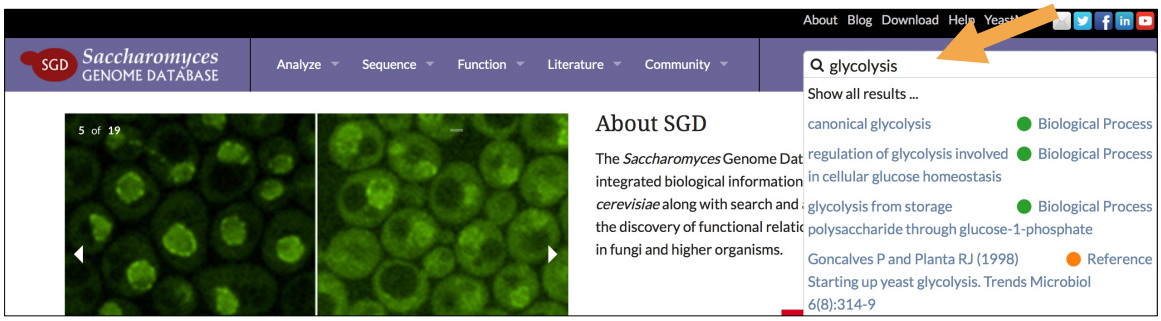
Using SPELL to Analyze Expression Datasets & Coexpressed Genes at SGD

SPELL (**S**erial **P**attern of **E**xpression **L**evels **L**ocator) is a query-driven search engine for large gene expression microarray compendia. Given a small set of query genes, SPELL identifies which datasets are most informative for these genes, then within those datasets additional genes are identified with expression profiles most similar to the query set.

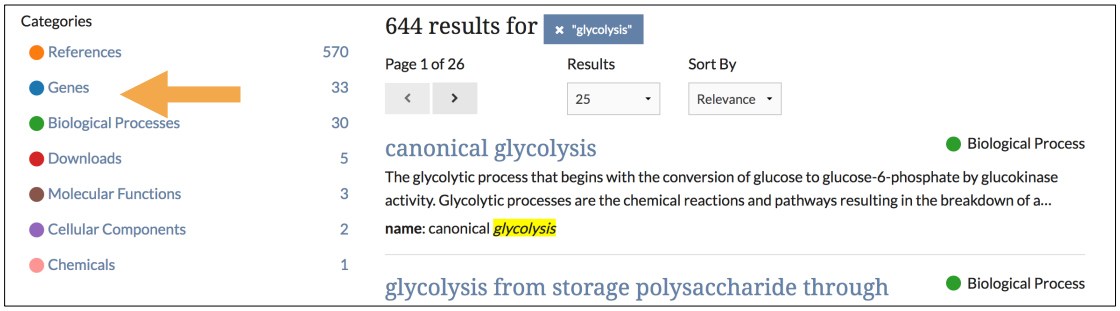
Use SPELL to find out which genes are coexpressed with genes involved in glycolysis.

Compile a list of genes involved in glycolysis.

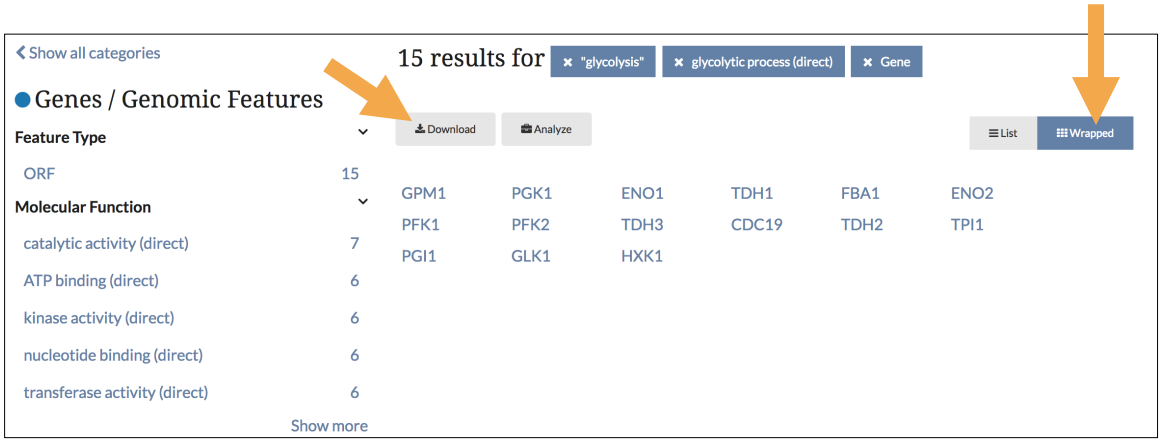
- On the SGD home page (www.yeastgenome.org), enter glycolysis into the search box and hit Enter.



- On the Results page, click on the **Genes** category.



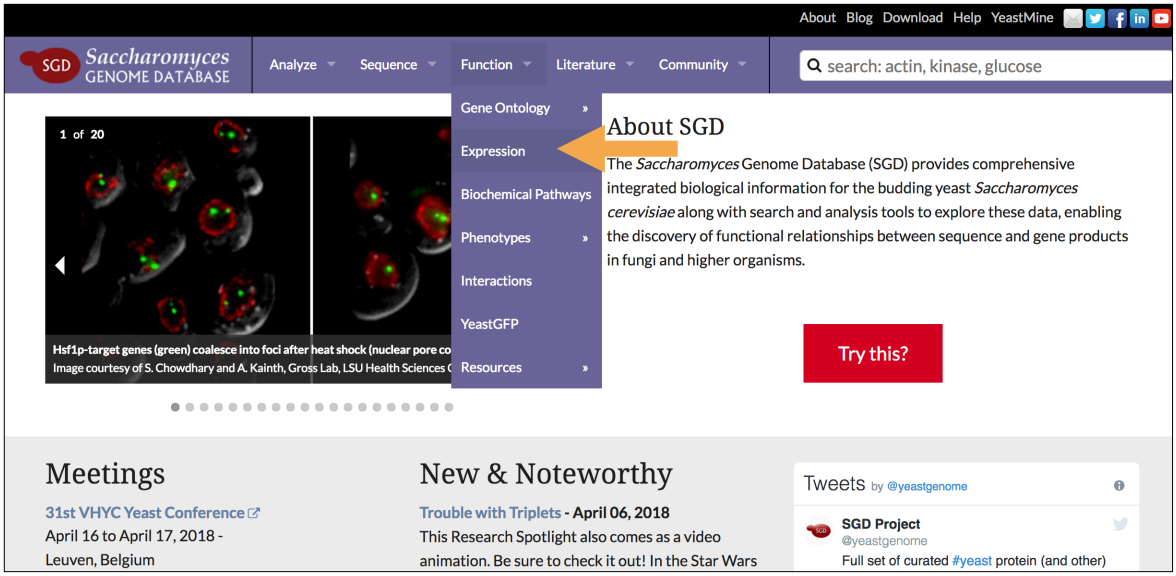
- Scroll down the page and find the **Biological Process** category on the left hand menu. Hit Show more and select **glycolytic process (direct).**
- To download the list of genes, click on **Wrapped** and then on **Download**.



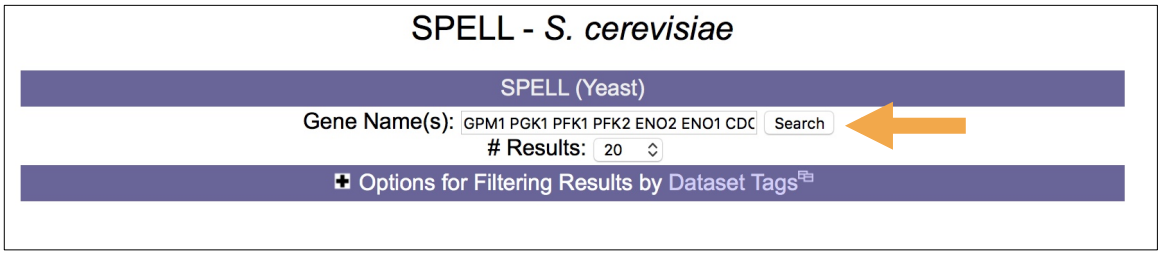
- The **Analyze** button, directly to the right of Download, enables you to import your search results directly into SPELL (among other tools at SGD). However, for the sake of demonstration, in this exercise we are instead going to enter our gene list into SPELL manually.

Import your gene list into SPELL and run a query:

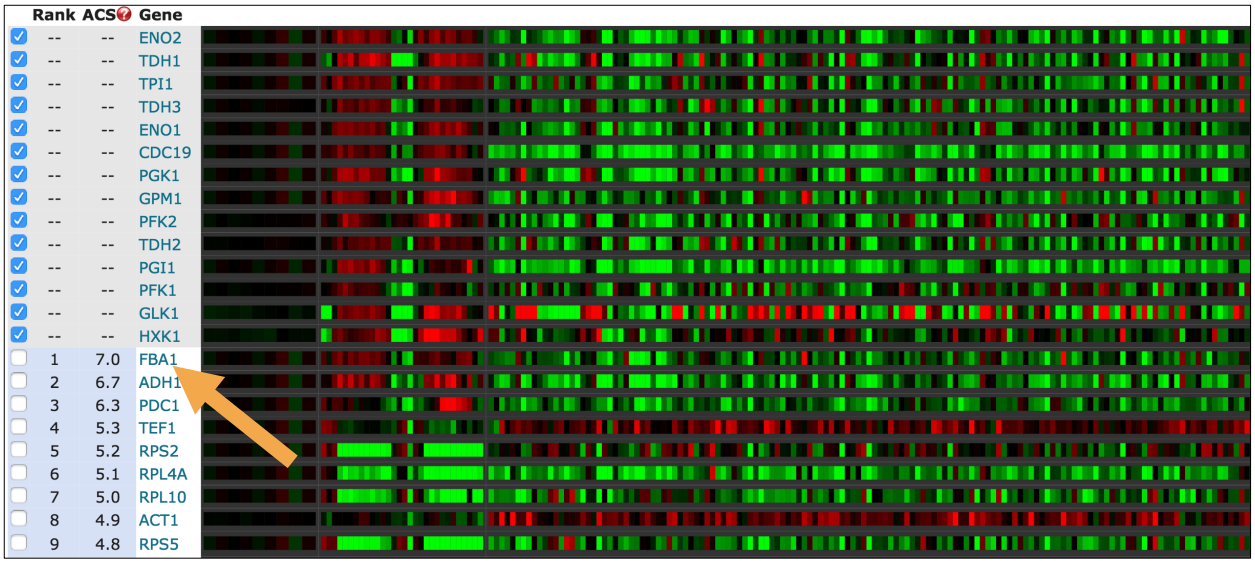
- To access SPELL, go to the SGD home page at www.yeastgenome.org, open the **Function** tab on top of the page and click on **Expression**. Or, if you are already on a Locus Summary page, open the Expression tab and click on the SPELL link under the histogram.



- On the SPELL page, copy and paste the list of glycolysis genes you downloaded in step 1 into the Gene Name(s) box. For the sake of demonstration, remove **FBA1** from your list before hitting Search. This is to test if SPELL can properly identify missing members of glycolysis based on coexpression.



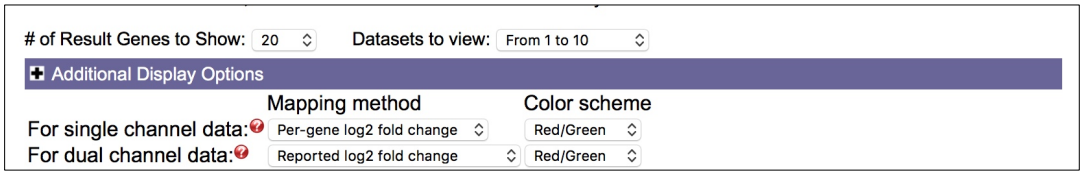
- Scroll down the list of genes on the left. Genes with checked boxes are from our query; the remaining genes are "hits", ordered from top to bottom according to their ranks. The rank reflects the correlation of expression of that gene with the query gene(s), given the relevance weight of that expression dataset. Thus, genes that show the highest degree of coexpression with the query genes in the most relevant datasets receive the highest rank.



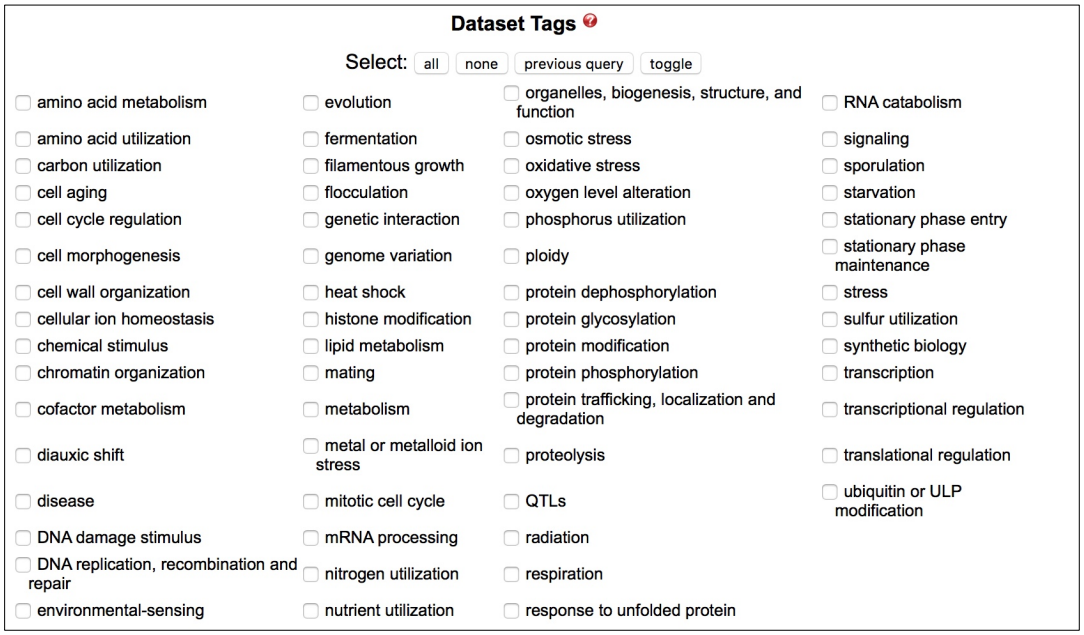
- Notice that the glycolysis gene we deleted earlier, FBA1, is indeed the highest-ranking gene!

- Examine other genes enriched for this query set. You can click on their names to be taken to their respective summary pages at SGD. Does it make sense for any of these genes to be highly coexpressed with members of glycolysis?

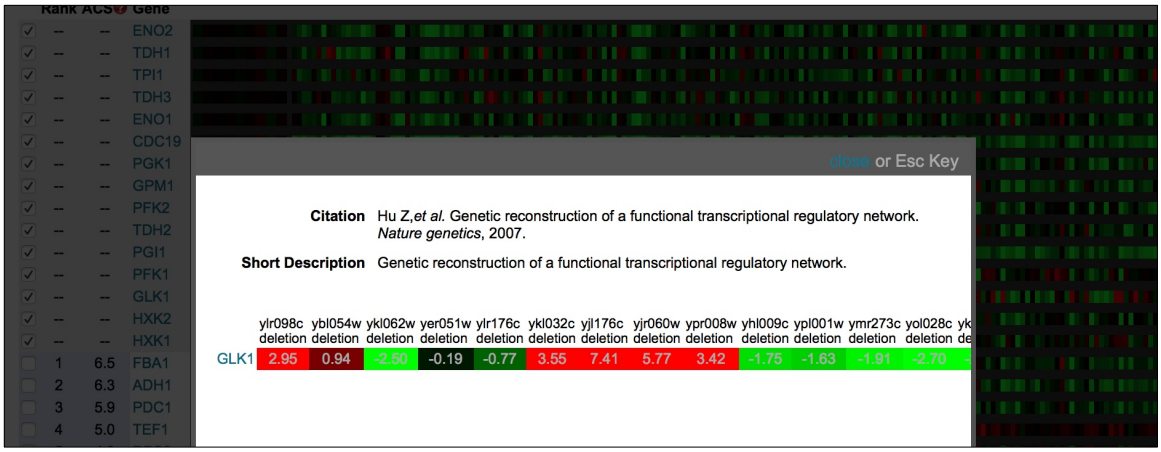
- Click on + **Additional Display Options** to change the default mapping method and color scheme to blue/yellow. Directly above this section are options to change the number of genes and datasets shown in your results.



- To select only datasets with particular tags, click on + **Options** for Filtering Results.



- Click on any patch in the heat map to open a page with information about its parent dataset.



- SPELL also runs a **Gene Ontology (GO) enrichment** for the results of your query. GO enrichments can tell you which gene ontology terms (in this case, biological process terms) are significantly associated with your set of genes. You can scroll down to the bottom of the page to view it.

GO Term Enrichment

GOTerm	P-val	% query	% genome	Annotated Genes
glucose catabolic process (biological_process)	1.33e-29	19 of 35	52 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
hexose catabolic process (biological_process)	2.39e-28	19 of 35	59 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
monosaccharide catabolic process (biological_process)	2.91e-27	19 of 35	66 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
glycolysis (biological_process)	4.79e-27	16 of 35	32 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, CDC19, PGK1, TDH2
glucose metabolic process (biological_process)	1.66e-23	19 of 35	99 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
single-organism carbohydrate catabolic process (biological_process)	3.62e-22	19 of 35	115 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
hexose metabolic process (biological_process)	4.32e-22	19 of 35	116 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
monosaccharide metabolic process (biological_process)	1.42e-21	19 of 35	123 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
carbohydrate catabolic process (biological_process)	1.97e-21	19 of 35	125 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
generation of precursor metabolites and energy (biological_process)	7.97e-18	19 of 35	190 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
single-organism carbohydrate metabolic process (biological_process)	1.60e-13	19 of 35	319 of 6381	FBA1, TDH3, ENO1, HXK1, HXK2, PFK2, GLK1, GPM1, PFK1, TPI1, TDH1, PGI1, ENO2, PDC1, ADH1, PDC5, CDC19, PGK1, TDH2
gluconeogenesis (biological_process)	3.72e-13	10 of 35	33 of 6381	FBA1, TDH3, ENO1, GPM1, TPI1, TDH1, PGI1, ENO2, PGK1, TDH2
hexose biosynthetic process (biological_process)	5.25e-13	10 of 35	34 of 6381	FBA1, TDH3, ENO1, GPM1, TPI1, TDH1, PGI1, ENO2, PGK1, TDH2
monosaccharide biosynthetic process (biological_process)	7.33e-13	10 of 35	35 of 6381	FBA1, TDH3, ENO1, GPM1, TPI1, TDH1, PGI1, ENO2, PGK1, TDH2