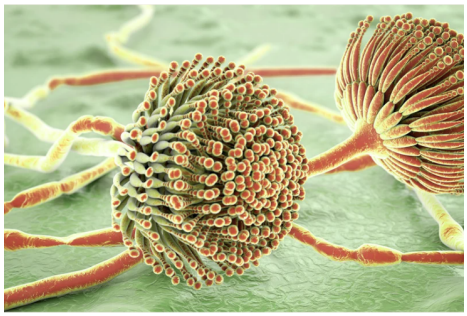
VEuPathDB
Eukaryotic Pathogen, Vector & Host Informatics Resources

Mining Transcriptomics Data
Co-expression of genes in *Aspergillus niger*

Learning objectives
- Review the types of expression searches in VEuPathDB
- Run a co-expression search

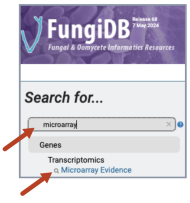
Introduction



A major obstacle in understanding biological systems lies in the vast number of genes in many genomes whose functions remain unknown. The fungal genus *Aspergillus* includes key human pathogens, model species, and industrially valuable microorganisms. *Aspergillus niger* is widely utilized for the production of organic acids, proteins, and holds potential for discovering novel bioactive secondary metabolites. But only a small minority of predicted open reading frames in the *A. niger* genome have been experimentally validated.

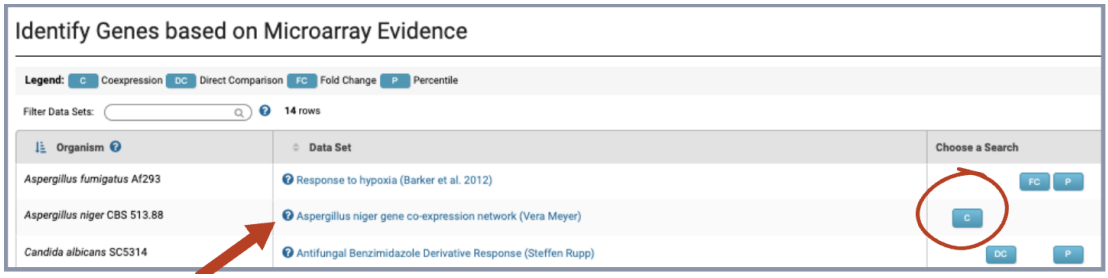
An04g07430 is an *Aspergillus niger* protein coding gene with little functional annotation. By finding genes that are expressed at the same time as An04g07430, we may find clues about its function and the biological processes that it participates in.

1. Go to FungiDB.org. This knowledgebase has data and informatics resources for oomycetes and diverse fungal taxa including *Aspergillus*.

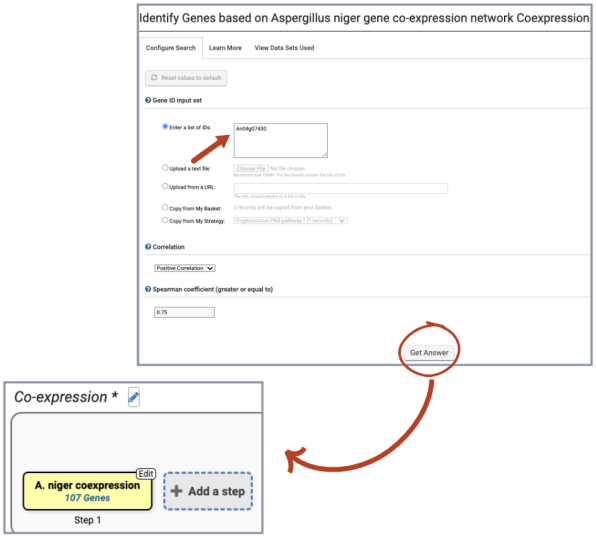


2. From the sidebar or header, search for “microarray” and click on Microarray Evidence

3. Next, choose the appropriate experiment/ samples within the search. In this case, we are looking for co-expression data. Choose the **Coexpression search (C)** for the data set titled *Aspergillus niger* gene co-expression network (Vera Meyer). This data is the result of a meta-analysis (Schape et al Nucleic Acids Research 2019) of 155 publicly available transcriptomics analyses for *A. niger*, which were used to generate a genome-level co-expression network and sub-networks for >9,500 genes.

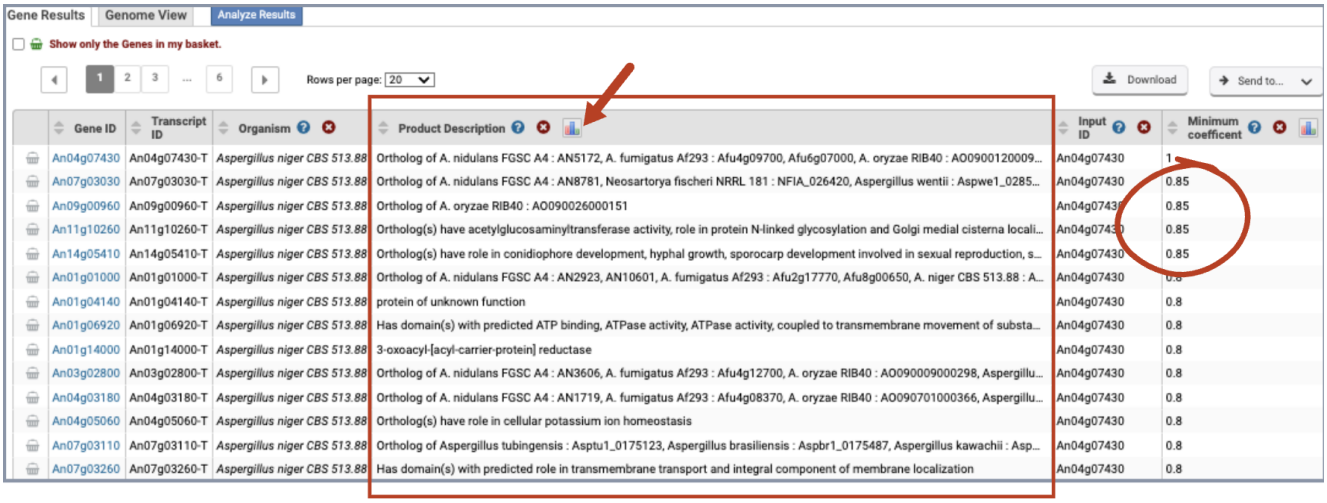


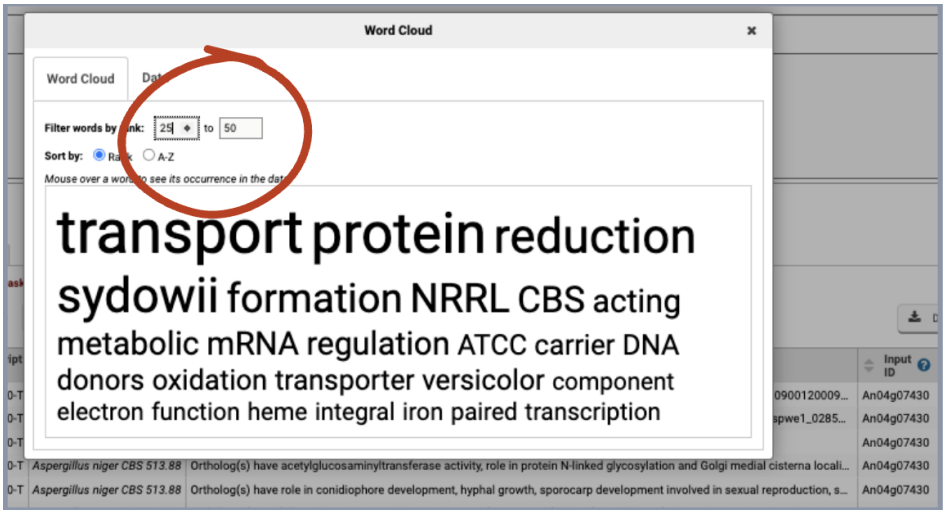
4. Configure the Coexpression search to find the co-expression network for the gene of interest:
    a. Enter **An04g07430** into the gene ID input set
    b. Set correlation to positive
    c. Set Spearman coefficient (greater or equal to) 0.75
    d. Get Answer



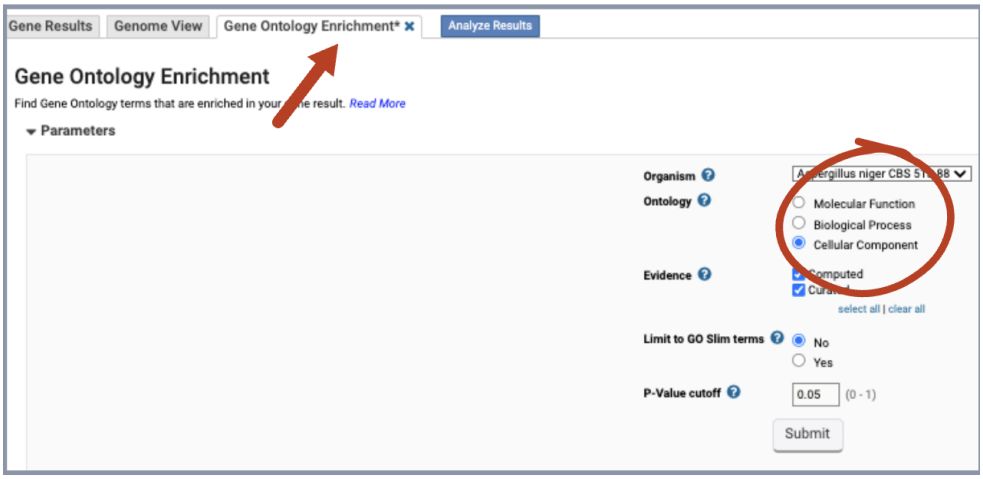
How many genes share the co-expression profile of An04g07430?

5. Explore the genes in the co-expression network.
    i. What genes share the co-expression profile of An04g07430? Several genes have a correlation coefficient of 0.85 (see red circle below). What are these genes? Visit their gene pages by clicking on the Gene ID link to learn more.
    ii. Scan the product description column (see red rectangle below) for genes with known functions.
    iii. Use the Column Histogram tool (see red arrow below) to view a word cloud of the product descriptions in the column. Set the rank range to 25-50. What words occur most often in the product descriptions of An04g07430 co-expressed genes?





6. Run the **Gene Ontology Enrichment** analyses for Molecular Function, Cellular Component and Biological Processes.



Do these provide information about what this group of co-expressed genes might be doing?