Search Strategies in SGD

In addition to a faceted search tool, SGD provides YeastMine

(<u>https://yeastmine.yeastgenome.org/</u>) 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 (<u>http://www.yeastgenome.org</u>); 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

GENOME	PROTEINS	FUNCTION	PHENOTYPES	INTERACTIONS	REGULATION	HOMOLOGY	EXPRESSION	LITERATURE
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Query for fu	unction:							
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• Enter mitochondrial ribosome into the query box; hit Show Results



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)

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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

GENOME	PROTEINS	FUNCTION	PHENOTYPES	INTERACTIONS	REGULATION	HOMOLOGY	EXPRESSION	LITERATURE
Read more								
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• 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 Interaction Retrieve all interactions for a specified ge	ene.	
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Show Results		Edit Query
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 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.

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Manage Filters	« Manage Relationships	▲ Save as List ◄							
Gene (92 Ger	nes)								
8 Gene > Orga	nism (1 Organism)								
Gene > Inter	actions > Details (11,842 Interaction	Details							
Gene > Interactions > Participant 2 (3,427 Genes)									
Gene > Inter	actions > Details > Experiment > In	eraction Detection Methods (23 Interaction Terms)							
er Gene > Inter	actions > Details > Experiment (305	Interaction Experiments)							
ar Pick items fro	om the table								
Y	Create List	Add to 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.

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	2000000	20100	Data Updated on: Ma	ır-21-2019			Contact Us	Video Tutorials	Help	Log in
Home	Templates	Lists	QueryBuilder	Tools	Regions	Data Sources	ΑΡΙ	🚨 MyMine		
Upload V	iew						Search:	e.g. act1		GO
	Lists View your own and select lists using cho	public lists, se eckboxes to p	arch by keyword and cor erform set operations. Cl	npare or combi ick 'Upload' abc	ne the contents of li ove to import a new	sts. Click on a list to view list.	graphs and sur	nmaries in an analy	ysis page	5,
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🕑 Uncha	racterized_ORFs 739	Genes								
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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.

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 select lists usin checkboxes to perform set operations. Click 'Upload' above to import a new list.	analysis page,
Filter: Reset	
Actions: 🛑 Union 🕦 Intersect 🚯 Subtract 🚯 Asymmetric Difference 📴 Copy 🍿 Delete Options: 🗸 Show descriptions	
You are not logged in. Log in to save lists permanently and to mark items as favourites $ m \hat{r}$.	

- 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

GENOME	PROTEINS	FUNCTION	PHENOTYPES	INTERACTIONS	REGULATION	HOMOLOGY	EXPRESSION	LITERATURE
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• Check the constrain to be IN checkbox and select your saved list ("List 3 uncharacterized MTR interactors"); click on Show Results

Gene Phenotype Retrieve all phenotypes for a specified ger	ne.	
Gene OOKUP: rad54 Constrain to be IN	Gene list List 3uncharacterized MTR interactors	≎ 1
Show Results		Edit Query
ee web service URL	Perl Python Ruby Java [help]	export XML

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 + + + + page 1 - + +												
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• In the Filter values box, enter respiratory and scroll down the list to check the box next to Respiratory growth; hit Filter.

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- 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.

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- 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 (<u>http://fungidb.org/</u>). 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".

Enter a list of IDs or text:	VDD326W				
	YUL336W YUL014C-A YJL0139W YCL001W-A				
Upload a text file:	Choose File No file chosen Maximum size: 10MB. The file should contain the list of IDs.				
O Copy from My Basket:	0 Genes will be copied from your Basket.				
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 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.

My Strategies:	New	Opened (1)	All (2)	Basket	Public Strategies (49)	Help	
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(Genes)							Strategy: Gene ID(s)(2) *
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 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.

First 1 2 3 4 5 Next Last Advanced Paging				Download Add to Basket Add Colum					
	韋 Gene ID	韋 Transcript ID	韋 Organism 🕹	Genomic Location (Gene) 3	Product Description				
	ACLA_086280	ACLA_086280-t26_1	A. clavatus NRRL 1	DS027060:2,044,0802,045,139(+)	GTP binding protein (EngB), putative	YDR336W			
6	AFLA_033930	AFLA_033930-t26_1	A. flavus NRRL3357	EQ963473:3,025,7573,026,783(-)	GTP binding protein (EngB), putative	YDR336W			
6	AFUB_001730	AFUB_001730-T	A. fumigatus A1163	scf_000001_A_fumigatus_A1163:485,315486,704(-)	Has domain(s) with predicted GTP binding activity and role in barrier septum assembly	YDR336W			
•	AGR57_3207	AGR57_3207T0	P. chrysosporium RP-78	PchrRP-78_SC003:600,486601,399(+)	P-loop containing nucleoside triphosphate hydrolase protein	YDR336W			
6	AGR95_111490	AGR95_111490.mRNA	H. capsulatum G217B	HISTO_ZT.Contig1089:445,461446,683(+)	unspecified product	YDR336W			
6	AKAW_06043	AKAW_06043-t41_1	A. kawachii IFO 4308	DF126461:135,225136,291(-)	GTP binding protein	YDR336W			
6	ALNC14_006000	ALNC14_006000:RNA	A. laibachii Nc14	FR824048:351,365352,417(-)	unspecified product	YDR336W			
•	AMAG_08869	AMAG_08869-t26_1	A. macrogynus ATCC 38327	GG745343:315,460317,068(+)	ribosome biogenesis GTP-binding protein YsxC	YDR336W			
6	AMAG_09047	AMAG_09047-t26_1	A. macrogynus ATCC 38327	GG745343:803,808805,364(-)	hypothetical protein	YDR336W			
	AMAG_12000	AMAG_12000-t26_1	A. macrogynus ATCC 38327	GG745353:588,076589,473(+)	hypothetical protein, hypothetical protein, variant	YDR336W			