putative
PFE0340c	hypothetical protein, conserved
PFI1180w	hypothetical protein
PFI1475w	merozoite surface protein 1, precursor
PFL0300c	phosphoesterase, putative
PFL0800c	hypothetical protein
PFL1395c	hypothetical protein
PFL1410c	hypothetical protein
PFL2520w	reticulocyte-binding protein, putative

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