

Mining Proteomics Data

PKA-regulated proteome of *Cryptococcus neoformans*

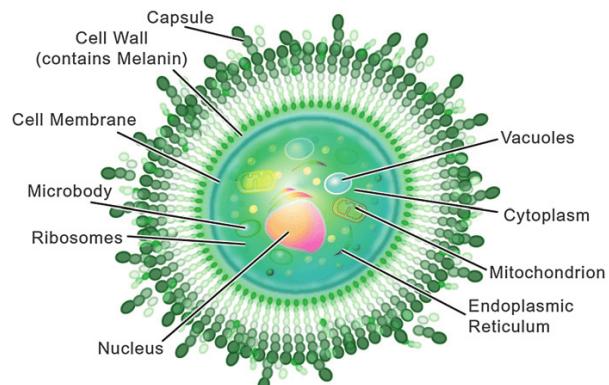
Learning objectives

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

Introduction

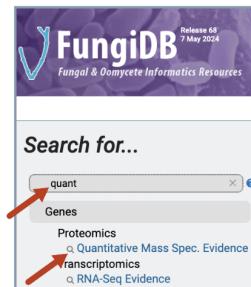
The opportunistic fungal pathogen *Cryptococcus neoformans* causes life-threatening meningitis in immunocompromised individuals. In *Cryptococcus*, the expression of virulence factors, including capsule and melanin, is in part regulated by the cyclic-AMP/protein kinase A (cAMP/PKA) signal transduction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

Identify Genes based on Quantitative Mass Spec. Evidence

Legend: DC Direct Comparison FC Fold Change

Filter Data Sets: 11 rows

Organism	Data Set	Choose a Search
Aspergillus clavatus NRRL 1	Proteomics changes in response to human serum (Wiedner et al. 2013)	FC
Aspergillus fischeri NRRL 181	Proteomics changes in response to human serum (Wiedner et al. 2013)	FC
Aspergillus fumigatus Af293	Proteomics changes in response to human serum (Wiedner et al. 2013)	FC
Aspergillus fumigatus Af293	Aspergillus fumigatus response to hypoxia (Barker et al. 2012)	FC
Aspergillus fumigatus Af293	Development stage specific proteome (Suh et al.)	FC
Aspergillus fumigatus Af293	Adaptive mechanisms of Aspergillus fumigatus' conidia to nutrient restriction Quant (Andjo et al.)	FC
Candida albicans SC5314	Extracellular vesicle and whole cell lysate proteomes for DAY226 yeast/biofilm, ATCC90028 and ATCC10231 strains. (Dawson et al. 2020)	FC
Candida auris strain B8441	Whole cell proteomics of Candida auris MMC1 and MMC2 strains (Zamith-Miranda et al. 2019)	FC
Cryptococcus neoformans var. grubii H99	Secretome profiling of Pka-1 regulated proteins in Cryptococcus neoformans (16, 48, 72, and 120 hr post inoculation) (Geddes et al.)	DC
Cryptococcus neoformans var. grubii H99	Analysis of the protein kinase A-regulated proteome of Cryptococcus neoformans (Geddes et al.)	DC
Neurospora crassa OR74A	Circadian time course data from wild type and delta csp-1 (Hurley et al.)	DC

Direct Comparison

Identify Genes based on *C. neoformans* var. *grubii* H99 Analysis of the protein kinase A-regulated proteome of *Cryptococcus neoformans* Proteomics (direct comparison)

Configure Search Learn More View Data Sets Used

Reset values to default

Experiment

Analysis of the protein kinase A-regulated proteome of *Cryptococcus neoformans*

Direction

up-regulated

Comparison

PGAL7::PKA1 + glucose (radio button)

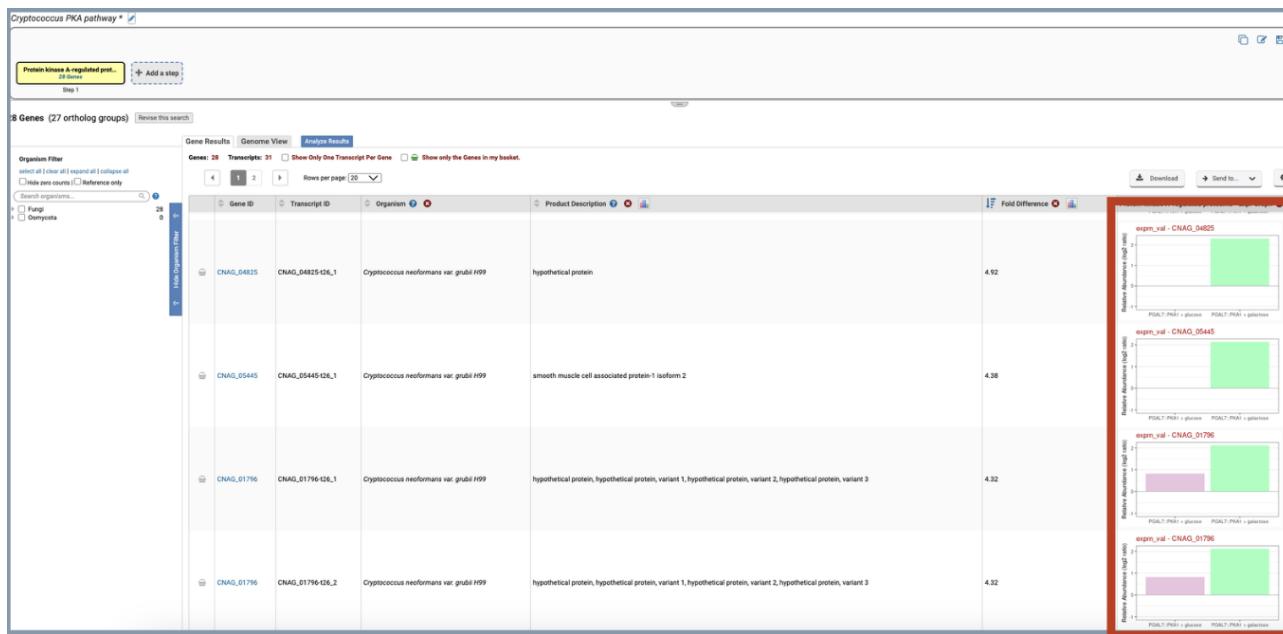
PGAL7::PKA1 + galactose (radio button)

Fold difference >=

3

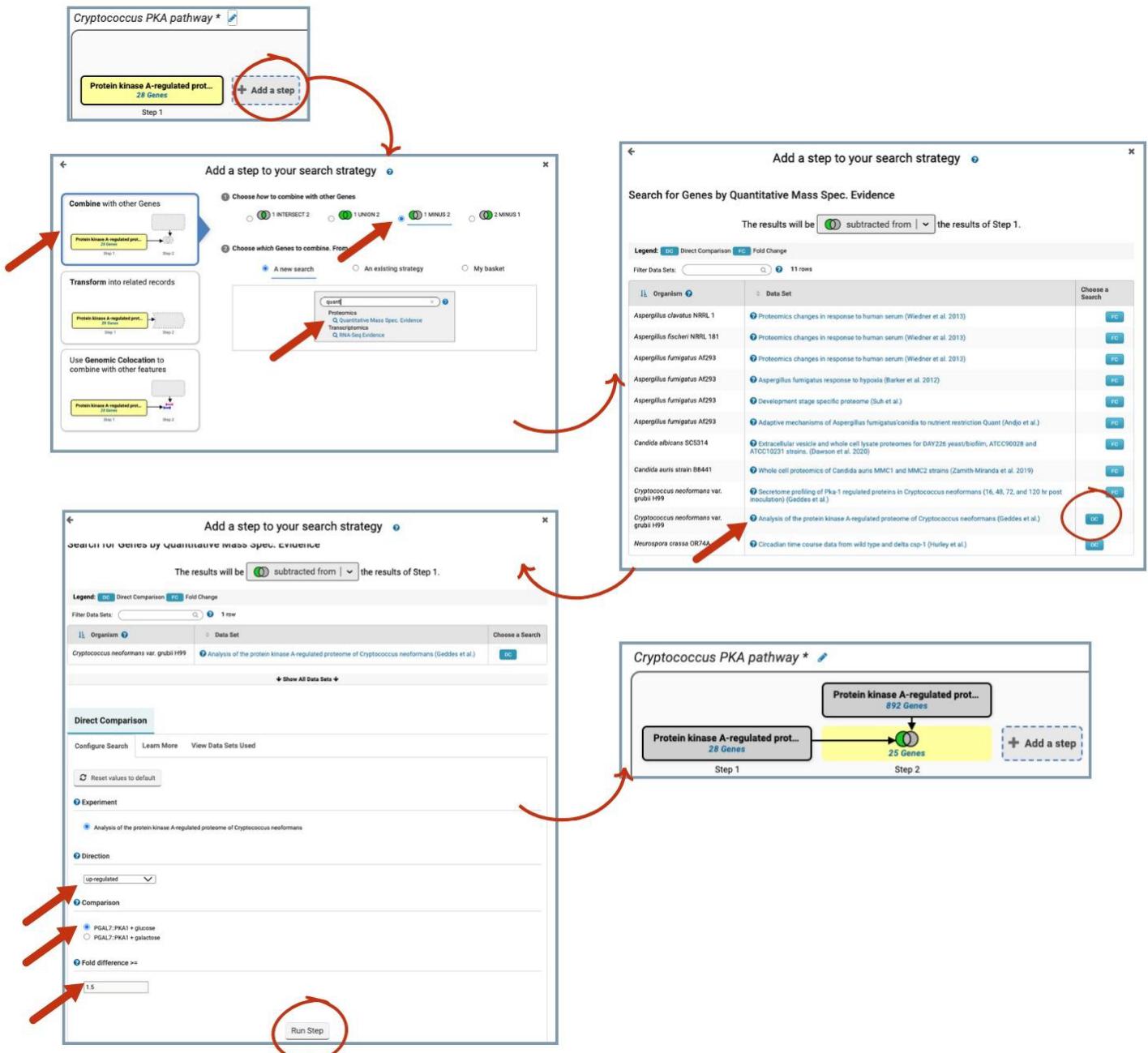
Get Answer

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?