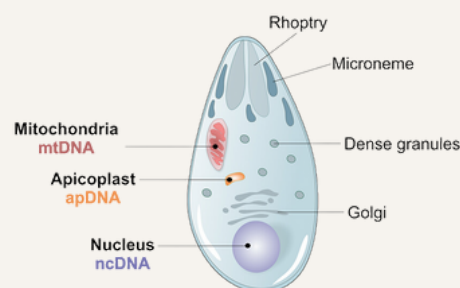




The search question

The malaria parasite *Plasmodium falciparum* and other *Plasmodium* species contain a non-photosynthetic plastid organelle called the **apicoplast** that is crucial to the malaria parasite's survival. Due to the algal origin of the apicoplast (which contains its own DNA), many proteins and pathways are not shared by the human host, making it an attractive target for antimalarial drugs.

To identify genes that are unique to the apicoplast and not present in human hosts, we could ask the question: **What genes in *Plasmodium falciparum* have protein products that are present at a higher concentration in the apicoplast compared to the endoplasmic reticulum (ER)?**



[Image credit](#)

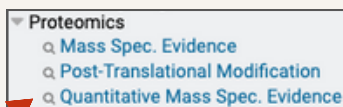
Furthermore, we can leverage protein subcellular localization data to limit the results to the apicoplast.

What platform is best suited for this question?



This knowledgebase has data on Haemoproteus, Hepatocystis, and Plasmodium spp.

What search is best suited for this question?



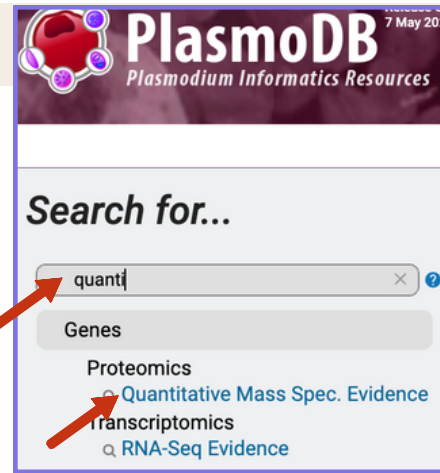
As we are seeking different in protein quantities between samples, data from quantitative proteomic experiments will be ideal for searching based on fold change or differential expression.

What is a possible search strategy that will answer this question?

Use **Quantitative Mass Spec. Evidence** search in two steps- (1) identify genes that are upregulated in apicoplast vs. ER, (2) intersect that search with an apicoplast localization search.

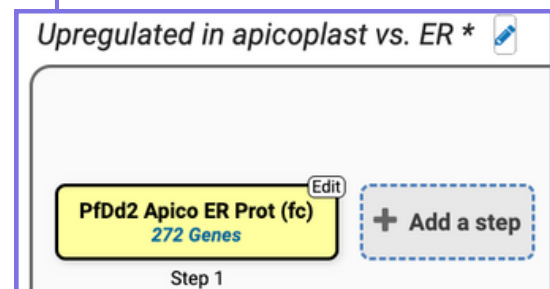
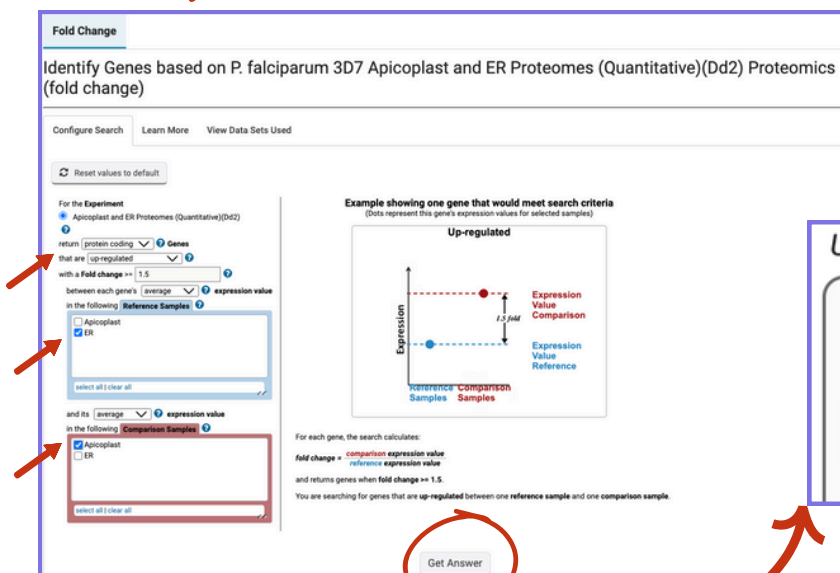
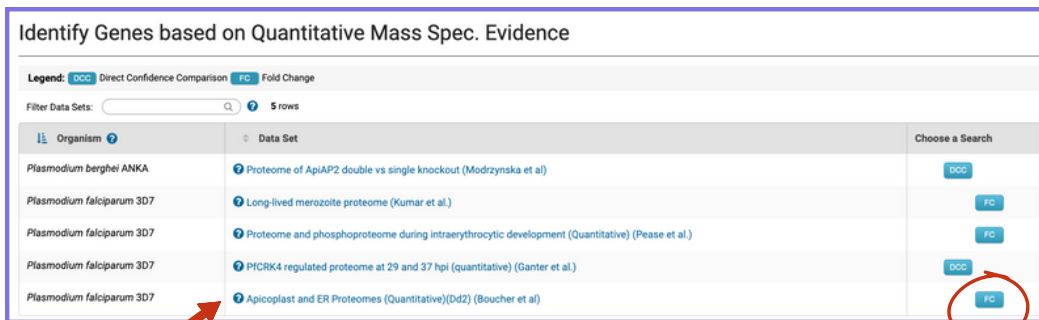
1. Navigate to the relevant search

- Navigate to PlasmoDB.org
- From the sidebar or header, search or scroll for “quantitative” and click on **Quantitative Mass Spec. Evidence**



2. Select an appropriate experiment & configure and run a search

1. Select the experiment called Apicoplast and ER Proteomes (Quantitative)(Dd2) (Boucher et al)- it compares the samples we are interested in.
2. Choose the fold change (FC) search.
3. Configure this search to return all genes that are upregulated by 1.5 fold in the apicoplast sample compared to the ER sample.



How many genes did you get that have upregulated protein expression in apicoplast compared to ER?

3. Limit the results by leveraging available subcellular localization data

PlasmoDB has a data set that returns genes with the transit peptides that mediate protein targeting to the apicoplast.

- Click on the **add step** button and find the **subcellular localization** search
- Make sure Apicoplast localization is selected and click on the Run Step button

The image consists of three screenshots from the PlasmoDB interface, illustrating the process of adding a subcellular localization step to a search strategy.

Top Left Screenshot: Shows a search result titled "Upregulated in apicoplast vs. ER *". Below the title, there is a yellow box labeled "PfDd2 Apico ER Prot (fc)" with "272 Genes" below it. To the right of this box is a red circle around the "Add a step" button.

Top Right Screenshot: Shows the "Add a step to your search strategy" dialog. It has two main sections: "1 Choose how to combine with other Genes" and "2 Choose which Genes to combine. From...". Under section 1, the "1 INTERSECT 2" radio button is selected. Under section 2, the "A new search" radio button is selected. A red arrow points from the "Add a step" button in the top left screenshot to the "1 INTERSECT 2" radio button.

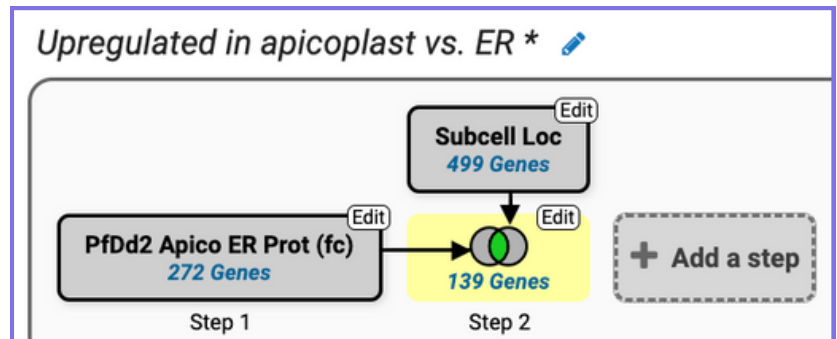
Bottom Screenshot: Shows the "Search for Genes by Pfal 3D7 Subcellular Localization" dialog. It has a "Localization" dropdown menu with "Apicoplast" selected. A red arrow points from the "Add a step" button in the top left screenshot to the "Apicoplast" dropdown. At the bottom right, the "Run Step" button is circled in red.

4. Explore your results

How many genes did you identify?

Are you more confident that these genes are apicoplast genes?

How would you use the PlasmoDB tools to boost your confidence in these so called apicoplast genes?



Questions? Comments? Write to
help@veupathdb.org