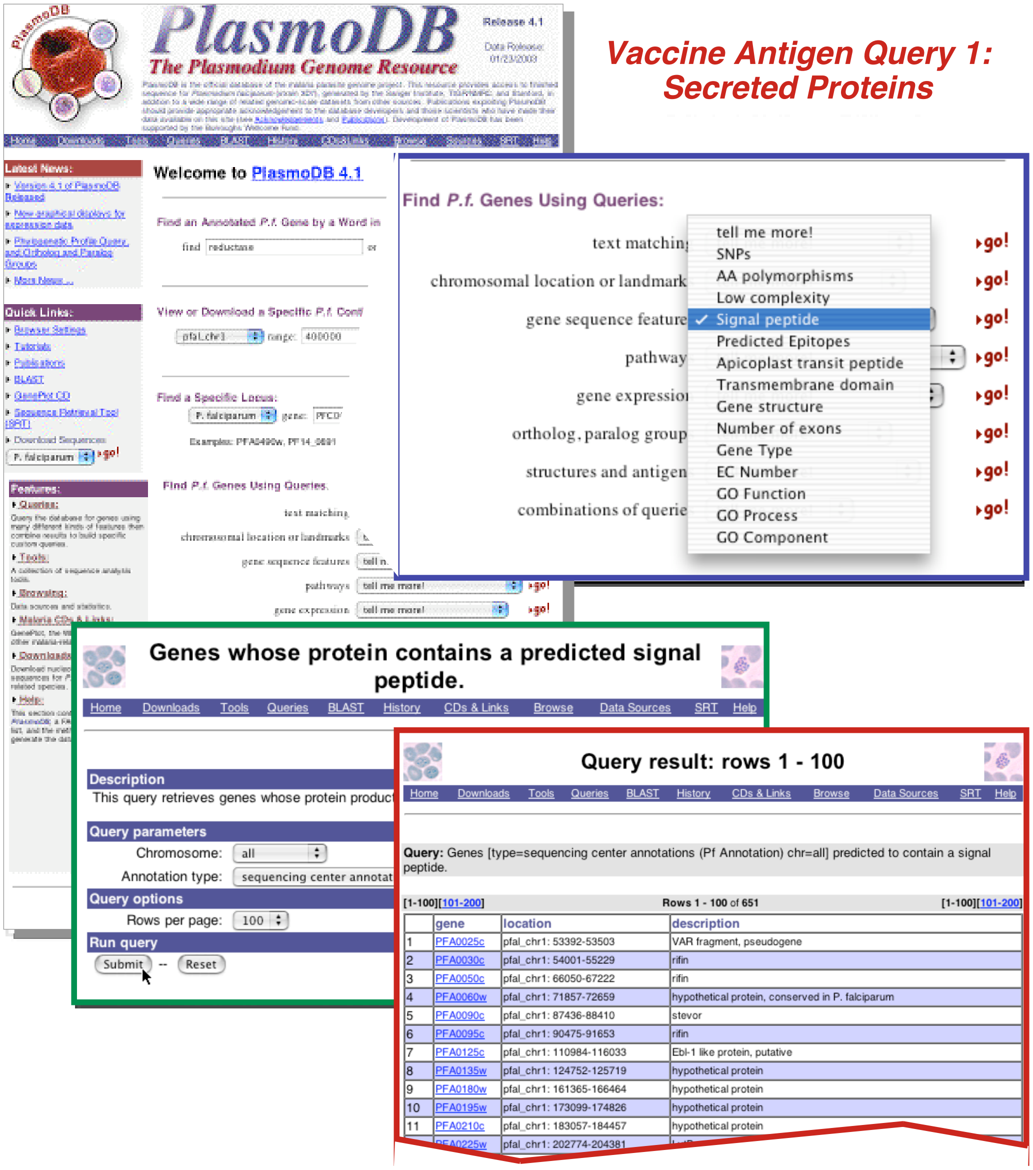
Vaccine Antigen Query 1: Secreted Proteins



Genes whose protein contains a predicted signal peptide.

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Description

This query retrieves genes whose protein product

Query parameters

Chromosome: all

Annotation type: sequencing center annotat

Query options

Rows per page: 100

Run query

Submit -- Reset

Query result: rows 1 - 100

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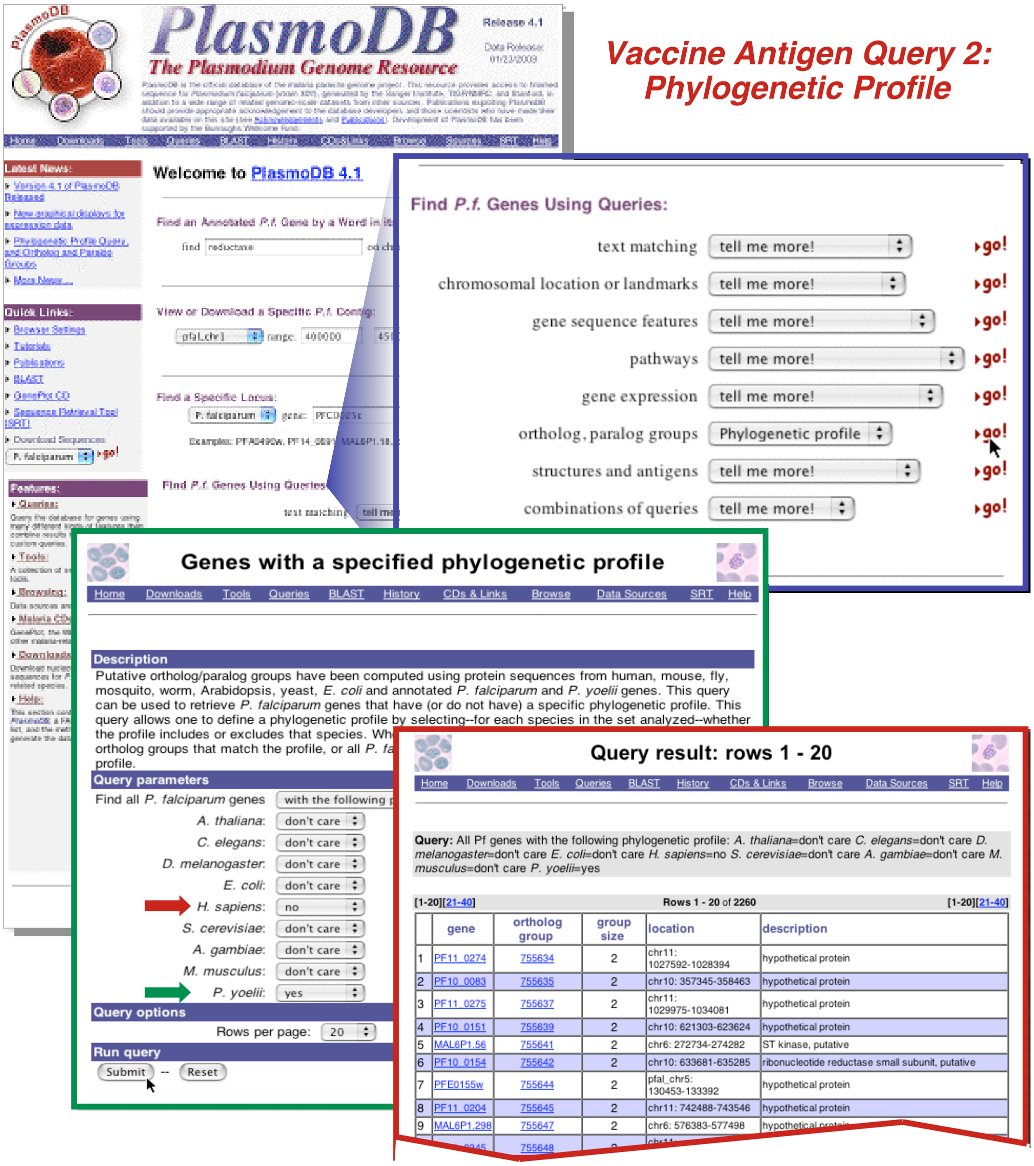
Query: Genes [type=sequencing center annotations (Pf Annotation) chr=all] predicted to contain a signal peptide.

[1-100][101-200] **Rows 1 - 100 of 651** [1-100][101-200]

	gene	location	description
1	PFA0025c	pfal_chr1: 53392-53503	VAR fragment, pseudogene
2	PFA0030c	pfal_chr1: 54001-55229	rifin
3	PFA0050c	pfal_chr1: 66050-67222	rifin
4	PFA0060w	pfal_chr1: 71857-72659	hypothetical protein, conserved in P. falciparum
5	PFA0090c	pfal_chr1: 87436-88410	stevor
6	PFA0095c	pfal_chr1: 90475-91653	rifin
7	PFA0125c	pfal_chr1: 110984-116033	Ebl-1 like protein, putative
8	PFA0135w	pfal_chr1: 124752-125719	hypothetical protein
9	PFA0180w	pfal_chr1: 161365-166464	hypothetical protein
10	PFA0195w	pfal_chr1: 173099-174826	hypothetical protein
11	PFA0210c	pfal_chr1: 183057-184457	hypothetical protein
	PFA0225w	pfal_chr1: 202774-204381	

Figure 3. Querying the curated annotation of *P. falciparum* genes in PlasmoDB 4.1 for signal peptides (identified using the neural net algorithm SignalP yields 651 proteins that are predicted to be secreted. Because accurate prediction of secretory signal sequences requires accurate assignment of the translational initiation, it is likely that this query misses many secreted proteins. Further refinements might include searching alternative gene models, or including proteins with predicted transmembrane domains.



Vaccine Antigen Query 2: Phylogenetic Profile

Find *P.f.* Genes Using Queries:

text matching	tell me more!	go!
chromosomal location or landmarks	tell me more!	go!
gene sequence features	tell me more!	go!
pathways	tell me more!	go!
gene expression	tell me more!	go!
ortholog, paralog groups	Phylogenetic profile	go!
structures and antigens	tell me more!	go!
combinations of queries	tell me more!	go!

Genes with a specified phylogenetic profile

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Description

Putative ortholog/paralog groups have been computed using protein sequences from human, mouse, fly, mosquito, worm, Arabidopsis, yeast, *E. coli* and annotated *P. falciparum* and *P. yoelii* genes. This query can be used to retrieve *P. falciparum* genes that have (or do not have) a specific phylogenetic profile. This query allows one to define a phylogenetic profile by selecting--for each species in the set analyzed--whether the profile includes or excludes that species. Wh ortholog groups that match the profile, or all *P. fa* profile.

Query parameters

Find all *P. falciparum* genes	with the following
A. thaliana:	don't care
C. elegans:	don't care
D. melanogaster:	don't care
E. coli:	don't care
H. sapiens:	no
S. cerevisiae:	don't care
A. gambiae:	don't care
M. musculus:	don't care
P. yoelii:	yes

Query options

Rows per page: 20

Run query

Submit -- Reset

Query result: rows 1 - 20

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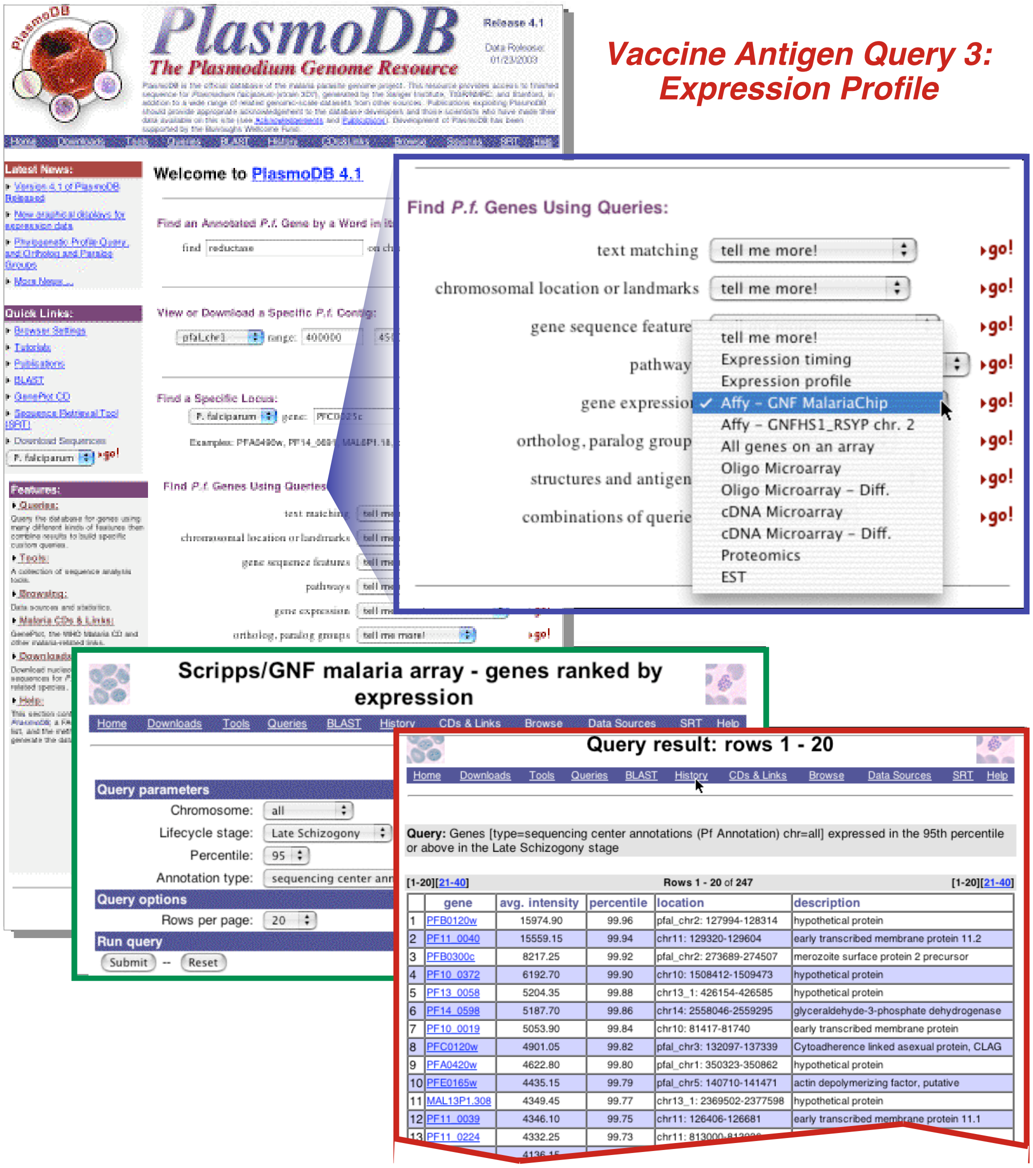
Query: All Pf genes with the following phylogenetic profile: *A. thaliana*=don't care *C. elegans*=don't care *D. melanogaster*=don't care *E. coli*=don't care *H. sapiens*=no *S. cerevisiae*=don't care *A. gambiae*=don't care *M. musculus*=don't care *P. yoelii*=yes

[1-20][21-40] **Rows 1 - 20 of 2260** [1-20][21-40]

	gene	ortholog group	group size	location	description
1	PF11_0274	755634	2	chr11: 1027592-1028394	hypothetical protein
2	PF10_0083	755635	2	chr10: 357345-358463	hypothetical protein
3	PF11_0275	755637	2	chr11: 1029975-1034081	hypothetical protein
4	PF10_0151	755639	2	chr10: 621303-623624	hypothetical protein
5	MAL6P1.56	755641	2	chr6: 272734-274282	ST kinase, putative
6	PF10_0154	755642	2	chr10: 633681-635285	ribonucleotide reductase small subunit, putative
7	PFE0155w	755644	2	pfal_chr5: 130453-133392	hypothetical protein
8	PF11_0204	755645	2	chr11: 742488-743546	hypothetical protein
9	MAL6P1.298	755647	2	chr6: 576383-577498	hypothetical protei
		755648			

Figure 4. Phylogenomic cross-comparisons with other genome sequence data can identify putative orthologous genes (Li *et al.*, 2003b), and genes that are phylogenetically restricted in their distribution (Ajioka *et al.*, 1998). In seeking candidate vaccine targets, one might wish to identify antigens that are highly conserved between *P. falciparum* and *P. yoelii*, but not shared with the human host. This query yields 2260 hits (>40% of the parasite genome).



Vaccine Antigen Query 3: Expression Profile

Find P.f. Genes Using Queries:

Scripps/GNF malaria array - genes ranked by expression

Query parameters

Chromosome: all

Lifecycle stage: Late Schizogony

Percentile: 95

Annotation type: sequencing center ann

Query options

Rows per page: 20

Run query

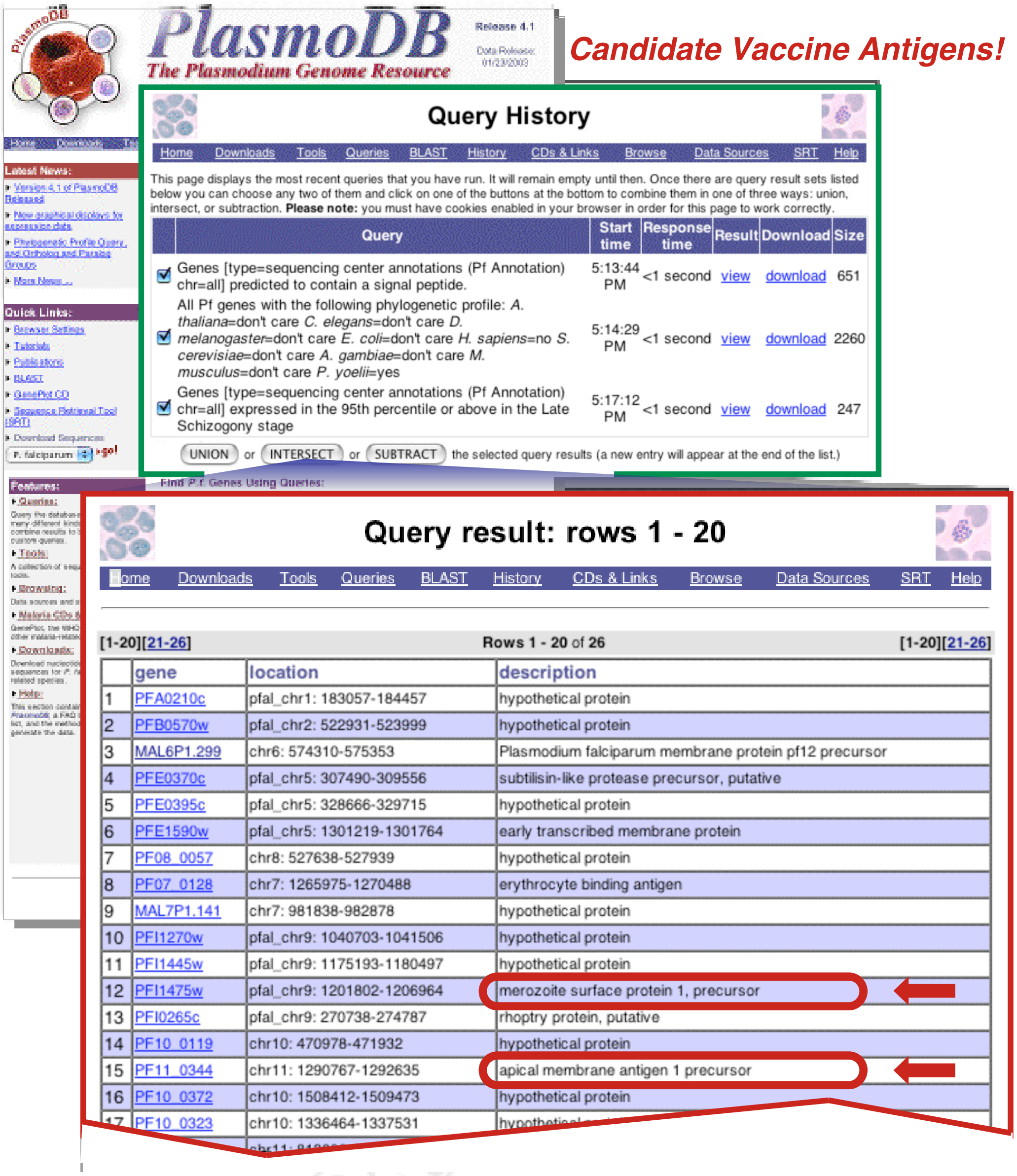
Query result: rows 1 - 20

Query: Genes [type=sequencing center annotations (Pf Annotation) chr=all] expressed in the 95th percentile or above in the Late Schizogony stage

[1-20][21-40] Rows 1 - 20 of 247 [1-20][21-40]

	gene	avg. intensity	percentile	location	description
1	PFB0120w	15974.90	99.96	pfal_chr2: 127994-128314	hypothetical protein
2	PF11_0040	15559.15	99.94	chr11: 129320-129604	early transcribed membrane protein 11.2
3	PFB0300c	8217.25	99.92	pfal_chr2: 273689-274507	merozoite surface protein 2 precursor
4	PF10_0372	6192.70	99.90	chr10: 1508412-1509473	hypothetical protein
5	PF13_0058	5204.35	99.88	chr13_1: 426154-426585	hypothetical protein
6	PF14_0598	5187.70	99.86	chr14: 2558046-2559295	glyceraldehyde-3-phosphate dehydrogenase
7	PF10_0019	5053.90	99.84	chr10: 81417-81740	early transcribed membrane protein
8	PFC0120w	4901.05	99.82	pfal_chr3: 132097-137339	Cytoadherence linked asexual protein, CLAG
9	PFA0420w	4622.80	99.80	pfal_chr1: 350323-350862	hypothetical protein
10	PFE0165w	4435.15	99.79	pfal_chr5: 140710-141471	actin depolymerizing factor, putative
11	MAL13P1.308	4349.45	99.77	chr13_1: 2369502-2377598	hypothetical protein
12	PF11_0039	4346.10	99.75	chr11: 126406-126681	early transcribed membrane protein 11.1
13	PF11_0224	4332.25	99.73	chr11: 813000-	
		4136.15			

Figure 5. In seeking and blood-stage vaccine, one might wish to prioritize antigens that are abundantly expressed in the extra-erythrocytic merozoite stage. This query focuses on experiments conducted by Le Roch et al (2003b) using an Affymetrix microarray to examine expression across the erythrocytic life cycle, and seeks genes that are among the top 5% in steady-state transcript abundance during late schizogony (many other expression datasets and query strategies could be also envisioned).



Query History

This page displays the most recent queries that you have run. It will remain empty until then. Once there are query result sets listed below you can choose any two of them and click on one of the buttons at the bottom to combine them in one of three ways: union, intersect, or subtraction. **Please note:** you must have cookies enabled in your browser in order for this page to work correctly.

	Query	Start time	Response time	Result	Download	Size
☑	Genes [type=sequencing center annotations (Pf Annotation) chr=all] predicted to contain a signal peptide.	5:13:44 PM	<1 second	view	download	651
☑	All Pf genes with the following phylogenetic profile: *A. thaliana*=don't care *C. elegans*=don't care *D. melanogaster*=don't care *E. coli*=don't care *H. sapiens*=no *S. cerevisiae*=don't care *A. gambiae*=don't care *M. musculus*=don't care *P. yoelii*=yes	5:14:29 PM	<1 second	view	download	2260
☑	Genes [type=sequencing center annotations (Pf Annotation) chr=all] expressed in the 95th percentile or above in the Late Schizogony stage	5:17:12 PM	<1 second	view	download	247

UNION or INTERSECT or SUBTRACT the selected query results (a new entry will appear at the end of the list.)

Query result: rows 1 - 20

[1-20][21-26] **Rows 1 - 20** of 26 [1-20][21-26]

	gene	location	description
1	PFA0210c	pfal_chr1: 183057-184457	hypothetical protein
2	PFB0570w	pfal_chr2: 522931-523999	hypothetical protein
3	MAL6P1.299	chr6: 574310-575353	Plasmodium falciparum membrane protein pf12 precursor
4	PFE0370c	pfal_chr5: 307490-309556	subtilisin-like protease precursor, putative
5	PFE0395c	pfal_chr5: 328666-329715	hypothetical protein
6	PFE1590w	pfal_chr5: 1301219-1301764	early transcribed membrane protein
7	PF08_0057	chr8: 527638-527939	hypothetical protein
8	PF07_0128	chr7: 1265975-1270488	erythrocyte binding antigen
9	MAL7P1.141	chr7: 981838-982878	hypothetical protein
10	PFI1270w	pfal_chr9: 1040703-1041506	hypothetical protein
11	PFI1445w	pfal_chr9: 1175193-1180497	hypothetical protein
12	PFI1475w	pfal_chr9: 1201802-1206964	merozoite surface protein 1, precursor
13	PFI0265c	pfal_chr9: 270738-274787	rhoptry protein, putative
14	PF10_0119	chr10: 470978-471932	hypothetical protein
15	PF11_0344	chr11: 1290767-1292635	apical membrane antigen 1 precursor
16	PF10_0372	chr10: 1508412-1509473	hypothetical protein
17	PF10_0323	chr10: 1336464-1337531	hypothetical

Figure 6. Using the 'Query History' feature of PlasmoDB to combine the queries illustrated in Figures 1-3 identifies only 26 genes exhibiting all three desired characteristics: antigens that are secreted, restricted to *Plasmodium* species, and abundantly transcribed just before merozoite emergence. Among these genes are both of the leading erythrocytic vaccine candidates: MSP1 and AMA1.