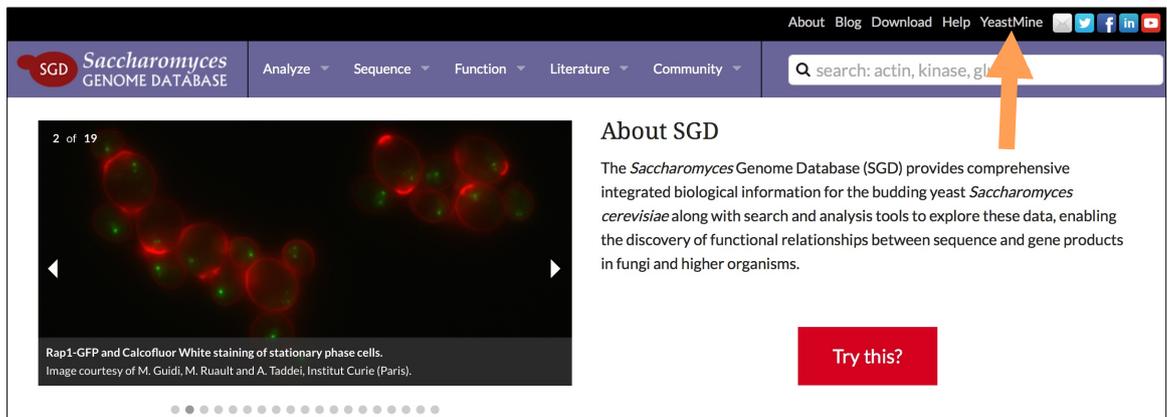


## Search Strategies in SGD

In addition to a faceted search tool, SGD provides **YeastMine** (<https://yeastmine.yeastgenome.org/>) as a means for users to conduct more advanced queries. YeastMine enables rapid retrieval and manipulation of curated biological data on *S. cerevisiae* genes and genomic features. By creating gene lists, users can retrieve data on multiple genes at once. Gene lists can then be continually modified, analyzed, and refined as desired, enabling you to answer complex biological questions such as, “How many plasma membrane proteins are required for viability?” or “Which kinases, if knocked out, increase chronological lifespan?”

In this exercise, we will use YeastMine to search for as-yet undiscovered mitochondrial ribosomal proteins in yeast.

- Access YeastMine from SGD home page (<http://www.yeastgenome.org>); click on YeastMine in the upper right corner above the search box.



### 1. Create a list of proteins that are known subunits of the mitochondrial ribosome (MTR):

- Open **FUNCTION** tab and select **GO Term name [and children of this term]** ->

**All genes**



- Enter **mitochondrial ribosome** into the query box; hit **Show Results**

**GO Term name [and children of this term] → All genes**  
 Retrieve all genes that are annotated to the specified GO term and children of that specified GO Term. Wild card queries (such as \*ascospore\*) are supported. Only manually curated and high-throughput GO annotations are included.

GO Term > Name - Show genes annotated with GO term (and any children of this GO term):

=

**Show Results**

[web service URL](#) [Perl](#) [Python](#) [Ruby](#) [Java](#) [\[help\]](#) [export XML](#)

- In the Results page, you should see a table with 108 rows. Click on **Save as List** and select the option **Gene (92 Genes)**. Give your list a name, such as "**List 1 MTR proteins**" and hit **Create List** (you should see a green **Success** banner on top)

Trail: Query  
**GO Term name [and children of this term] → All genes**  
 Retrieve all genes that are annotated to the specified GO term and children of that specified GO Term. Wild card queries (such as \*ascospore\*) are supported. Only manually curated and high-throughput GO annotations are included.

Manage Columns  Manage Filters  Manage Relationships

Showing rows 1 to 25 of 110 Rows per page: 25

Gene Primary DBID	Gene Systematic Name	Gene Standard Name	Gene Feature Type	Gene Qualifier	GO Annotation Ontology Term . Identifier	GO Annotation Ontology Term . Name	GO Annotation Ontology Term . Namespace	GO Code Code	GO Annotation Qualifier	GO Code With Text	GO Annotation Extension	GO Code Annot Type	Parents Identifier	Parents Name
S000000134	YBL038W	MRPL16	ORF	Verified	GO:0005762	mitochondrial large ribosomal subunit	cellular_component	IDA	NO VALUE	NO VALUE	NO VALUE	manually curated	GO:0005761	mitochondr ribosome
S000000134	YBL038W	MRPL16	ORF	Verified	GO:0005762	mitochondrial large ribosomal subunit	cellular_component	IDA	NO VALUE	NO VALUE	NO VALUE	manually curated	GO:0005761	mitochondr ribosome
S000000186	YBL090W	MRP21	ORF	Verified	GO:0005763	mitochondrial small ribosomal subunit	cellular_component	IDA	NO VALUE	NO VALUE	NO VALUE	manually curated	GO:0005761	mitochondr ribosome

Relationships

**Gene (92 Genes)**

- Gene > GO Annotation > Ontology Term (3 GO Terms)
- Gene > GO Annotation > Evidence > Code (7 GO Evidence Codes)
- Gene > GO Annotation (110 GO Annotations)
- Gene > GO Annotation > Ontology Term > Parents (1 GO Term)
- Gene > GO Annotation > Evidence > Publications (23 Publications)
- Gene > Organism (1 Organism)

Pick items from the table

**Create a new List of 92 Genes**

List Name

List Description

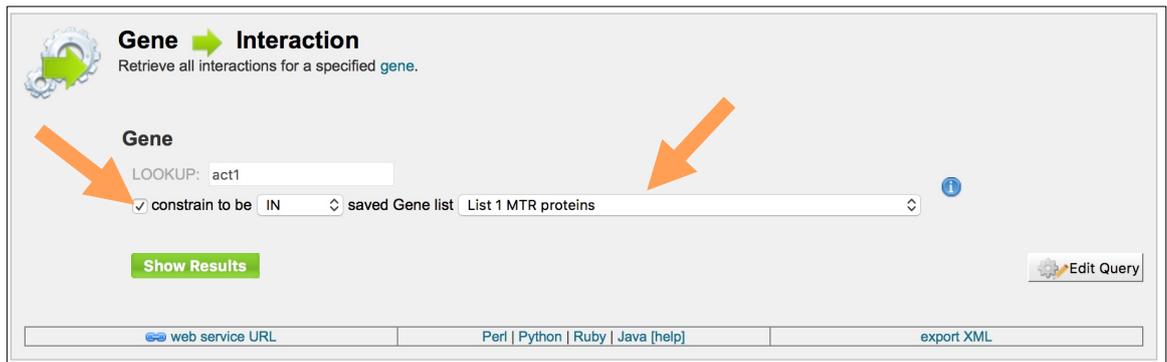
NO TAGS

## 2. Find genes/proteins that interact with MTR proteins:

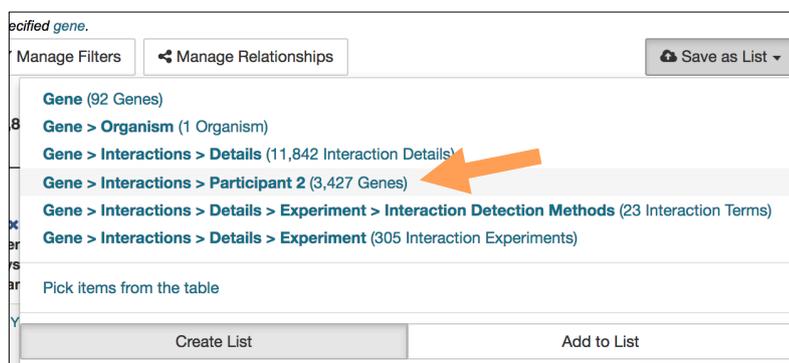
- Go back to YeastMine home page (click on **Home** in the purple banner on top). Open the **INTERACTIONS** tab and select **Gene -> Interaction**



- Check the box next to **constrain to be IN** and select your previously created list ("**List 1 MTR proteins**") from the menu; hit **Show Results**

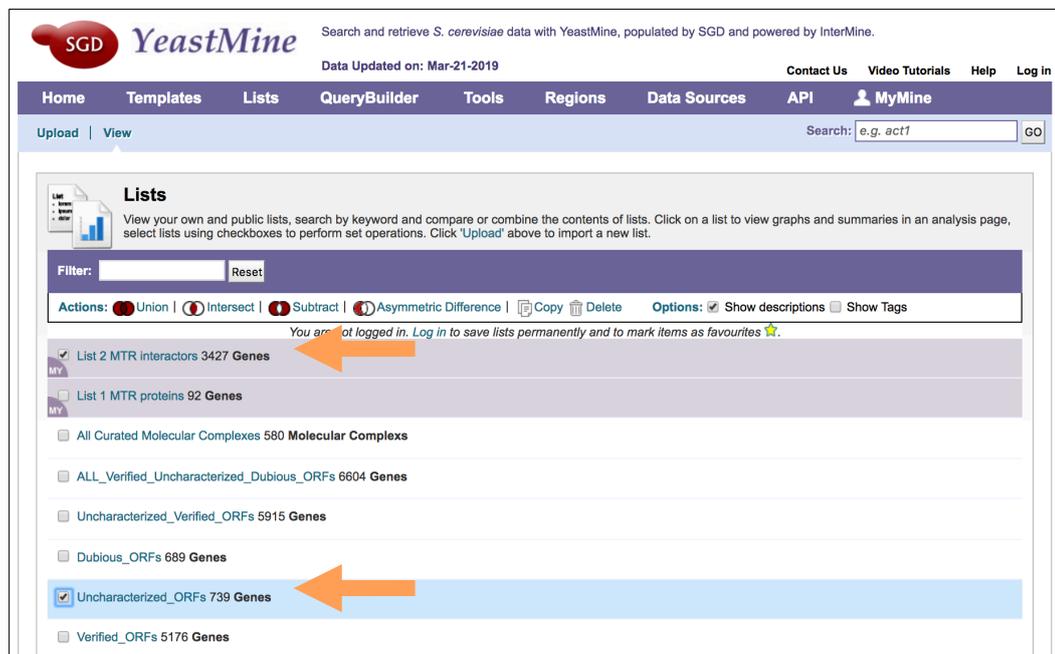


- The results page shows all genes/proteins with genetic or physical interactions with the MTR proteins from List 1. Save the MTR interactors by clicking on **Save as List** and selecting **Gene > Interactions > Participant 2**. Give your list a name ("**List 2 MTR interactors**") and hit **Create List**.



### 3. Find MTR interactors that are uncharacterized:

- Use a pre-made list of uncharacterized yeast genes: select **Lists** from the purple banner on top and click on **View** in the upper left corner. Scroll down the page to check the box next to **Uncharacterized\_ORFs**. Also check your previously saved list ("**List 2 MTR interactors**") that should be on top, highlighted in purple.



- From the **Actions**, click on **Intersect**, give your list a name ("**List 3 uncharacterized MTR interactors**") and click on **Save**; a green confirmation banner should appear on top.

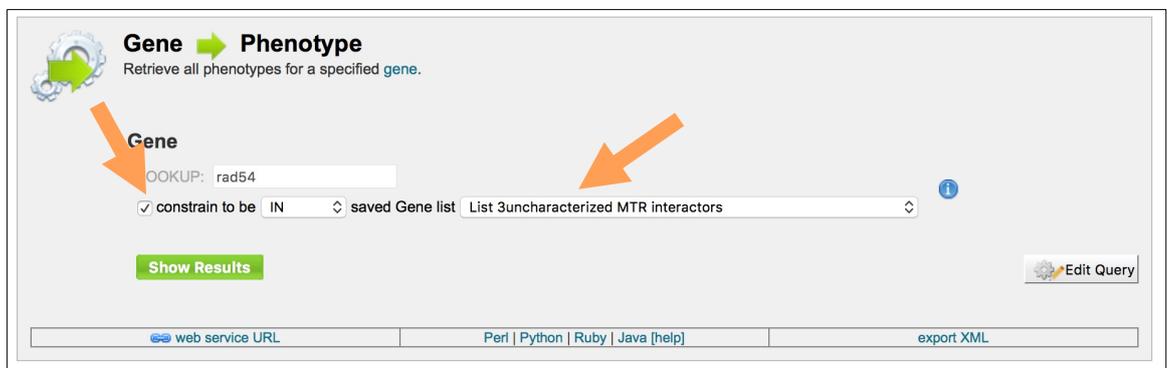


- Click on your list to see the results.
- Because we have over 200 genes in our results, it would be a good idea to narrow down our candidates even more. For example, because the MTR is a mitochondrial complex, we would expect that deleting bona fide subunits of the MTR would disrupt aerobic respiration. Let's refine our list of predicted MTR subunits by seeing which genes disrupt respiratory growth when deleted.

- Return to YeastMine home page, open up **PHENOTYPES** tab and select the **Gene -> Phenotype** query



- Check the **constrain to be IN** checkbox and select your saved list ("**List 3 uncharacterized MTR interactors**") ; click on **Show Results**



- In the Results table, find a column labeled **Phenotypes Observable**. Hover your mouse over the small icons above the column name and click on **View Column Summary** (the bar graph icon on the right).

Showing rows 1 to 25 of 2,471

Rows per page: 25

Gene Primary DBID	Gene Standard Name	Gene Systematic Name	Gene Sgd Alias	Gene Qualifier	Phenotypes Experiment Type	Phenotypes Mutant Type	Phenotypes Observable	Phenotypes Qualifier	Phenotypes Allele	Phenotypes Allele Comment	Phenotypes Strain Background	Phenotypes Chemical
S000000035	NO VALUE	YAL037W	NO VALUE	Uncharacterized	competitive growth	null	competitive fitness	increased	NO VALUE	NO VALUE	S288c	
S000000035	NO VALUE	YAL037W	NO VALUE	Uncharacterized	heterozygous diploid, competitive growth	null	haploinsufficient	NO VALUE	NO VALUE	NO VALUE	S288c	

- In the **Filter values** box, enter **respiratory** and scroll down the list to check the box next to **Respiratory growth**; hit **Filter**.

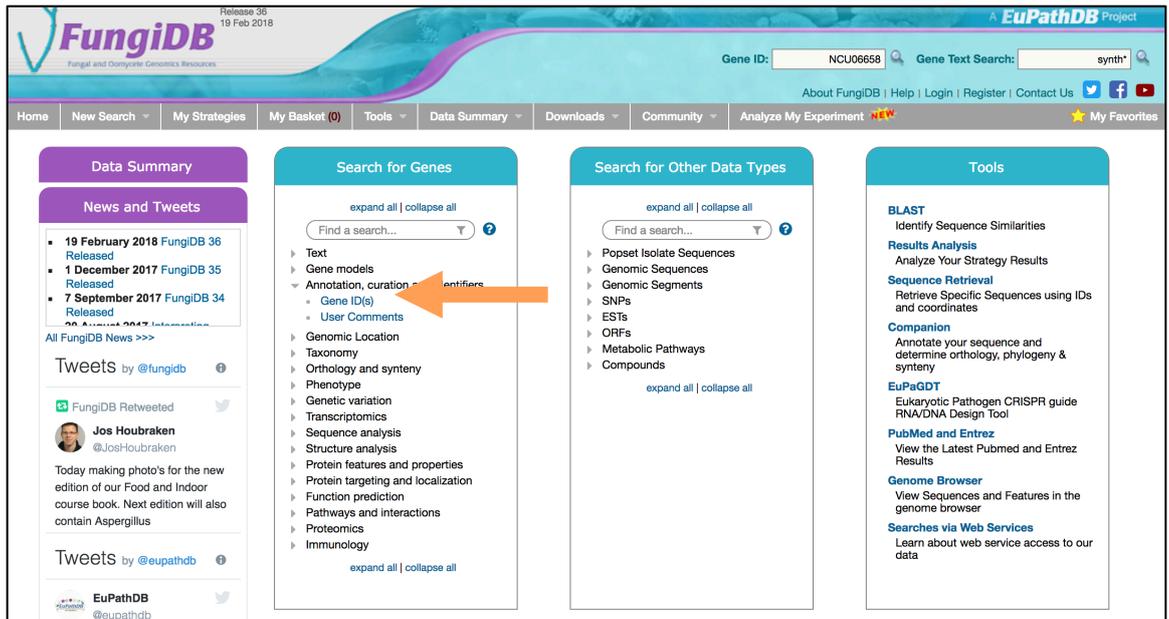
The screenshot shows a data table with columns for Gene Qualifier, Phenotypes Experiment Type, Phenotypes Mutant Type, and Phenotype Observable. A pop-up window titled "68 Phenotype Observables" is open, displaying a search for "respiratory". The search results show "respiratory growth" with a count of 12. An orange arrow points to the "Filter" button in the pop-up, and another orange arrow points to the "Filter" button in the table header.

- To filter the phenotypes for those where respiratory growth is impeded, find the **Phenotype Qualifiers** column and open the **View Column Summary** menu. Select all items that refer to hindering respiratory growth: “decreased”, “decreased rate”, “absent”, etc. Then, hit Filter.
- You should now have a list of uncharacterized yeast genes whose products interact with mitochondrial ribosomes and mutations lead to respiratory growth defects. Export the results into a .tsv file by clicking on the **Export** button, and then on the **“Download file”** button in the resulting pop-up window.

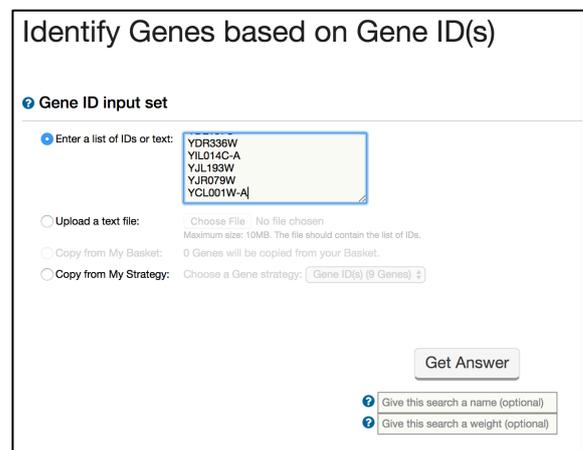
The screenshot shows a data table with columns for Gene Primary DBID, Gene Standard Name, Gene Systematic Name, Gene Sgd Alias, Gene Qualifier, Phenotypes Experiment Type, Phenotypes Mutant Type, Phenotypes Observable, Phenotypes Qualifier, Phenotypes Allele, Phenotypes Comment, Phenotypes Strain Background, Phenotypes Chemical, and Phenotypes Condition. An orange arrow points to the "Export" button in the top right corner of the table interface.

Gene Primary DBID	Gene Standard Name	Gene Systematic Name	Gene Sgd Alias	Gene Qualifier	Phenotypes Experiment Type	Phenotypes Mutant Type	Phenotypes Observable	Phenotypes Qualifier	Phenotypes Allele	Phenotypes Comment	Phenotypes Strain Background	Phenotypes Chemical	Phenotypes Condition
S000000191	MRX3	YBL095W	NO VALUE	Uncharacterized	classical genetics	null	respiratory growth	decreased	NO VALUE	NO VALUE	Other	glycerol, ethanol	Media: nonfermenting carbon (YPEG)
S0000002316	NO VALUE	YDL157C	NO VALUE	Uncharacterized	systematic mutation set	null	respiratory growth	absent	NO VALUE	NO VALUE	S288c		Media: carbon

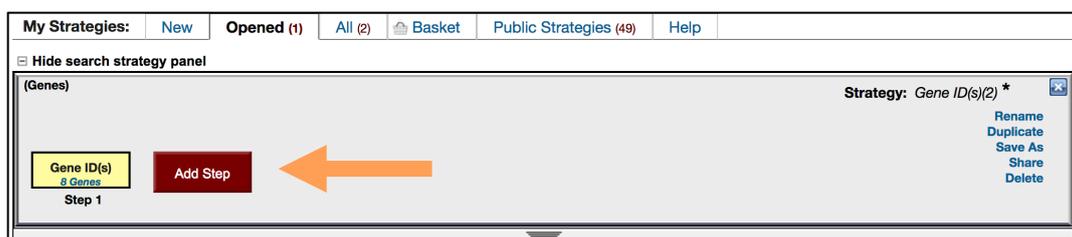
- The results of the above YeastMine analysis suggest 8 genes that potentially encode undiscovered subunits of the mitochondrial ribosome. Although these genes are uncharacterized, more data may exist on their orthologs in other organisms. Use FungiDB to survey the function of orthologs in Fungi and Oomycetes.
- Open the FungiDB homepage (<http://fungidb.org/>). In the “Search for Genes” box, open the “Annotation, curation and identifiers” section and click on “Gene ID(s)”.



- Using your exported .tsv file from YeastMine, copy and paste the systematic names of your results into the box. Click on “Get Answer”.



- Click on the red “Add Step” button. In the resulting pop-up window, click on **Transform by orthology**. Select **Fungi** and **Oomycetes**, then click on **Run Step**.



- Orthologs from multiple species will be shown in the results table. Peruse the “Product Description” column. Do the descriptions of these orthologs support the prediction that the 8 yeast genes encode subunits of the mitochondrial ribosome? Click on the bar graph icon by the Product Description column to see a word cloud of entries in this column.

Gene Results   Genome View   Analyze Results

Genes: 606   Transcripts: 626    Show Only One Transcript Per Gene

First 1 2 3 4 5 Next Last   Advanced Paging   Download   Add to Basket   Add Columns

Gene ID	Transcript ID	Organism	Genomic Location (Gene)	Product Description	Ortholog(s)
<a href="#">ACLA_086280</a>	ACLA_086280-t26_1	<i>A. clavatus</i> NRRL 1	DS027060:2,044,080..2,045,139(+)	GTP binding protein (EngB), putative	YDR336W
<a href="#">AFLA_033930</a>	AFLA_033930-t26_1	<i>A. flavus</i> NRRL3357	EQ963473:3,025,757..3,026,783(-)	GTP binding protein (EngB), putative	YDR336W
<a href="#">AFUB_001730</a>	AFUB_001730-T	<i>A. fumigatus</i> A1163	scf_000001_A_fumigatus_A1163:485,315..486,704(-)	Has domain(s) with predicted GTP binding activity and role in barrier septum assembly	YDR336W
<a href="#">AGR57_3207</a>	AGR57_3207T0	<i>P. chrysosporium</i> RP-78	PchrRP-78_SC003:600,486..601,399(+)	P-loop containing nucleoside triphosphate hydrolase protein	YDR336W
<a href="#">AGR95_111490</a>	AGR95_111490.mRNA	<i>H. capsulatum</i> G217B	HISTO_ZT.Contig1089:445,461..446,683(+)	unspecified product	YDR336W
<a href="#">AKAW_06043</a>	AKAW_06043-t41_1	<i>A. kawachii</i> IFO 4308	DF126461:135,225..136,291(-)	GTP binding protein	YDR336W
<a href="#">ALNC14_006000</a>	ALNC14_006000:RNA	<i>A. laibachii</i> Nc14	FR824048:351,365..352,417(-)	unspecified product	YDR336W
<a href="#">AMAG_08869</a>	AMAG_08869-t26_1	<i>A. macrogynus</i> ATCC 38327	GG745343:315,460..317,068(+)	ribosome biogenesis GTP-binding protein YsxC	YDR336W
<a href="#">AMAG_09047</a>	AMAG_09047-t26_1	<i>A. macrogynus</i> ATCC 38327	GG745343:803,808..805,364(-)	hypothetical protein	YDR336W
<a href="#">AMAG_12000</a>	AMAG_12000-t26_1	<i>A. macrogynus</i> ATCC 38327	GG745353:588,076..589,473(+)	hypothetical protein, hypothetical protein, variant	YDR336W