

FungiDB: Proteomics

1. Identify genes using evidence from quantitative mass spec data.

In the example described here, quantitative proteomics data from Suh *et al.* (PMID: 22545825) are examined to identify *A. fumigatus* genes up-regulated in the growing conidia and then cross referenced with *Gene Models* data for *Exon Count* to identify genes with no more than 5 exons.

- Deploy *Quantitative Mass Spec. Evidence Search* from the *Proteomics* section under the *Search for Genes* category.
 - In the proteomics dataset selection window click on the *Fold Change (FC)* button next to the Suh *et al.* study.
 - To identify genes that are upregulated by at least 2-fold in the 4–8hr time frame compared to the 0hr time point, set the regulation direction to up-regulated, modify the Fold Change parameter to 2, and select 0hr from the *Reference Samples* and 4, 6, and 8hr from the *Comparison Samples*
 - Click *Get Answer*.

The screenshot shows the 'Search for Genes' interface. On the left is a sidebar with a search bar and a list of categories. The 'Proteomics' category is expanded, and 'Quantitative Mass Spec. Evidence' is selected. The main search area is titled 'Identify Genes based on A. fumigatus Af293 Development stage specific proteome Proteomics (fold change)'. It contains several input fields: 'Experiment' (Development stage specific proteome), 'Regulation' (up-regulated), 'Fold Change' (>= 2), 'Reference Samples' (0hr), and 'Comparison Samples' (4hr, 6hr, 8hr). An example graph shows 'Up-regulated' genes with a 2-fold increase in expression from a reference sample (0hr) to comparison samples (4hr, 6hr, 8hr). A 'Get Answer' button is at the bottom.

Strategy: AfumCEA10 stage-specific Quant (fc)(3) *

102 Genes from Step 1 [Review](#)

Strategy: AfumCEA10 stage-specific Quant (fc)(3)

Click on a number in this table to limit/filter your results

Gene ID	Transcript ID	Organism	Product Description	Fold Difference	Chosen Ref (log2)	Chosen Comp (log2)	AfumCEA10 stage-specific Quant - Expr Graph
Afu4g06620	Afu4g06620-T	A. fumigatus Af293	Glutamata,Leucine/Phenylalanine/Valine dehydrogenase	151.1	9.21	16.45	

The search strategy returned 102 genes that are up-regulated during conidial growth.

b) Expand this search strategy and determine how many of these genes have multiple exons

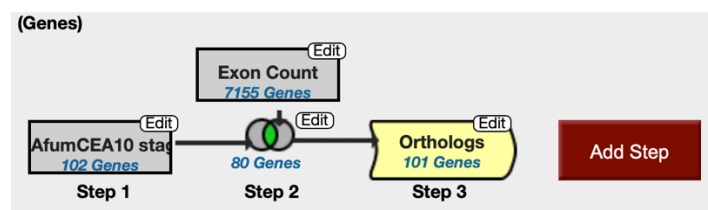
- Click on the *Add Step* button and choose to *Run a New Search for, Genes, Genes models, Exon Count* (min =2, max =5).
- Intersect the second search with the first one.

Examine or revise results, explore additional data by adding more columns via the *Add Columns* button, or export records via the *Download* link.

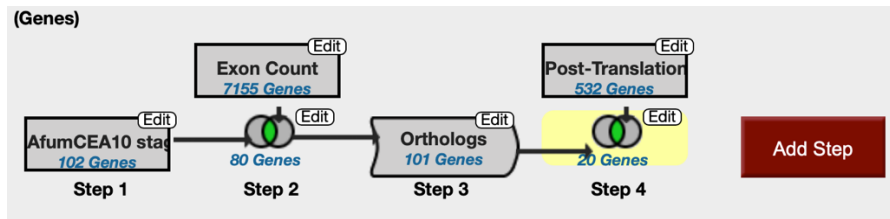
2. Identify proteins modified post-translationally.

Using the query developed above to identify which genes may be post-translationally modified using post-translation modification data from *A. nidulans*.

- Add step and transform genes into orthologs in *A. nidulans*



- Add Step and then select *Proteomics, Post-Translational Modification* dataset in *A. nidulans*



Determine how many of these phosphorylated proteins are also likely secreted.

- Add Step and Run a New Search for Protein Targeting and Localization, Predicted Signal Peptide

