

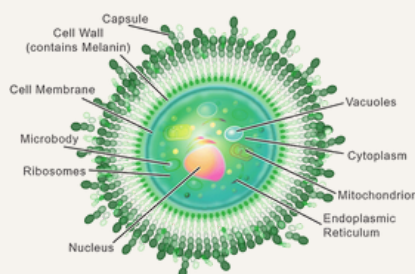


The search question

The opportunistic fungal pathogen *Cryptococcus neoformans* causes life-threatening meningitis in immunocompromised individuals. In *Cryptococcus*, the expression of virulence factors, including capsule and melanin, is in part regulated by the cyclic-AMP/protein kinase A (cAMP/PKA) signal transduction pathway.

Investigating the influence of PKA on the composition of the intracellular proteome can contribute to a comprehensive understanding of the regulation that underpins virulence. *C. neoformans* PGAL7::PKA1 strain can be used to induce the PKA pathway in galactose media and repress the pathway in glucose media.

In this exercise, the goal is to **identify *Cryptococcus neoformans* genes that are upregulated in a protein kinase A dependent (PKA) manner and not in a non-PKA dependent manner.**



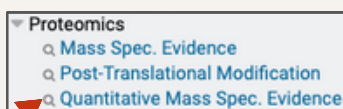
[Image credit](#)

What platform is best suited for this question?



This knowledgebase has data on oomycetes & diverse fungal taxa, including *Cryptococcus*.

What search is best suited for this question?



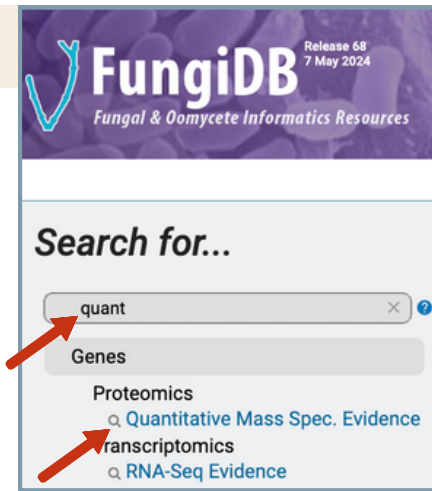
As we are seeking differences in the proteome between two culture conditions, data from quantitative proteomic experiments will be ideal for this search.

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 by galactose induction of PKA pathway, (2) remove genes that are upregulated by glucose media.

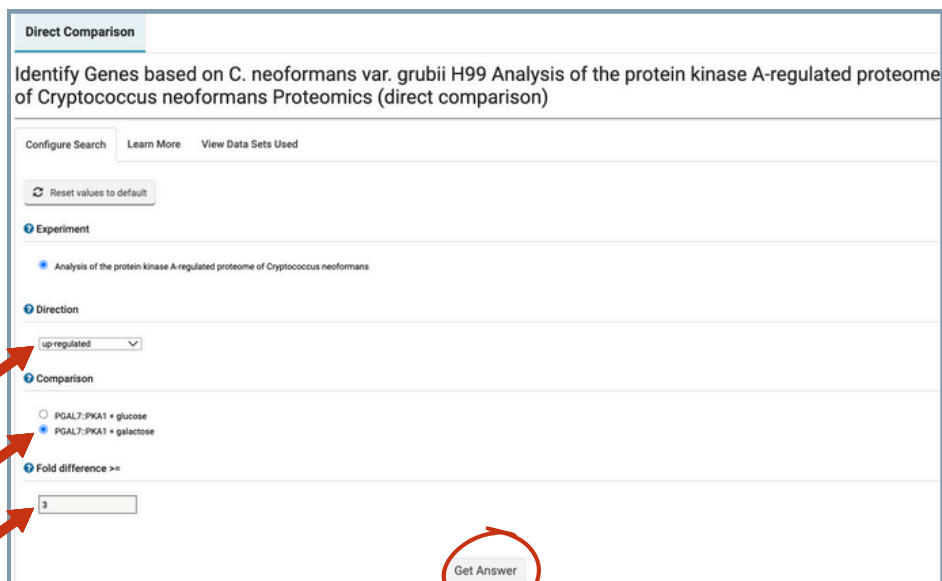
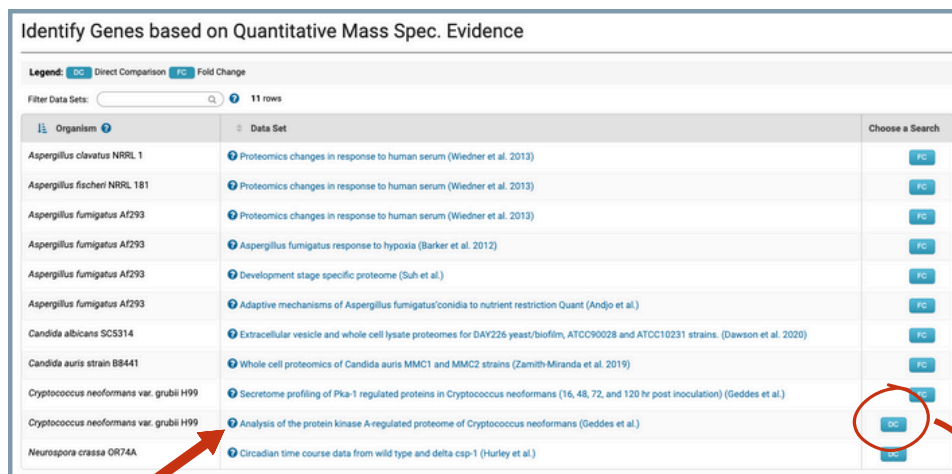
1. Navigate to the appropriate search

- Navigate to [FungiDB.org](https://fungi.org/fungi/FungiDB)
- From the sidebar or header, search for “quantitative” and click on **Quantitative Mass Spec. Evidence**



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

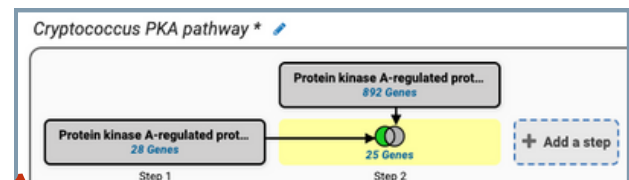
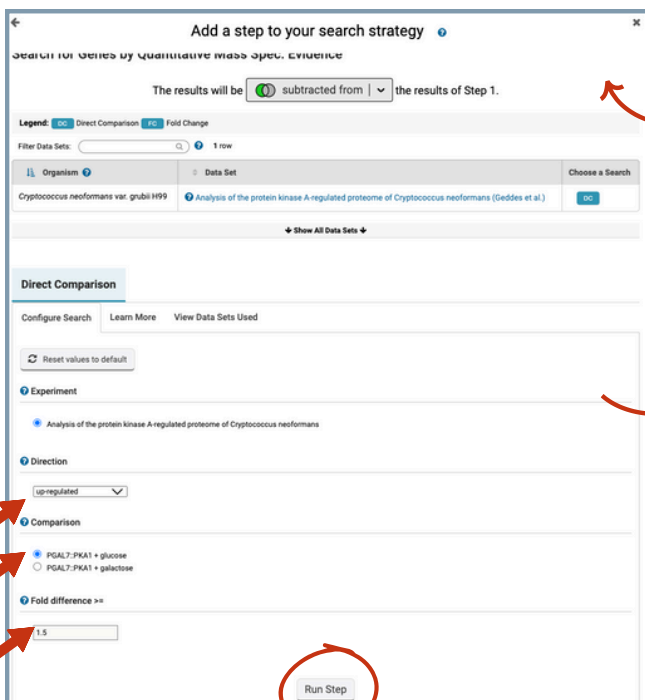
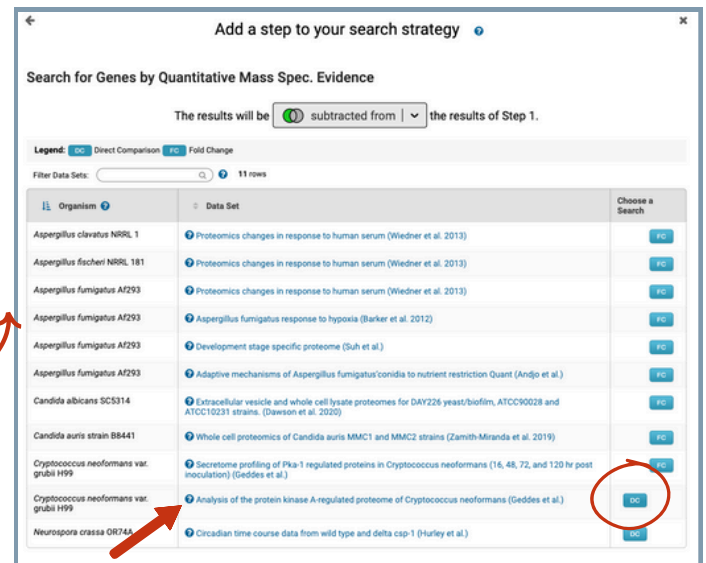
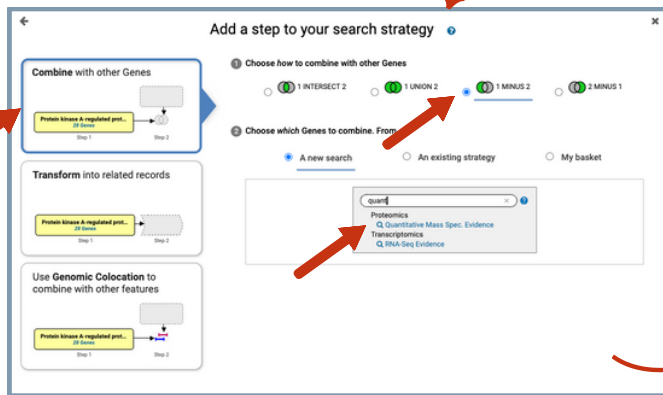
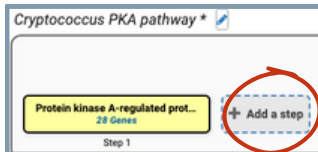
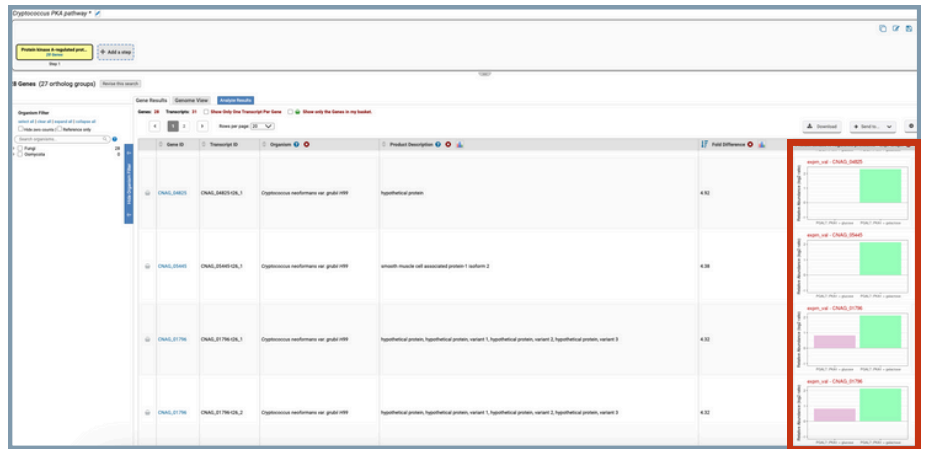
1. find the experiment called “Analysis of the protein kinase A-regulated proteome of *Cryptococcus neoformans* (Geddes et al.)”
2. Choose the Direct Comparison (FC) search.
3. Configure the direct comparison search to identify genes that are upregulated by 3 fold in galactose media. Run the search by clicking on “Get answer”.



3. Explore results and add a step to your search strategy

Explore your results. Do the expression graphs in the table of gene results meet the criteria you selected?

- Add a step and remove from this list any gene that is upregulated by 1.5 fold in glucose media.



Can you reconfigure the above searches to identify genes that are downregulated as opposed to upregulated?

Did your results change?

Questions? Comments? Write to help@veupathdb.org