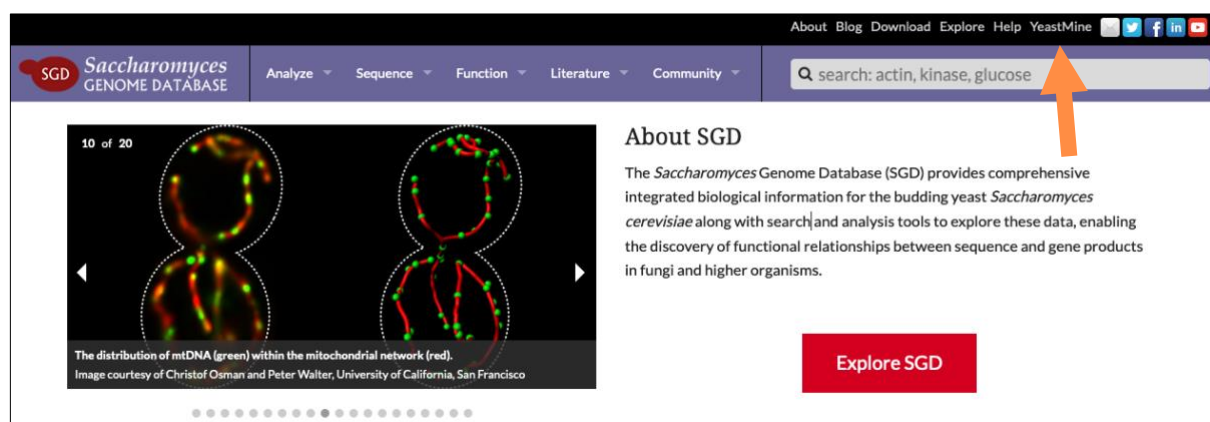


## Search Strategies in SGD

In addition to searching for data using our faceted search tool, SGD provides **YeastMine** (<https://yeastmine.yeastgenome.org/>), a multifaceted search and retrieval environment that provides access to diverse datatypes. 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 sequentially modified, analyzed, and refined, enabling you to answer more complex biological questions such as, “How many plasma membrane proteins are required for viability?” or “Which kinases, if knocked out, increase chronological lifespan?”

YeastMine can be accessed from the SGD home page (<http://www.yeastgenome.org>).



YeastMine contains several basic functionalities:

- Predefined queries (templates) (access via tab at the top (1) or tabbed bar middle (2))
  - Filter by category
  - Filter by keyword(s)
- List creation
  - Create and save list (name and add description), rename, share (MyMine)
  - Add to list
- List operations (access via Lists tab at top)
  - Union – all genes in two lists
  - Intersect - overlap of genes in two lists
  - Subtract – total unique non-overlapping genes
  - Asymmetric Difference – unique to one list of non-overlapping genes

 Union |  Intersect |  Subtract |  Asymmetric Difference

Template results page options (top of page):





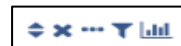





 Manage Columns	_____	Re-arrange, add/remove columns, change sort order
 Save as List ▾	_____	Save items, like genes, in a list
 Export	_____	Download results in different formats
Rows per page: 50 ▾	 page 1	Navigation aids








Table functions (top of each column on results page):



	_____	Column sort
	_____	Remove column
	_____	Toggle column visibility
	_____	Filter by values in a column
	_____	View column summary









**Feature Type** → **Features of a selected feature Type** ☆

Retrieve all chromosomal features of a selected feature type.

 Manage Columns
  Manage Filters
  Manage Relationships
  Undo ▾
  Save as List ▾
  Generate Python code ▾
  Export

Showing 1 to 25 of 6,604 rows

Rows per page: 25 ▾

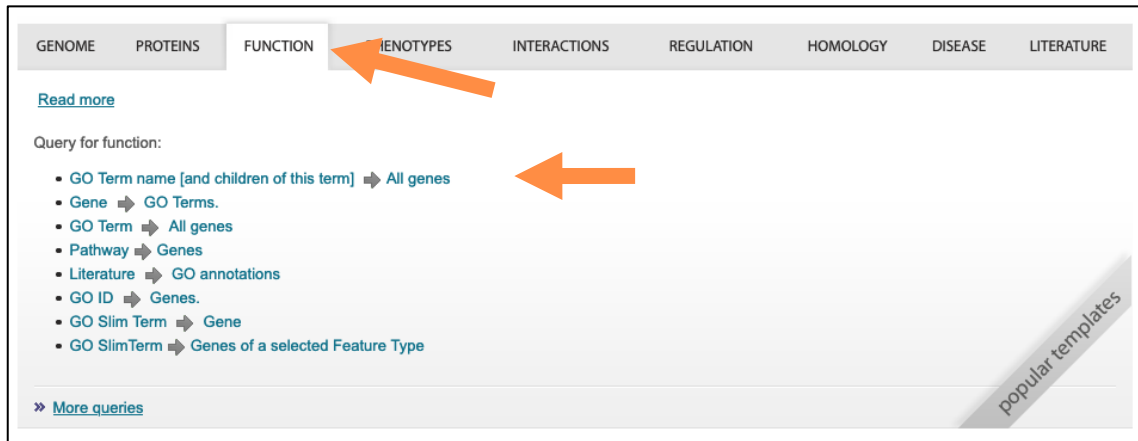
							
Sequence Feature Primary DBID	Sequence Feature Systematic Name	Sequence Feature Standard Name	Sequence Feature Sgd Alias	Sequence Feature Description		Sequence Feature Feature Type	Sequence Feature Qualifier

In the following exercise, we will use YeastMine to search for as yet under- and/or uncharacterized mitochondrial ribosomal proteins in yeast.

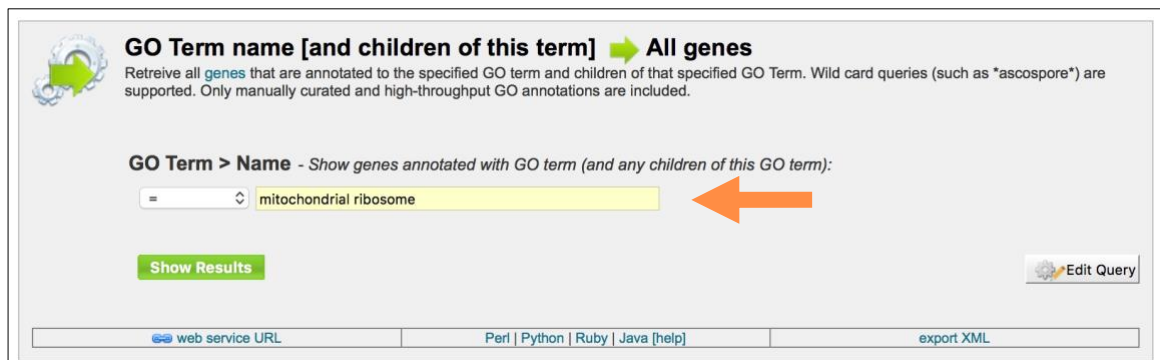
- Access YeastMine from SGD home page (<http://www.yeastgenome.org>); click on YeastMine in the upper right corner above the search box.

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

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



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



- On the Results page, you should see a table with 110 rows. Click on **Save as List** and select the option **Gene (91 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 Save as List Generate Python code Export

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

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

Relationships Save as List

Gene (91 Genes)

- Gene > GO Annotation > Ontology Term (3 GO Terms)
- Gene > GO Annotation > Evidence > Code (6 Ontology Annotation Evidence Codes)
- Gene > GO Annotation (110 GO Annotations)
- Gene > GO Annotation > Ontology Term > Parents (1 GO Term)
- Gene > GO Annotation > Evidence > Publications (24 Publications)
- Gene > Organism (1 Organism)

Pick items from the table

Create List Add to List

Create a new List of 91 Genes

List Name

List 1 MTR proteins

Optional attributes

List Description

Enter a description

NO TAGS Add a new tag add

Close Create List

## 2. Find genes/proteins that genetically/physically 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 -> Genetic Interaction**

GENOME PROTEINS FUNCTION PHENOTYPES **INTERACTIONS** REGULATION HOMOLOGY DISEASE LITERATURE

[Read more](#)

Query for interactions:

- Literature → Interaction
- Gene → Genetic Interactions
- Gene → Physical Interactions
- Complex → Details + Participants
- Gene → Complex + Details

» [More queries](#)

popular templates

- 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**

**Gene** → **Genetic Interactions** ☆  
Retrieve all genetic interactions for a specified **gene**.

**Gene**  
LOOKUP:

☒ constrain to be **IN** saved Gene list **List 1 MTR proteins**

**Show Results** [Edit Query](#)

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

- The result shows all genes that interact genetically with MTR genes from List 1. Save the MTR genetic interactors by clicking on **Save as List** and selecting **Gene > Interactions > Participant 2**. Give your list a name (“**List 2 MTR genetic interactors**”) and hit **Create List**.

Save as List ▾

- Gene (89 Genes)
- Gene > Organism (1 Organism)
- Gene > Interactions > Details (8,874 Interaction Details)
- Gene > Interactions > Participant 2 (3,257 Genes)
- Gene > Interactions > Details > Experiment > Interaction Detection Methods (11 Interaction Terms)
- Gene > Interactions > Details > Experiment (192 Interaction Experiments)
- Gene > Interactions > Alleleinteractions > Allele 1 (1,043 Alleles)
- Gene > Interactions > Alleleinteractions > Allele 2 (2,627 Alleles)
- Gene > Interactions > Alleleinteractions (7,299 Allele Interactions)

Pick items from the table

Create List Add to List

- Now go back to the YeastMine home page, open the **INTERACTIONS** tab again but this time select **Gene -> Physical Interactions**

GENOME PROTEINS FUNCTION PHENOTYPES **INTERACTIONS** REGULATION HOMOLOGY DISEASE LITERATURE

[Read more](#)

Query for interactions:

- Literature → Interaction
- Gene → Genetic Interactions
- Gene → Physical Interactions
- Complex → Details + Participants
- Gene → Complex + Details

» [More queries](#)

popular templates

- 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**

**Gene Physical Interactions** ☆  
Retrieve all physical interactions for a specified **gene**.

**Gene**  
LOOKUP:

☒ constrain to be **IN** saved Gene list **List 1 MTR proteins**

**Show Results** Edit Query

web service URL Perl | Python | Ruby | Java [help] export XML

- This results page shows all proteins that interact physically with the MTR proteins from List 1. Save the MTR physical interactors by clicking on **Save as List** and selecting **Gene > Interactions > Participant 2**. Give your list a name (“**List 3 MTR physical interactors**”) and hit **Create List**.

**Gene (91 Genes)**

**Gene > Organism (1 Organism)**

**Gene > Interactions > Details (3,883 Interaction Details)**

**Gene > Interactions > Participant 2 (517 Genes)**

**Gene > Interactions > Details > Experiment > Interaction Detection Methods (14 Interaction Terms)**

**Gene > Interactions > Details > Experiment (147 Interaction Experiments)**

Pick items from the table

**Create List** **Add to List**

- Now combine the genetic and physical interactors by performing a “Union” to get a combined list of both genetic AND physical interactors. Go to the Lists tab, select the check boxes next to **List 2 MTR genetic interactors** and **List 3 MTR physical interactors** and select **Union**, and enter the name “**List 4 MTR interactors**”

**Lists**

View your own and public lists, search by keyword and compare or combine the contents of lists. Click on a list to view graphs and summaries in an analysis page, select lists using checkboxes, perform set operations. Click 'Upload' above to import a new list.

Filter:  Filter:  -- filter by a tag -- Reset

**Actions:** ☒ Union ☐ Intersect ☐ Subtract ☐ Asymmetric Difference Show descriptions Show Tags

☒ List 3 MTR physical interactors ☆ 517 Genes

☒ List 2 MTR genetic interactors ☆ 3257 Genes

Enter a new List name:  
 Save

### 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 4 MTR interactors**) that should be on top, highlighted in purple.
- 

SGD YeastMine Search and retrieve *S. cerevisiae* data with YeastMine, populated by SGD and powered by InterMine.

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Upload View Search: e.g. act1 GO

### Lists

View your own and public lists, search by keyword and compare or combine the contents of lists. Click on a list to view graphs and summaries in an analysis page, select lists using checkboxes to perform set operations. Click 'Upload' above to import a new list.

Filter: Filter: H Y -- filter by a tag -- Reset

Actions: Union Intersect Subtract Asymmetric Difference Copy Delete Options: ☒ Show descriptions ☐ Show Tags

- ☒ List 4 MTR interactors 3957 Genes
- ☐ List 3 MTR physical interactors 517 Genes
- ☐ List 2 MTR genetic interactors 3257 Genes
- ☐ List 1 MTR proteins 91 Genes

- ☐ ALL\_Verified\_Uncharacterized\_Dubious\_ORFs 6605 Genes
- ☐ Uncharacterized\_Verified\_ORFs 5917 Genes
- ☐ Dubious\_ORFs 688 Genes
- ☒ Uncharacterized\_ORFs 722 Genes

- From the **Actions**, click on **Intersect**, give your list a name ("**List 5 uncharacterized MTR interactors**") and select **Save**; a green confirmation banner should appear.

### Lists

View your own and public lists, search by keyword and compare or combine the contents of lists. Click on a list to view graphs and summaries in an analysis page, select lists using checkboxes to perform set operations. Click 'Upload' above to import a new list.

Filter: Filter: H Y -- filter by a tag -- Reset

Actions: Union Intersect Subtract Asymmetric Difference Copy Delete Options: ☒ Show descriptions ☐ Show Tags

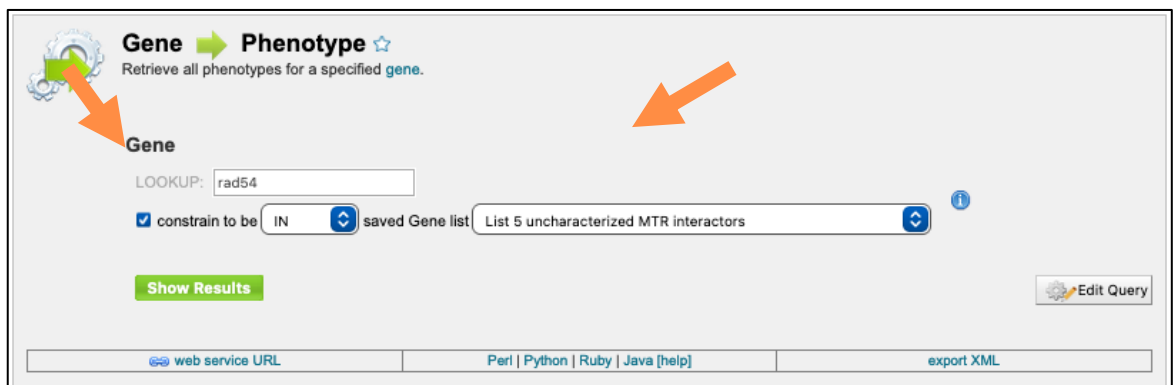
- Click on your list to see the results.
- Because we have over 200 genes in our results, it would be a good idea to narrow down our candidates further. For example, because the MTR is a mitochondrial

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



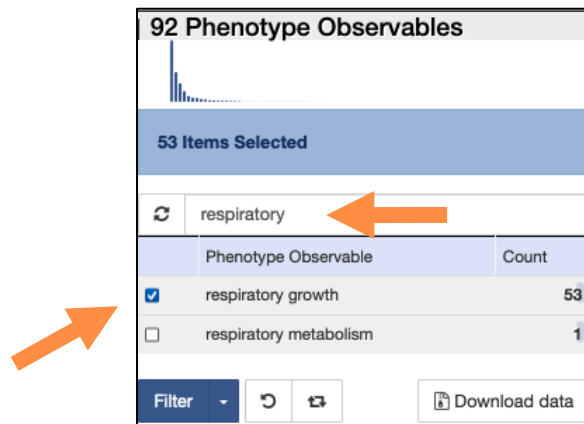
- Check the **constrain to be IN** checkbox and select your saved list ("**List 5 uncharacterized MTR interactors**") ; click on **Show Results**



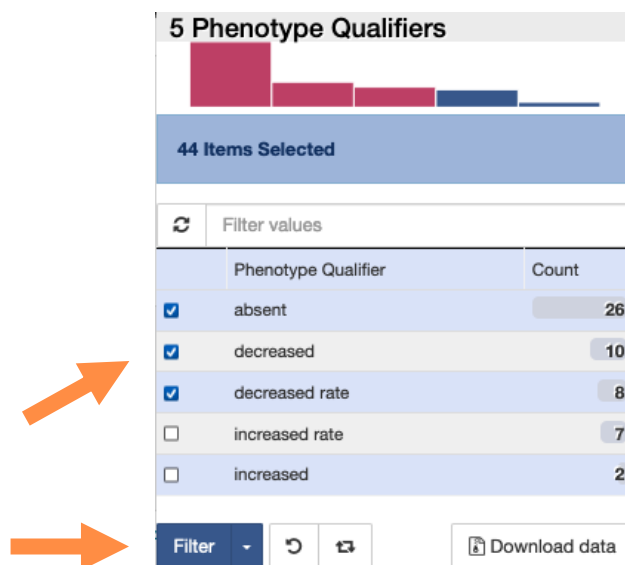
In the Results table, find a column labelled **Phenotypes Observable**. Hover your mouse over the small icons above the column name and click on **View Column Summary** (the bar graph icon on the right).

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

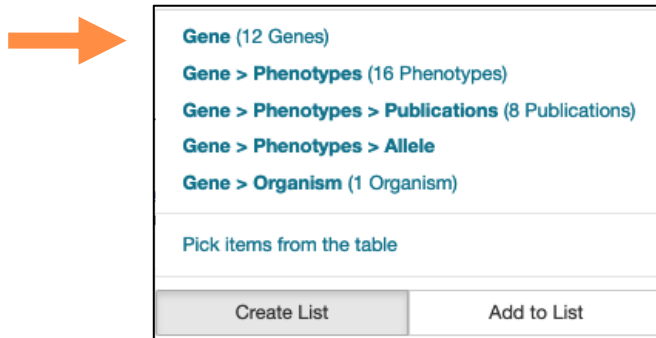




- To filter the phenotypes for those where respiratory growth is impeded, find the **Phenotype Qualifiers** column and open the **View Column Summary** menu. Select all items that refer to hindering respiratory growth: “decreased”, “decreased rate”, “absent”, etc. Then, hit Filter.



- You should now have a list of uncharacterized yeast genes whose products interact with mitochondrial ribosomes and mutations lead to respiratory growth defects. Use the **Save as List** function to save the list of genes and enter the name “**List 6 uncharacterized MTR interactors with respiratory growth phenotype**”



- View the list and save 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.

**List Analysis for List 6 uncharacterized MTR interactors with respiratory growth phenotype (12 Genes)**

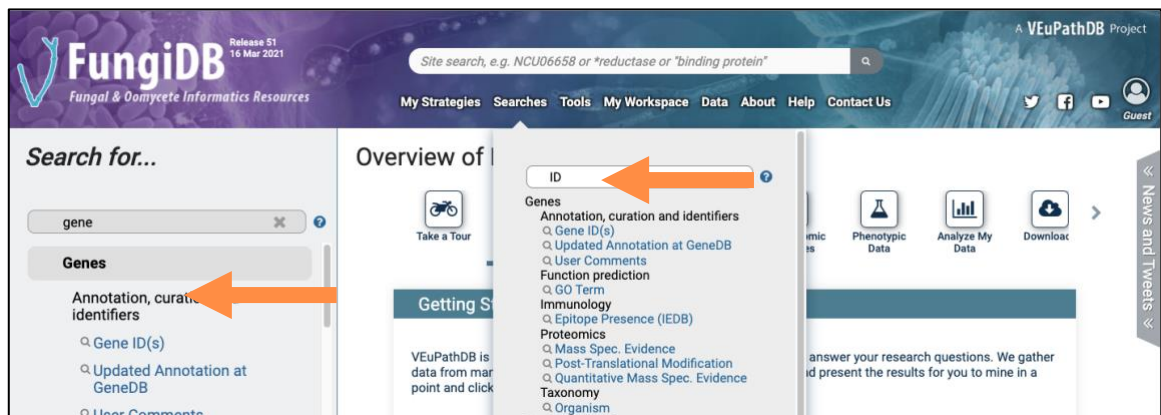
Manage Columns Manage Filters Manage Relationships Save as List Generate Python code Export

Showing 1 to 12 of 12 rows Rows per page: 10

Gene Primary DBID	Gene Systematic Name	Gene Organism . Short Name	Gene Standard Name	Gene Name
S000000191	YBL095W	S. cerevisiae	MRX3	Mitochondrial oRganization of gene eXpression (MIOREX)
S000000879	YER077C	S. cerevisiae	MRX1	Mitochondrial oRganization of gene eXpression (MIOREX)
S000002272	YDL114W	S. cerevisiae	NO VALUE	NO VALUE
S000002316	YDL157C	S. cerevisiae	NO VALUE	NO VALUE
S000002744	YDR336W	S. cerevisiae	MRX8	Mitochondrial oRganization of gene eXpression (MIOREX)
S000003536	YIL014C-A	S. cerevisiae	NO VALUE	NO VALUE
S000003729	YJL193W	S. cerevisiae	NO VALUE	NO VALUE
S000003840	YJR079W	S. cerevisiae	NO VALUE	NO VALUE
S000004040	YLR050C	S. cerevisiae	EMA19	Efficient Mitochondria targeting-Associated protein
S000005522	YOL162W	S. cerevisiae	NO VALUE	NO VALUE
S000007221	YCL001W-A	S. cerevisiae	NO VALUE	NO VALUE
S000028832	YHR050W-A	S. cerevisiae	NO VALUE	NO VALUE

- The results of the above YeastMine analysis suggest 12 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 (<https://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 into related records > Orthology**. Select **Fungi** and **Oomycetes**, then click on **Run Step**.

### Identify Genes based on Gene ID(s)

Reset values

Gene ID input set

Enter a list of IDs or text:

YLR050C  
YLR077C  
YLR095W  
YLR114W  
YLR162W

- Orthologs from multiple species will be shown in the results table. Peruse the “Product Description” column. Click on the columns button. Do the descriptions of these orthologs support the prediction that the 12 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: 1,334		Transcripts: 1,361		<input type="checkbox"/> Show Only One Transcript Per Gene			
1 2		Rows per page: 1000		Download Add to Basket Add Columns			
Gene ID	Transcript ID	Organism	Product Description	Product	Ortholog Group	Pair	Col
ACLA_007740	ACLA_007740-t26_1	Aspergillus clavatus NRRL 1	integral membrane protein, putative	YLR050C	OG6_104415	0	
ACLA_013870	ACLA_013870-t26_1	Aspergillus clavatus NRRL 1	pentatricopeptide repeat protein	YER077C	OG6_100693	0	
ACLA_024710	ACLA_024710-t26_1	Aspergillus clavatus NRRL 1	thioesterase family protein	YBL095W	OG6_103459	2	
ACLA_028340	ACLA_028340-t26_1	Aspergillus clavatus NRRL 1	short-chain dehydrogenase/reductase family protein, putative	YDL114W	OG6_100599	2	
ACLA_043130	ACLA_043130-t26_1	Aspergillus clavatus NRRL 1	short-chain dehydrogenase/reductase 2, putative	YDL114W	OG6_100599	2	