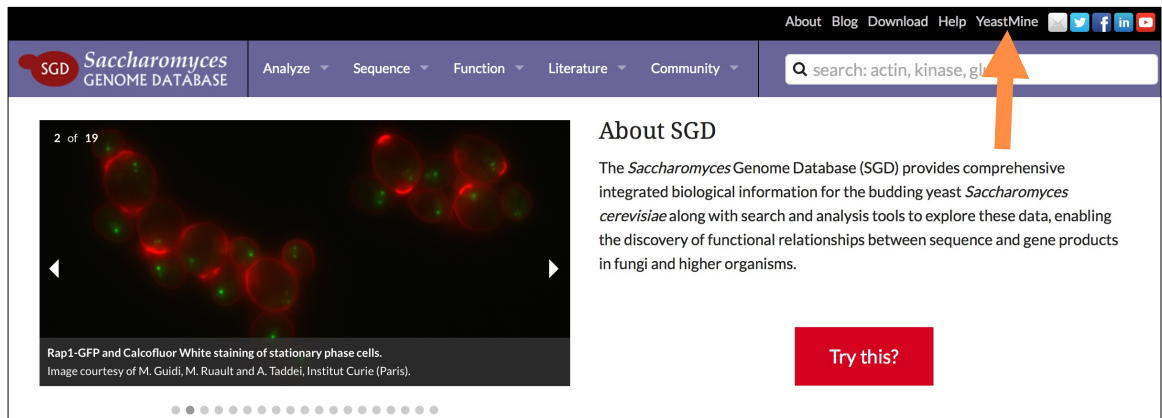


Search Strategies in SGD

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.

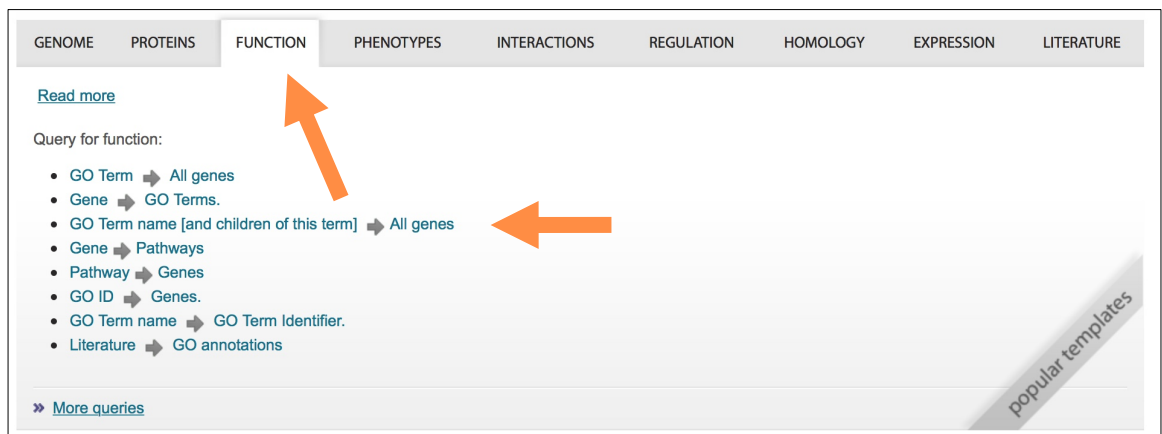
- Access YeastMine from SGD home page (<http://www.yeastgenome.org>); click on YeastMine in the upper right corner above the search box.




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  Edit Query

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

- In 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

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	GO Annotation Code Code	GO Annotation Qualifier	GO Annotation 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	mitochondr
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
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

[Relationships](#) [Save as List](#)


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 List **Add to List**

Create a new List of 92 Genes

List Name 
 List 1 MTR proteins

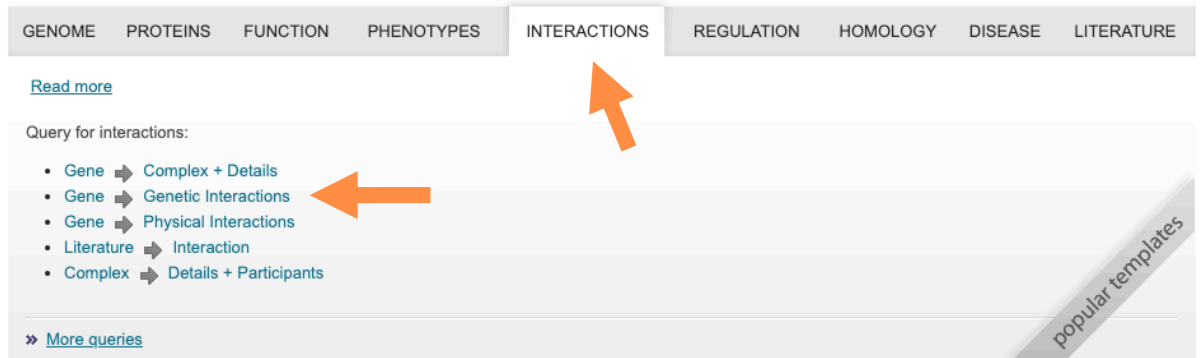
List Description
 Enter a description

Optional attributes
 NO TAGS **add**

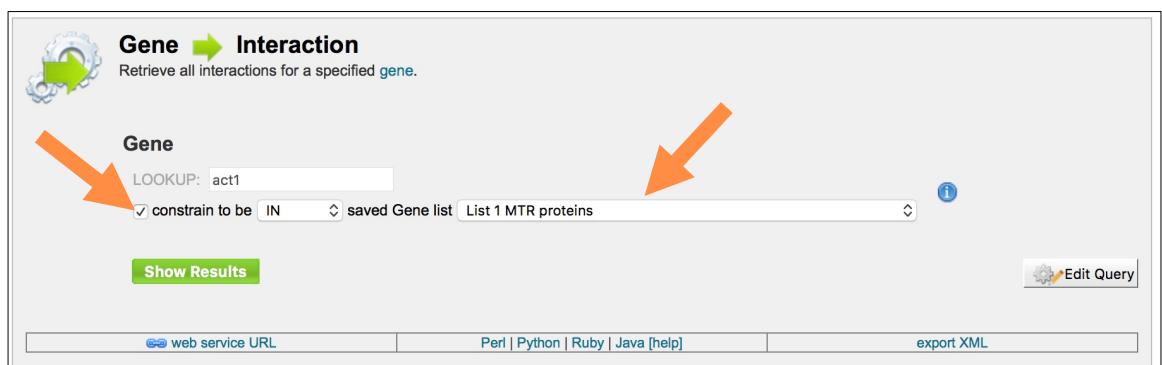
Create List

2. Find proteins that genetically interact with MTR proteins:

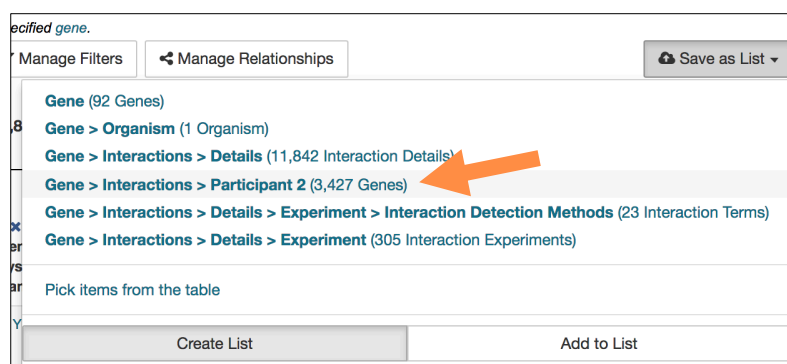
- Go back to YeastMine home page (click on **Home** in the purple banner on top). Open the **INTERACTIONS** tab and select **Gene -> Genetic Interactions**



- 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**

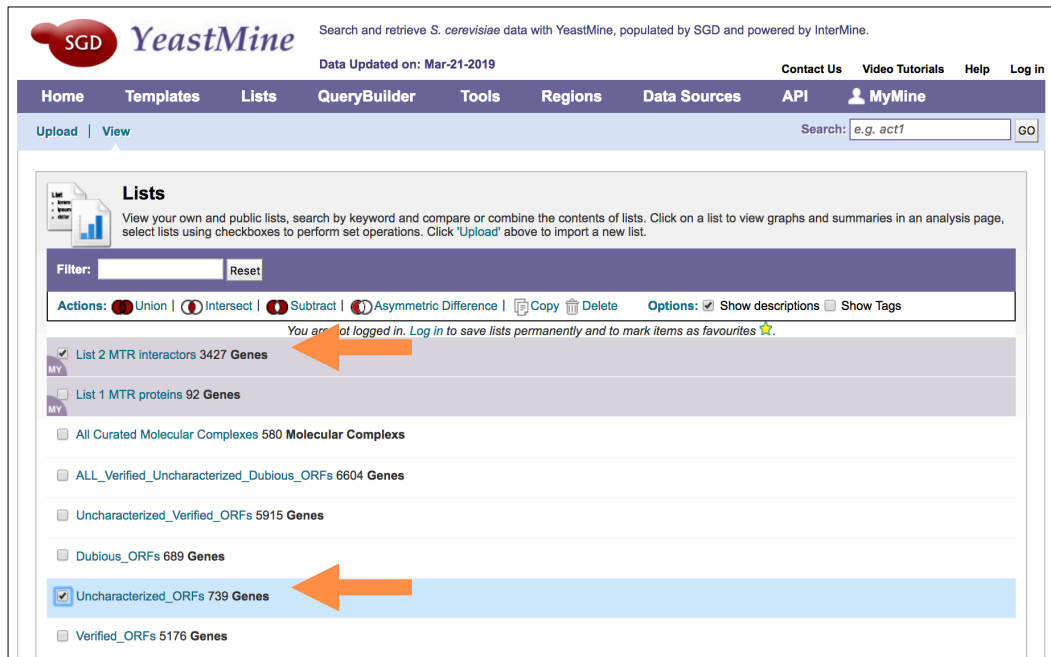


- The results page shows all genes/proteins with genetic or physical interactions with the MTR proteins from List 1. Save the MTR interactors by clicking on **Save as List** and selecting **Gene > Interactions > Participant 2**. Give your list a name ("**List 2 MTR interactors**") and hit **Create List**.



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.

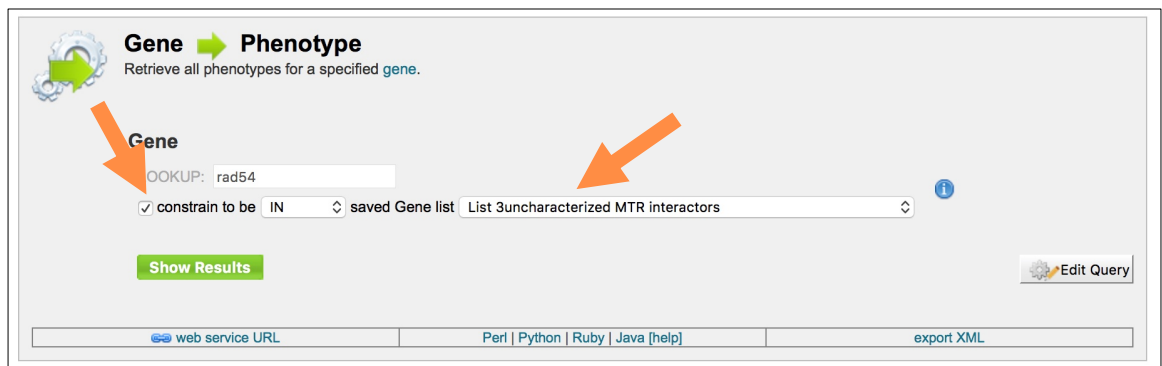


- Click on your list to see the results.
- Because we have over 200 genes in our results, it would be a good idea to narrow down our candidates even more. For example, because the MTR is a mitochondrial complex, we would expect that deleting uncharacterized (but bona fide) subunits of the MTR would disrupt 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: Gene Qualifier, Phenotypes Experiment Type, Phenotypes Mutant Type, Phenotype Observable, and Phenotypes. A pop-up window titled "68 Phenotype Observables" is open, showing a search for "respiratory" with 12 items selected. The selected item is "respiratory growth" with a count of 12. An orange arrow points to the "Filter" button in the pop-up.

- 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.

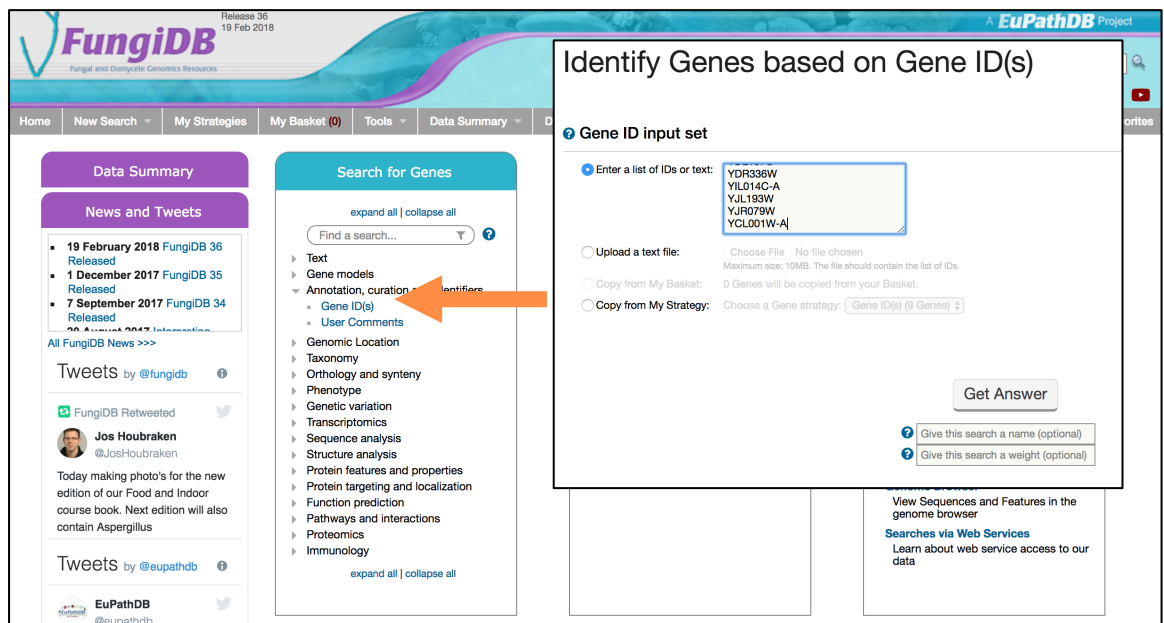
Trail: Query
Gene → **Phenotype**
 Retrieve all phenotypes for a specified gene.

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

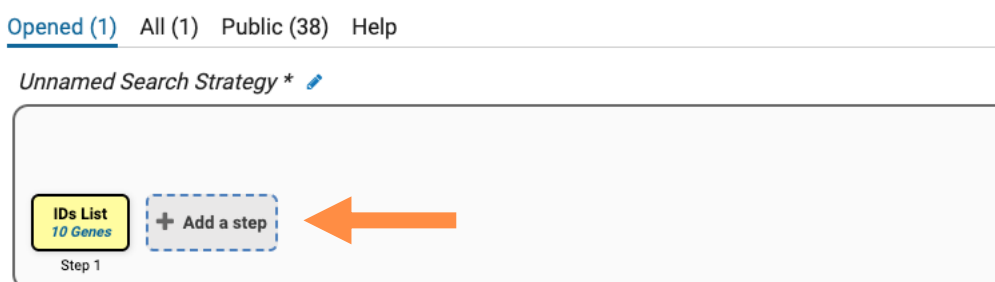
Showing rows 1 to 2 of 2

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	Phenotypes Condition
S000000191	MRX3	YBL095W	NO VALUE	Uncharacterized	classical genetics	null	respiratory growth	decreased	NO VALUE	NO VALUE	Other	glycerol, ethanol	Media: nonfermentable carbon (YPEG)
S0000002316	NO VALUE	YDL157C	NO VALUE	Uncharacterized	systematic mutation set	null	respiratory growth	absent	NO VALUE	NO VALUE	S288c		Media: carbon

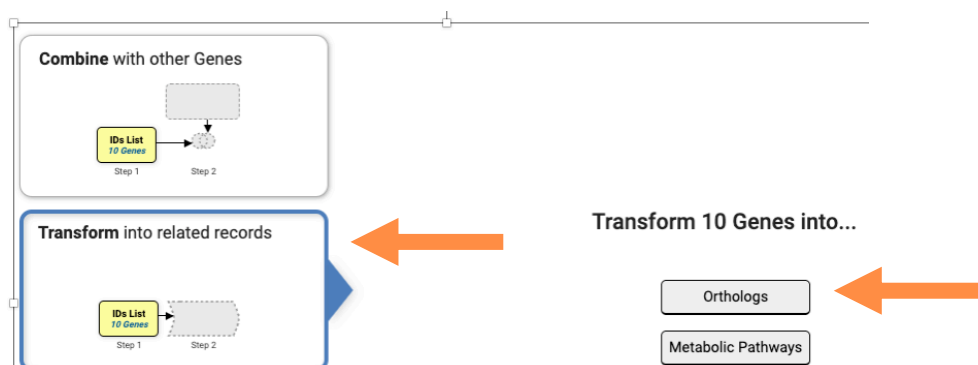
- The results of the above YeastMine analysis suggest 10 genes that potentially encode undiscovered subunits of the mitochondrial ribosome. Although these genes are uncharacterized, more data may exist on their orthologs in other organisms. Use FungiDB to survey the function of orthologs in Fungi and 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 “**Add a step**” button.



- In the resulting pop-up window, click on **Transform into Related Records**. Select **Orthologs** and then **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)
ACLA_086280	ACLA_086280-t26_1	<i>A. clavatus</i> NRRL 1	DS027060:2,044,080..2,045,139(+)	GTP binding protein (EngB), putative	YDR336W
AFLA_033930	AFLA_033930-t26_1	<i>A. flavus</i> NRRL3357	EQ963473:3,025,757..3,026,783(-)	GTP binding protein (EngB), putative	YDR336W
AFUB_001730	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
AGR57_3207	AGR57_3207T0	<i>P. chrysosporium</i> RP-78	PchrRP-78_SC003:600,486..601,399(+)	P-loop containing nucleoside triphosphate hydrolase protein	YDR336W
AGR95_111490	AGR95_111490.mRNA	<i>H. capsulatum</i> G217B	HISTO_ZT.Contig1089:445,461..446,683(+)	unspecified product	YDR336W
AKAW_06043	AKAW_06043-t41_1	<i>A. kawachii</i> IFO 4308	DF126461:135,225..136,291(-)	GTP binding protein	YDR336W
ALNC14_006000	ALNC14_006000:RNA	<i>A. laibachii</i> Nc14	FR824048:351,365..352,417(-)	unspecified product	YDR336W
AMAG_08869	AMAG_08869-t26_1	<i>A. macrogynus</i> ATCC 38327	GG745343:315,460..317,068(+)	ribosome biogenesis GTP-binding protein YsxC	YDR336W
AMAG_09047	AMAG_09047-t26_1	<i>A. macrogynus</i> ATCC 38327	GG745343:803,808..805,364(-)	hypothetical protein	YDR336W
AMAG_12000	AMAG_12000-t26_1	<i>A. macrogynus</i> ATCC 38327	GG745353:588,076..589,473(+)	hypothetical protein, hypothetical protein, variant	YDR336W

