VEuPathDB
Eukaryotic Pathogen, Vector & Host Informatics Resources

Mining Proteomics Data
PKA-regulated proteome of *Cryptococcus neoformans*
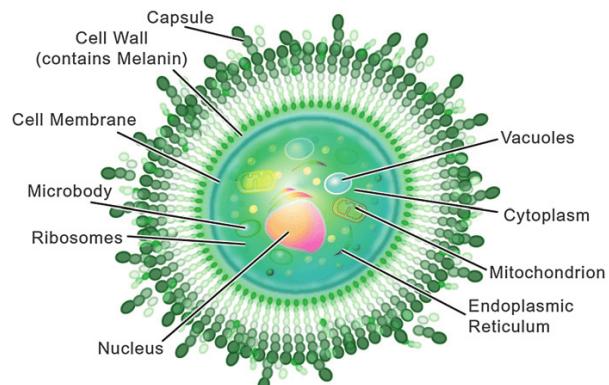

Learning objectives
- Explore proteomics datasets on VEuPathDB
- Identify upregulated genes using the Quantitative Mass Spec. Evidence search


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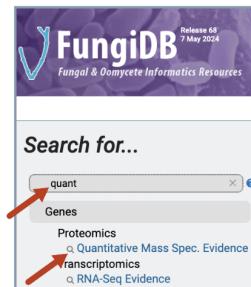
The opportunistic fungal pathogen *Cryptococcus neoformans* causes life-threatening meningitis in immunocompromised individuals. In Cryptococcus, the expression of virulence factors, including capsule and melanin, is in part regulated by the cyclic-AMP/protein kinase A (cAMP/PKA) signal transduction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

1. Navigate to FungiDB.org
2. From the sidebar or header, search for "quantitative" and click on **Quantitative Mass Spec. Evidence**

3. Find genes upregulated in galactose media
   a. Find the experiment called "Analysis of the protein kinase A-regulated proteome of Cryptococcus neoformans (Geddes et al.)"
   b. Choose the Direct Comparison (**DC**) search.
   c. 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".
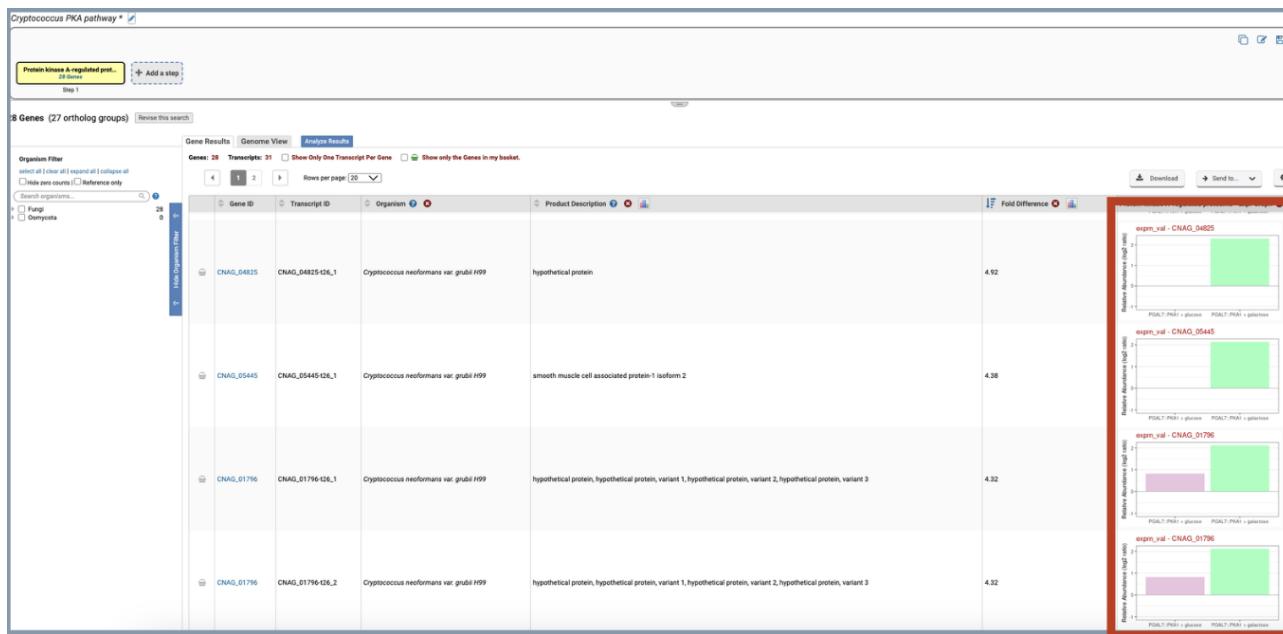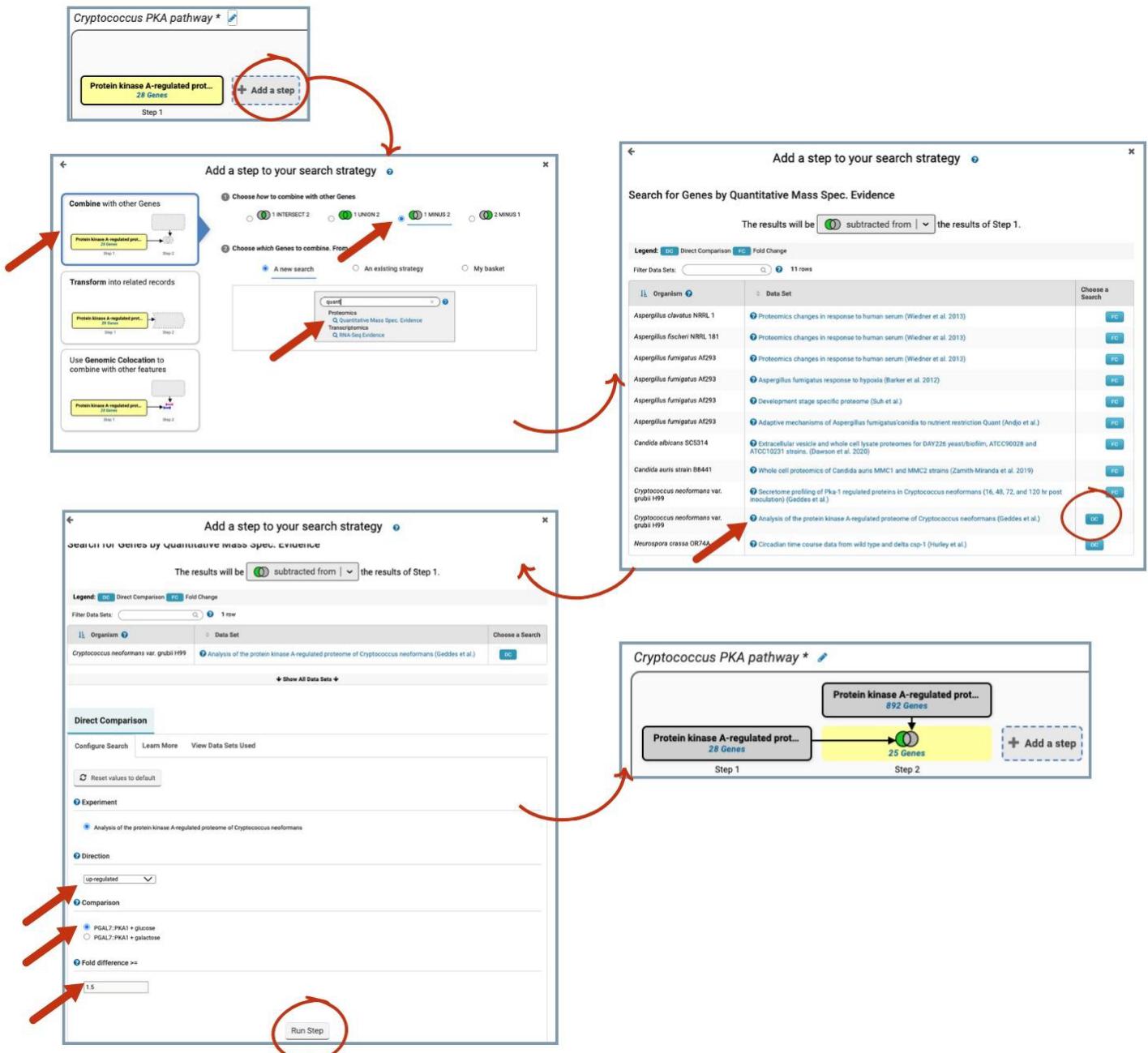
4. **Explore your results.**

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

5. **Add a step and remove from this list any gene that is upregulated by 1.5-fold in glucose media.**
   How many genes did you identify?

6. Can you reconfigure the above searches to identify genes that are downregulated as opposed to upregulated? Did your results change?