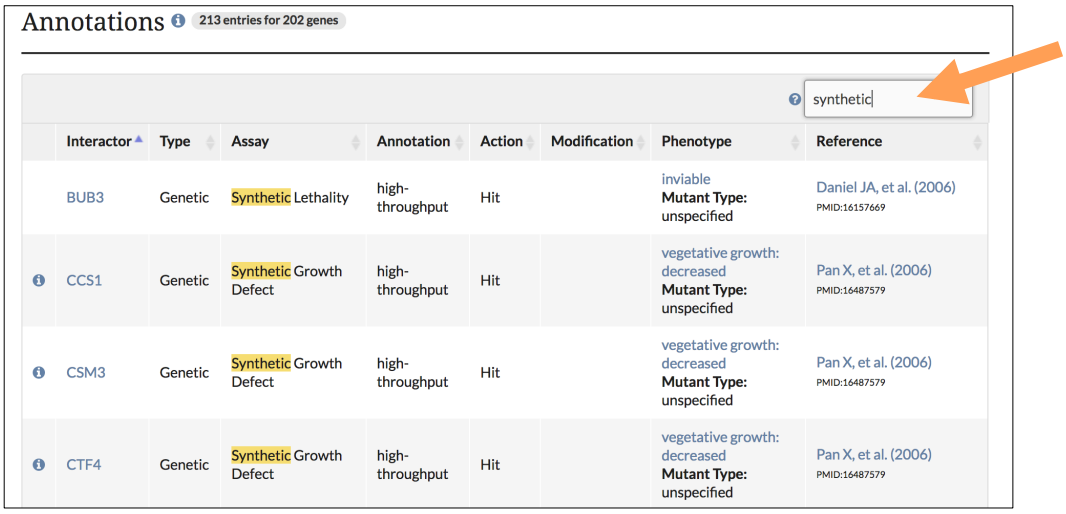
Using SGD GO Slim Mapper and Interaction Data to Predict Gene Function

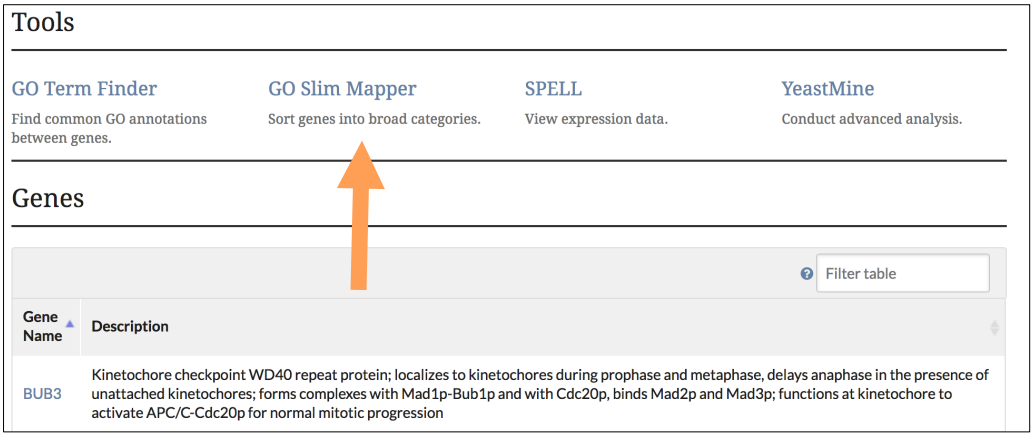
The Gene Ontology (GO) is structured in a hierarchy, such that granular terms ("perinuclear space") are connected and further down the hierarchy than their related broader terms ("nucleus"). However, for many purposes, such as reporting the upregulated cellular functions of a transcriptomics experiment, is very useful to focus on the broad, high-level part of the GO. For example, if you were interested in which of your upregulated genes are involved in DNA replication, it would be useful to map genes that have been annotated to specific terms (e.g. "synthesis of RNA primer involved in nuclear cell cycle DNA replication") to more general terms (e.g. "DNA replication").

The **Gene Ontology (GO) Slim Mapper** at SGD maps granular GO annotations of a group of genes to more general terms and/or bins them into broad categories, ie. "**GO Slim**" terms. Using GO Slim Mapper, predict what biological processes an uncharacterized gene may be involved in based on its genetic interactions.

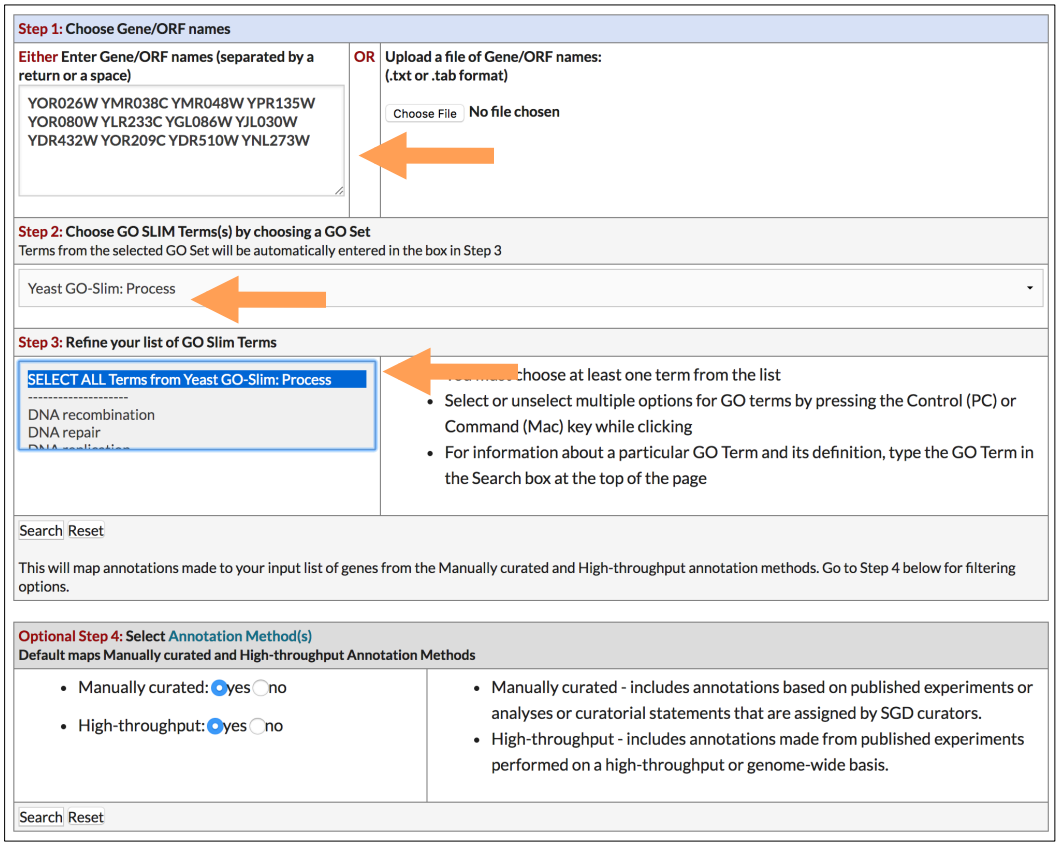
- From the SGD home page (www.yeastgenome.org), go to the Locus Summary page for the uncharacterized gene **YLR287C.**
- Select **Interactions** tab. Here, we are interested in finding genes that have a genetic interaction with YLR287C, as the function of these genes may provide hints about the function of YLR287C.
- Scroll to the **Annotations** table and search for "synthetic". This will filter the table for genes that, when knocked in combination with YLR287C, elicit some sort of synthetic growth defect, haploinsufficiency, lethality, etc. These harsh phenotypes may suggest clues about related functions in YLR287C.



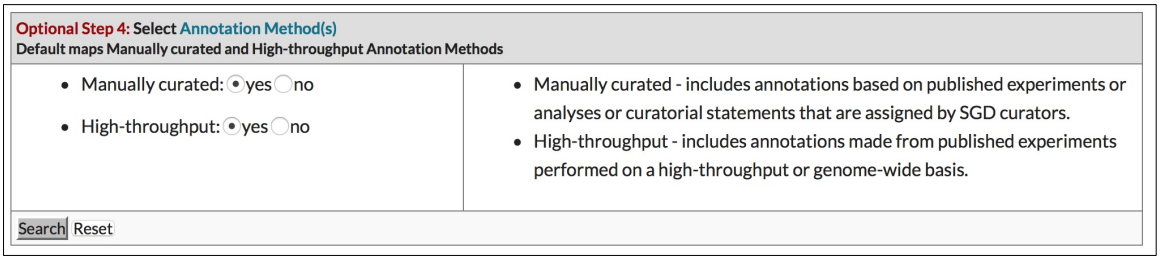
- Find and click on the **Analyze** button at the bottom of the Annotation table. This will import the table you filtered to a page where you can send the genes to other SGD tools.
- On the next page that lists the YLR287C interactors, select **GO Slim Mapper**.



- The GO Slim Mapper has three steps (plus one optional step) in which you can specify your query. In Step 1, the input box is preloaded with the list of genes you imported.
- In Step 2, choose a **GO Set** by selecting **Yeast GO-Slim: Process** from the pull-down.
- In Step 3, highlight **SELECT ALL Terms from Yeast GO-Slim: Process.**



- Click the **Search** button to use the default settings or go further down to customize your query.
    - Optional Step 4 allows excluding manually curated or high-throughput annotations; leave the **yes** options checked for both.



- Results appear in a table with four columns:
    a. GO Slim terms picked by GO Slim Mapper
    b. Cluster frequency, the number and percentage of genes in your list annotated to each term
    c. Genome frequency, the number and percentage of all genes in the genome annotated to each term
    d. Genes from your list that are annotated to that term, hyperlinked to their Locus Summary pages. You can also download the results in a tab-delimited file.
- Based on the results, what biological processes might YLR287C be involved in?