# 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).
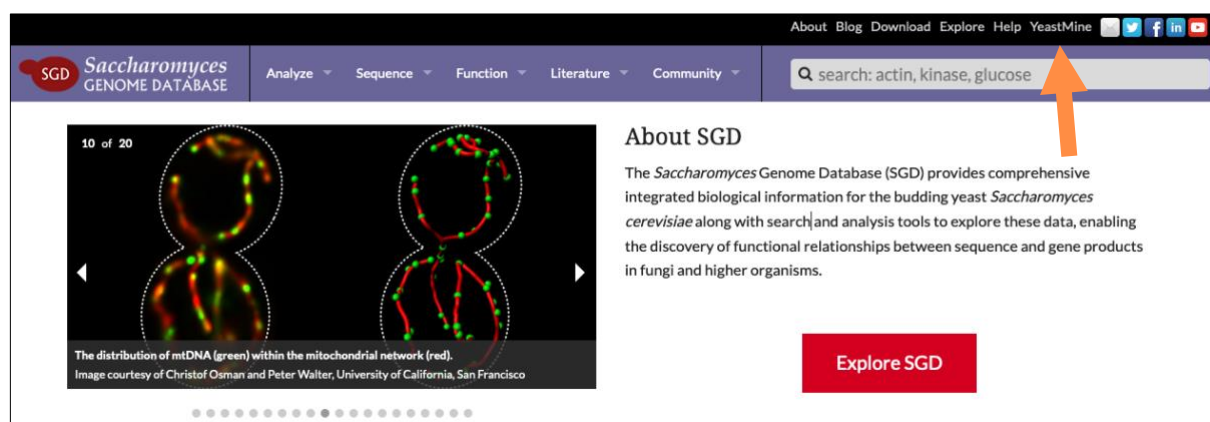
YeastMine contains several basic functionalities:

- 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

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):   ⇕ ✖ ⋯ ▼ ⏷
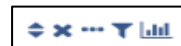
⇕	————————	Column sort
✖	————————	Remove column
⋯	————————	Toggle column visibility
▼	————————	Filter by values in a column
⏷	————————	View column summary

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**
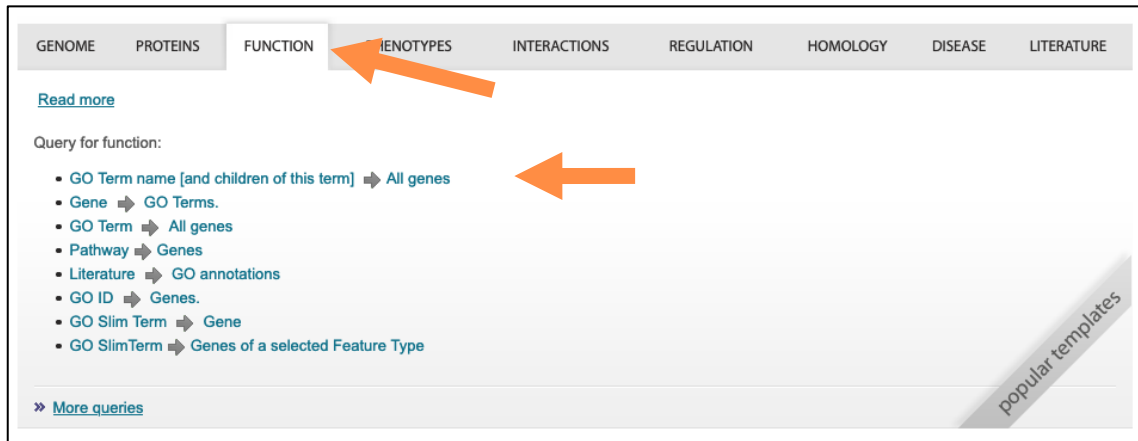
- Enter **mitochondrial ribosome** into the query box; hit **Show Results**
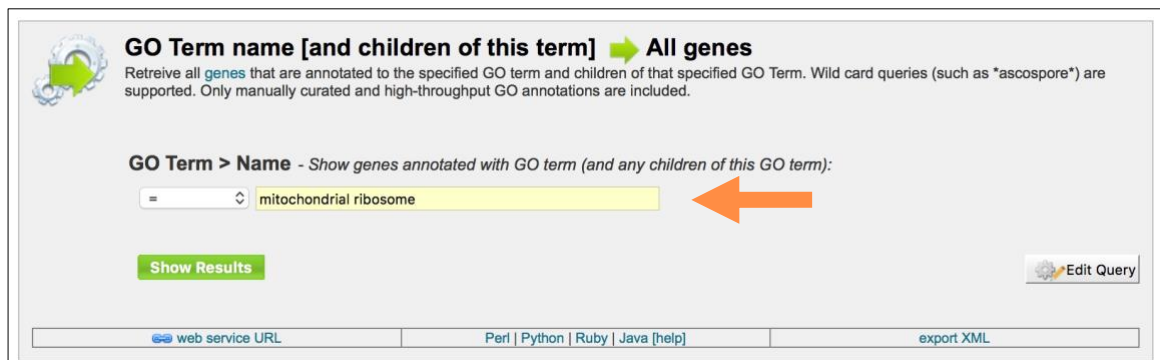
- On the Results page, you should see a table with 110 rows. Click on **Save as List** and select the option **Gene (91 Genes).** Give your list a name, such as "**List 1 MTR proteins**" and hit **Create List** (you should see a green **Success** banner on top)

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 Ontology Term . Identifier	GO Annotation Ontology Term . Name	GO Annotation Ontology Term . Namespace	Code Code	GO Annotation Qualifier	Code With Text	GO Annotation 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	mitochondrial 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	mitochondrial 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	mitochondrial ribosome

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**

- 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.**

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

- 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**

- 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.**

- 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**"

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.

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- 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.


- 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**
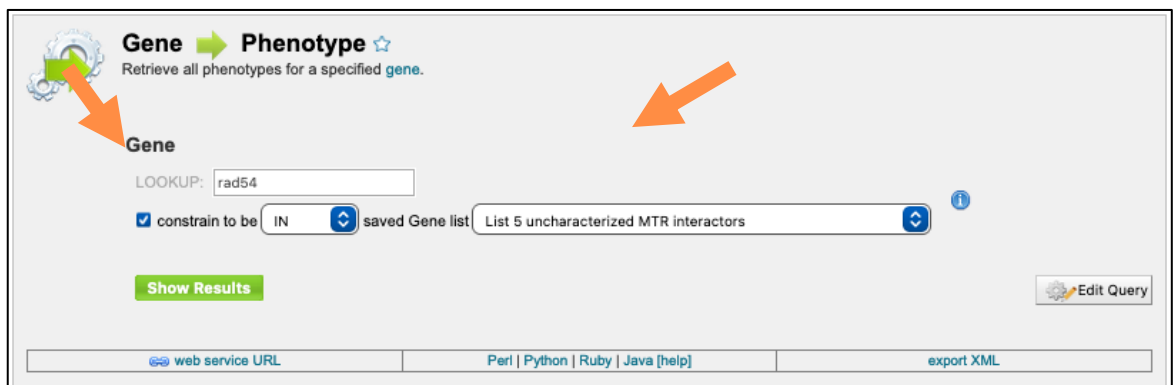

In the Results table, find a column labelled **Phenotypes Observable**. Hover your mouse over the small icons above the column name and click on **View Column Summary** (the bar graph icon on the right).

In the **Filter values** box, enter **respiratory** and scroll down the list to check the box next to **Respiratory growth**; hit **Filter**.
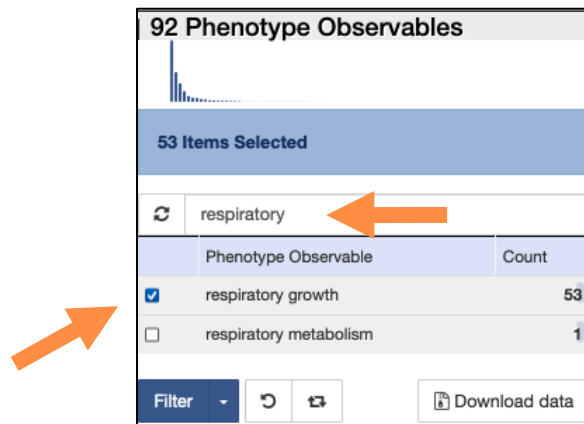
- To filter the phenotypes for those where respiratory growth is impeded, find the **Phenotype Qualifiers** column and open the **View Column Summary** menu. Select all items that refer to hindering respiratory growth: "decreased", "decreased rate", "absent", etc. Then, hit Filter.
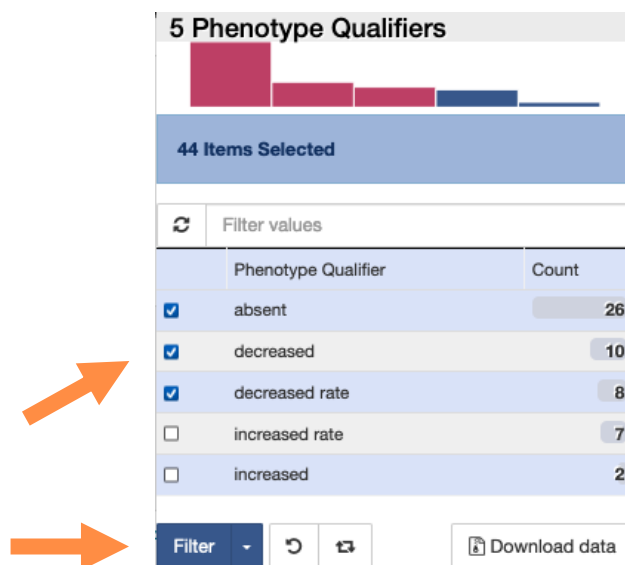
- You should now have a list of uncharacterized yeast genes whose products interact with mitochondrial ribosomes and mutations lead to respiratory growth defects. Use the **Save as List** function to save the list of genes and enter the name "**List 6 uncharacterized MTR interactors with respiratory growth phenotype**"
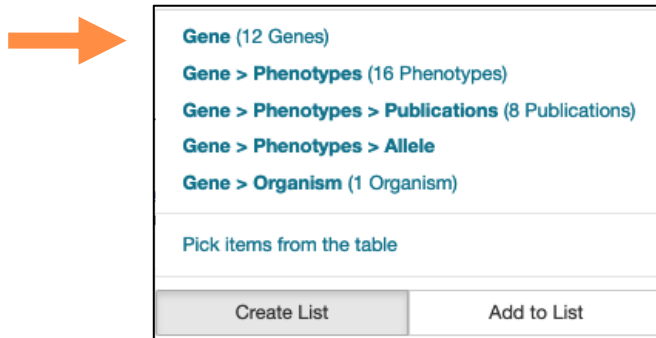
- View the list and save the results into a .tsv file by clicking on the **Export** button, and then on the "**Download file**" button in the resulting pop-up window.

- 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**".
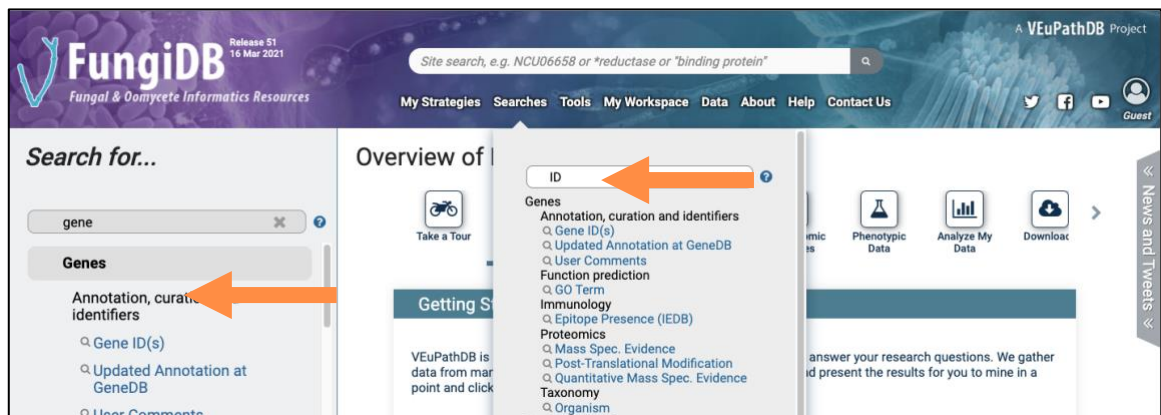
- Click on the red "**Add Step**" button. In the resulting pop-up window, click on **Transform into related records > Orthology**. Select **Fungi** and **Oomycetes**, then click on **Run Step**.

- 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.