



YeastMine: An Advanced Search and Analysis Tool for SGD Data



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The Saccharomyces Genome Database (SGD; <http://www.yeastgenome.org/>) provides high-quality curated genomic, genetic, and molecular information on the genes and gene products of the budding yeast *Saccharomyces cerevisiae*. YeastMine provides a sophisticated tool for searching SGD data with a list of genes, GO terms and other data types. Pre-made queries called templates can be used to get results for most commonly asked questions. For more complex questions, one can use multiple templates, intermediate steps and list operations to get answers. Registered users can store their queries and results in MyMine. Regulatory relationships, human homolog and disease connections, and protein complex data are the most recent data types loaded into YeastMine. YeastMine is built using the open source software InterMine (<http://www.intermine.org/>), a data warehouse solution for biological data.

Search:

GO

Search Methods



Templates

Templates are predefined queries, each has a simple form and a description, by category.

Filter: Filter: -- all categories --

Actions: Options: ☒ Show descriptions ☐ Show Tags

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☐ Yeast gene --> OMIM human homolog(s) --> OMIM Disease Phenotype(s)
Retrieve human homolog(s) of yeast gene(s) and any of their associated OMIM

3. Type/Paste in genomic regions in ☒ base coordinate ☐ interbase coordinate
(click to see an example)
chrIII:1356..20455
chrVI:11331..18001
chrVI:9856..100010

Home Templates Lists QueryBuilder

Model browser

Individual fields to the results. Use [\[edit query\]](#) links to cons value in the query.

Gene [\[edit query\]](#) [\[edit query\]](#)
Brief Description [\[edit query\]](#) [\[edit query\]](#)
Cytological Location [\[edit query\]](#) [\[edit query\]](#)
Description [\[edit query\]](#) [\[edit query\]](#)
Feature Type [\[edit query\]](#) [\[edit query\]](#)
Function Summary [\[edit query\]](#) [\[edit query\]](#)
Length [\[edit query\]](#) [\[edit query\]](#)
Name [\[edit query\]](#) [\[edit query\]](#)
Phenotype Summary [\[edit query\]](#) [\[edit query\]](#)
Primary DBID [\[edit query\]](#) [\[edit query\]](#)
Qualifier [\[edit query\]](#) [\[edit query\]](#)
Systematic Name [\[edit query\]](#) [\[edit query\]](#)
Spt Alias [\[edit query\]](#) [\[edit query\]](#)
Status [\[edit query\]](#) [\[edit query\]](#)
Standard Name [\[edit query\]](#) [\[edit query\]](#)
Child Features Sequence Feature [\[edit query\]](#) [\[edit query\]](#)
Chromosome Chromosome [\[edit query\]](#) [\[edit query\]](#)
Chromosome Location Location [\[edit query\]](#) [\[edit query\]](#)
Complements Complement [\[edit query\]](#) [\[edit query\]](#)
Cross References Cross Reference [\[edit query\]](#) [\[edit query\]](#)
Data Sets Data Set [\[edit query\]](#) [\[edit query\]](#)

•Keyword
•Templates
•Regions
•Querybuilder
•Programmatic

API

1 Upload list of identifiers 2 Verify identifier matches 3 List analysis

Create a new list
Select the type of list to create and either enter in a list of identifiers or upload identifiers from a file. A search will be performed for all the identifiers in your list.

- Separate identifiers by a comma, space, tab, new line or semi-colon.
- Qualify any identifiers that contain whitespace with double quotes like so: "even skipped".

Select Type:
for Organism:
Type/Paste in identifiers (click to see an example)

or Upload identifiers from a .txt file... No file chosen
☐ Match on case

Question based List Analysis

Lists

- [ALL_Verified_Uncharacterized_Dubious_ORFs](#) (6604 Genes)
This List includes ALL ORFs
- [Centromeres](#) (16 Centromeres)
- [Human genes complementing or complemented by yea](#)
- [Human genes with yeast homologs](#) (6626 Genes)
- [Long Terminal Repeat](#) (383 LongTerminalRepeats)
- [Not In Systematic Sequence Of S288C](#) (55 NotInSysteme)
List of genes that are not present in the S288C referenc
- [RetroTransposons](#) (50 Retrotransposons)
- [Telomeres](#) (32 Telomeres)
- [Uncharacterized_Verified_ORFs](#) (5915 Genes)
This List excludes Dubious ORFs

New mito
ribosome
subunits?

Predicting
chemotherapy
targets

MyMine

Actions: ☒ Union | ☐ Intersect | ☐ Subtract | ☐ Asymmetric Difference |



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<https://www.facebook.com/yeastgenome/>



<https://www.youtube.com/SaccharomycesGenomeDatabase>

