



The search question

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.

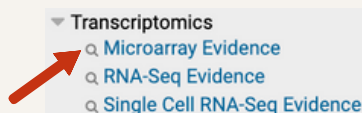


What platform is best suited for this question?



This knowledgebase has data and informatics resources for oomycetes and diverse fungal taxa including *Aspergillus*.

What search is best suited for this question?



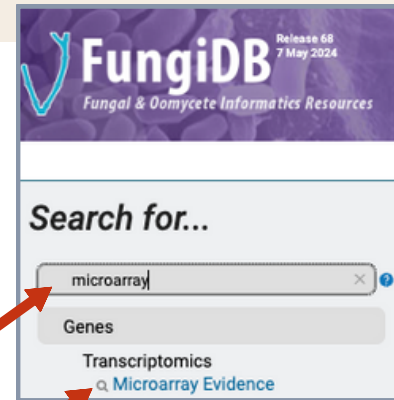
The analysis of gene expression data from **microarray data** can identify groups of genes that exhibit similar expression levels across different conditions.

What is a possible search strategy that will answer this question?

Use the **Microarray Evidence** data and **Co-expression search** to find the co-expression network for the gene of interest. Further, explore the genes in this network using the column histogram tool and enrichment analyses to glean information about the function of this group of co-expressed genes.

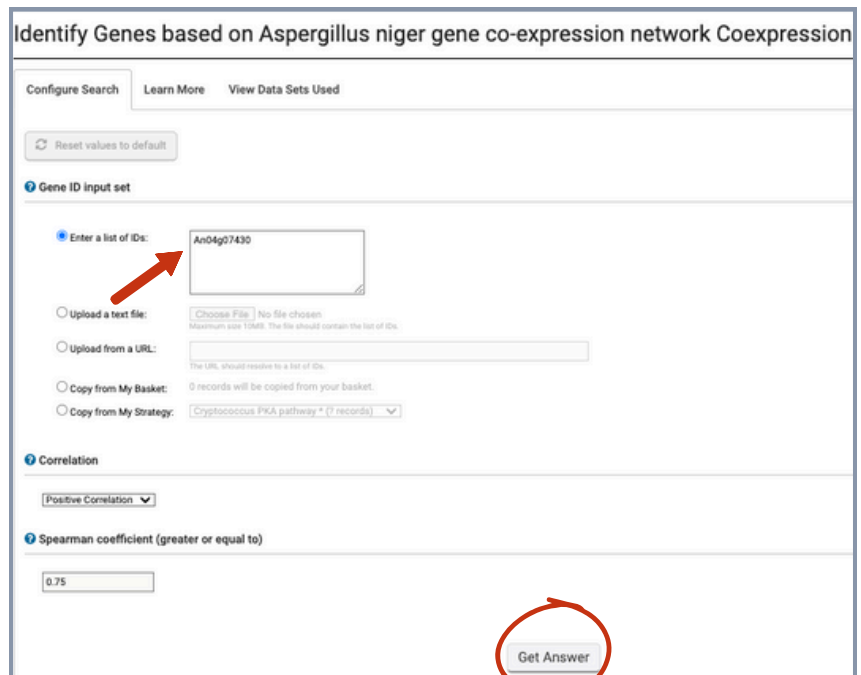
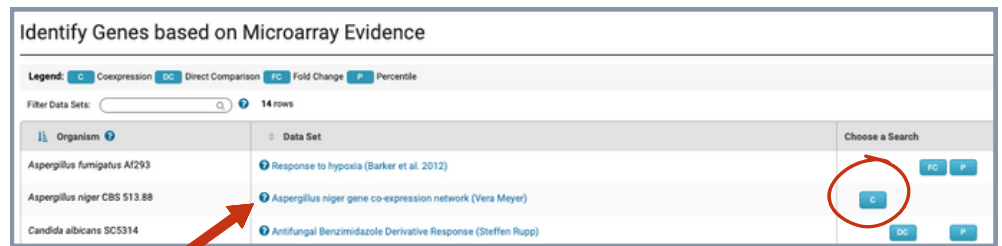
1. Navigate to the appropriate search

- Navigate to [FungiDB.org](https://fungi.org/fungi/FungiDB)
- From the sidebar or header, search for "microarray" and click on Microarray Evidence

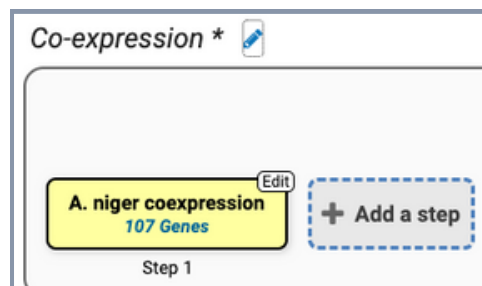


2. Choose the appropriate experiments/ samples & parameters within the search

- Choose the Coexpression search 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.
- Configure the **Coexpression search** to find the co-expression network for the gene **An04g07430**.



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



3. Explore the genes in the co-expression network

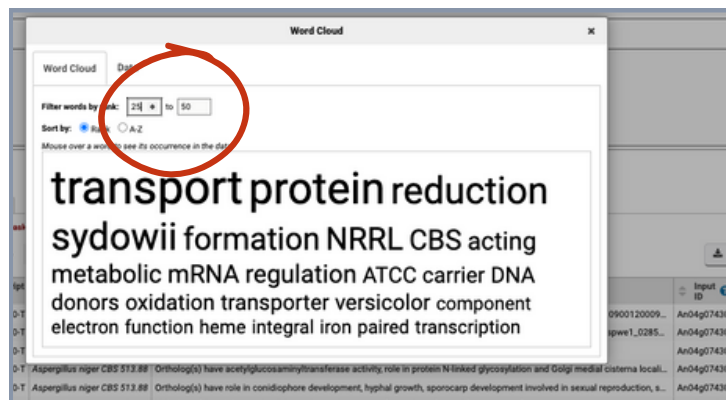
Gene Results | Genome View | **Analyze Results**

☐ Show only the Genes in my basket.

Rows per page: 20

Gene ID	Transcript ID	Organism	Product Description	Input ID	Minimum coefficient
An04g07430	An04g07430-T	Aspergillus niger CBS 513.88	Ortholog of A. nidulans FGSC A4 : AN5172, A. fumigatus Af293 : Afu4g09700, Afu6g07000, A. oryzae RIB40 : AO0900120009...	An04g07430	1
An07g03030	An07g03030-T	Aspergillus niger CBS 513.88	Ortholog of A. nidulans FGSC A4 : AN8781, Neosartorya fischeri NRRL 181 : NFIA_026420, Aspergillus wentii : Aspwe1_0285...	An04g07430	0.85
An09g00960	An09g00960-T	Aspergillus niger CBS 513.88	Ortholog of A. oryzae RIB40 : AO090026000151	An04g07430	0.85
An11g10260	An11g10260-T	Aspergillus niger CBS 513.88	Ortholog(s) have acetylglucosaminyltransferase activity, role in protein N-linked glycosylation and Golgi medial cisterna local...	An04g07430	0.85
An14g05410	An14g05410-T	Aspergillus niger CBS 513.88	Ortholog(s) have role in conidiophore development, hyphal growth, sporocarp development involved in sexual reproduction, s...	An04g07430	0.85
An01g01000	An01g01000-T	Aspergillus niger CBS 513.88	Ortholog of A. nidulans FGSC A4 : AN2923, AN10601, A. fumigatus Af293 : Afu2g17770, Afu8g00650, A. niger CBS 513.88 : A...	An04g07430	0.8
An01g04140	An01g04140-T	Aspergillus niger CBS 513.88	protein of unknown function	An04g07430	0.8
An01g06920	An01g06920-T	Aspergillus niger CBS 513.88	Has domain(s) with predicted ATP binding, ATPase activity, ATPase activity, coupled to transmembrane movement of substa...	An04g07430	0.8
An01g14000	An01g14000-T	Aspergillus niger CBS 513.88	3-oxoacyl-[acyl-carrier-protein] reductase	An04g07430	0.8
An03g02800	An03g02800-T	Aspergillus niger CBS 513.88	Ortholog of A. nidulans FGSC A4 : AN3606, A. fumigatus Af293 : Afu4g12700, A. oryzae RIB40 : AO090009000298, Aspergillu...	An04g07430	0.8
An04g03180	An04g03180-T	Aspergillus niger CBS 513.88	Ortholog of A. nidulans FGSC A4 : AN1719, A. fumigatus Af293 : Afu4g08370, A. oryzae RIB40 : AO090701000366, Aspergillu...	An04g07430	0.8
An04g05060	An04g05060-T	Aspergillus niger CBS 513.88	Ortholog(s) have role in cellular potassium ion homeostasis	An04g07430	0.8
An07g03110	An07g03110-T	Aspergillus niger CBS 513.88	Ortholog of Aspergillus tubingensis : Asptu1_0175123, Aspergillus brasiliensis : Aspbr1_0175487, Aspergillus kawachii : Asp...	An04g07430	0.8
An07g03260	An07g03260-T	Aspergillus niger CBS 513.88	Has domain(s) with predicted role in transmembrane transport and integral component of membrane localization	An04g07430	0.8

- What genes share the co-expression profile of An04g07430? Several genes have a correlation coefficient of 0.85 (see **red circle** above). What are these genes? Visit their gene pages by clicking on the Gene ID link to learn more.
- Scan the product description column (see **red rectangle** above) for genes with known functions.
- Use the Column Histogram tool (see **red arrow** above) 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?**



Gene Results | Genome View | **Gene Ontology Enrichment*** | Analyze Results

Find Gene Ontology terms that are enriched in your gene result. [Read More](#)

Parameters

Organism: **Aspergillus niger CBS 513.88**

Ontology: ☐ Molecular Function ☐ Biological Process ☒ Cellular Component

Evidence: ☒ Computed ☐ Curated

Limit to GO Slim terms: ☐ No ☐ Yes

P-Value cutoff: 0.05 (0 - 1)

Submit

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?



Questions? Comments? Write to help@veupathdb.org