



# YeastMine: An Advanced Search and Analysis Tool for SGD Data



Stanford  
MEDICINE

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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: e.g. act1

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

You are not logged in. [Log in](#) to...

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  
chrIV:11331..18001  
chrV:9856..100010

Home Templates Lists QueryBuilder

### Model browser

Individual fields to the results. Use [CONSTRAINTS](#) links to constrain value in the query.

Gene  [CONSTRAINTS](#)  
Brief Description  [CONSTRAINTS](#)  
Cytological Location  [CONSTRAINTS](#)  
Definition  [CONSTRAINTS](#)  
Feature Type  [CONSTRAINTS](#)  
Function Summary  [CONSTRAINTS](#)  
Location  [CONSTRAINTS](#)  
Name  [CONSTRAINTS](#)  
Phenotype Summary  [CONSTRAINTS](#)  
Primary DBID  [CONSTRAINTS](#)  
Qualifiers  [CONSTRAINTS](#)  
Systematic Name  [CONSTRAINTS](#)  
Synonyms  [CONSTRAINTS](#)  
Status  [CONSTRAINTS](#)  
Standard Name  [CONSTRAINTS](#)  
Child Features/Sequence Features  [CONSTRAINTS](#)  
Chromosome Chromosome  [CONSTRAINTS](#)  
Chromosome Location/Location  [CONSTRAINTS](#)  
Cross References Cross Reference  [CONSTRAINTS](#)  
Data Sets Data Set  [CONSTRAINTS](#)  
Data Sets Data Set  [CONSTRAINTS](#)

- Keyword
- Templates
- Regions
- Querybuilder
- Programmatic

API

1 Upload list of identifiers 2 Verify identifier matches [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

or Upload identifiers from a .txt file...

Match on case

## Question based List Analysis

### Lists

- [ALL\\_Verified\\_Uncharacterized\\_Dubious\\_ORFs](#) (6604 G)  
This List includes ALL ORFs
- [Centromeres](#) (16 Centromeres)
- [Human genes complementing or complemented by yeast](#)
- [Human genes with yeast homologs](#) (6626 Genes)
- [Long Terminal Repeat](#) (383 LongTerminalRepeats)
- [Not In Systematic Sequence Of S288C](#) (55 NotInSyste  
List of genes that are not present in the S288C reference
- [RetroTransposons](#) (50 Retrotransposons)
- [Telomeres](#) (32 Telomeres)
- [Uncharacterized\\_Verified\\_ORFs](#) (5915 Genes)  
This List excludes Dubious ORFs

Actions:

New mito  
ribosome  
subunits?

Predicting  
chemotherapy  
targets

MyMine



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

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