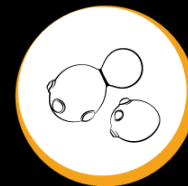



# Finding Data(files) at SGD

Yeast Genetics Meeting, Stanford, CA

August 24, 2018



# General search box

 **Saccharomyces**  
GENOME DATABASE

Analyze ▾ Sequence ▾ Function ▾ Literature ▾ Community ▾

8 of 20



Peroxisome (red) and mitochondrial (green) fission defects in *vps1 fis1* double deletion strain transformed with *FIS1*.  
Image courtesy of S. Lefevre, S. Kumar and I. van der Klei, University of Groningen.

## About SGD

The *Saccharomyces* Genome Database (SGD) provides comprehensive integrated biological information for the budding yeast *Saccharomyces cerevisiae* along with search and analysis tools to explore these data, enabling the discovery of functional relationships between sequence and gene products in fungi and higher organisms.

Try this?

## Categories

- References 97,806
- Biological Processes 24,765
- Colleagues 12,417
- Molecular Functions
- Genes
- Downloads
- Cellular Components
- Chemicals
- Phenotypes
- Observables
- Strains
- Resources
- Reserved Gene Names

169,013 results

Page 1 of 6,761



◀ Show all categories

## References

Author

Journal

Year

Associated Genes

## Colleagues

Last Name

Position

Institution

Country

Genes Of Interest

## Genes / Genomic Features

Feature Type

Molecular Function

Cellular Component

Biological Process

Status

## Downloads

Topic

Data

Keyword

Format

Status

• Active

○ Archived

Year

◀ Show all categories

## Phenotypes


References

Phenotype Loci

Chemical

Mutant Type

# All Matches for a Gene Name

**Saccharomyces**  
GENOME DATABASE

MENU

Categories

- Phenotypes 36
- References 24
- Biological Processes 8
- Molecular Functions 3
- Cellular Components 3
- Genes 1
- Colleagues 1

76 results for **"whi3"**

Page 1 of 4

< >

25

**WHI3 / YNL197C**

RNA binding protein that sequester  
involved in the cell cycle, sister chro

protein: mRNA-binding protein **WH**

name: **WHI3** / YNL197C

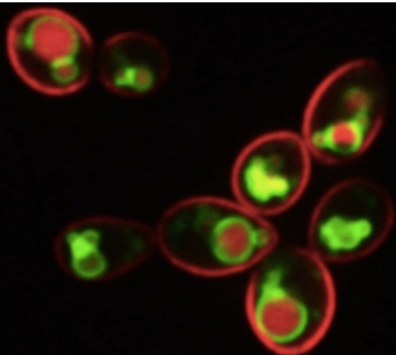
Caudron F and Barral

Q whi3 \*

Show all results ...

- WHI3 / YNL197C Gene
- WHI2 / YOR043W Gene
- WHI4 / YDL224C Gene
- WHI5 / YOR083W Gene
- WSC3 / YOL105C Gene
- WTM2 / YOR229W Gene
- WSC4 / YHL028W Gene
- WWM1 / YFL010C Gene
- WTM1 / YOR230W Gene
- WSS1 / YHR134W Gene

3 of 20



Pma1-mCherry and Vma1-GFP localization in mitotic cells.

Image courtesy of M. Eastwood, Fred Hutch and M. Meneghini, University of Toronto.



## About SGD

The *Saccharomyces* Genome Database (SGD) integrated biological information for the budding yeast *S. cerevisiae* along with search and analysis tools, enabling the discovery of functional relationships between gene products in fungi and higher organisms.

[Try this?](#)

Q expres

Show all results ...

Expression

● Resource

EXA2

● Gene

EXP1 / YDL121C

● Gene

● Download

Expression\_connection\_data.zip

EXO70 / YJL085W

● Gene

EXO1 / YOR033C

● Gene

EXG1 / YLR300W

● Gene

EXO5 / YBR163W

● Gene

EXO84 / YBR102C

● Gene

EXG2 / YDR261C

● Gene

# Tools

YeastMine: [Batch Analysis](#) or [Advanced Search](#)

[Home](#)

[Analyze](#)

[Sequence](#)

[Function](#)

[Literature](#)

[Community](#)

## SPELL - *S. cerevisiae*

SPELL (Yeast)

Gene Name(s):

# Results: 20

**Options for Filtering Results by Dataset Tags**

### Dataset Tags

Select:

- |  |  |  |   |
|--|--|--|---|
| <input type="checkbox"/> disease   | <input type="checkbox"/> DNA replication, recombination and repair | <input type="checkbox"/> mRNA processing         | <input type="checkbox"/> response to unfolded protein |
| <input type="checkbox"/> organelles, biogenesis, structure, and function | <input type="checkbox"/> environmental-sensing                     | <input type="checkbox"/> nitrogen utilization    | <input type="checkbox"/> RNA catabolism               |
| <input type="checkbox"/> amino acid metabolism                           | <input type="checkbox"/> evolution                                 | <input type="checkbox"/> nutrient utilization    | <input type="checkbox"/> signaling                    |
| <input type="checkbox"/> amino acid utilization                          | <input type="checkbox"/> fermentation                              | <input type="checkbox"/> osmotic stress          | <input type="checkbox"/> sporulation                  |
| <input type="checkbox"/> carbon utilization                              | <input type="checkbox"/> filamentous growth                        | <input type="checkbox"/> oxidative stress        | <input type="checkbox"/> starvation                   |
| <input type="checkbox"/> cell aging                                      | <input type="checkbox"/> flocculation                              | <input type="checkbox"/> oxygen level alteration | <input type="checkbox"/> stationary phase entry       |
| <input type="checkbox"/> cell cycle regulation                           | <input type="checkbox"/> genetic interaction                       | <input type="checkbox"/> phosphorus utilization  | <input type="checkbox"/> stationary phase maintenance |

[New Search](#)

[Dataset Listing](#)

[Show Expression Levels](#)

[Download Expression Data](#)

[About the Website](#)

SPELL Version 2.0.3

# JBrowse datasets

The image displays the JBrowse genome browser interface. The top navigation bar includes 'Genome', 'Track', 'View', and 'Help'. The main view shows a genomic track for chromosome VI, with coordinates ranging from 0 to 200,000. A red box highlights the coordinate '50,000'. Below the coordinate bar, there are navigation controls (left arrow, right arrow, zoom in, zoom out) and a 'Select tracks' button. The track list on the left includes 'All Annotated Sequence Features', 'htz1\_0\_to\_60\_mins', 'Michel\_2017\_Vps13D716H', 'Mancera\_2008\_meiotic\_recombination\_hotspots\_V64', 'Arribere\_2013\_GSE39074\_TATL-SeqCombined', and 'Zhang\_2007\_intron\_tiling\_array\_log2\_ratios\_V64'. A red circle highlights the context menu for the 'Mancera\_2008\_meiotic\_recombination\_hotspots\_V64' track, which includes options: 'About this track', 'Pin to top', 'Edit config', 'Delete track', 'Save track data' (highlighted), 'Display mode', and 'Show labels'. A red arrow points from the 'Save track data' option in the context menu to a 'Save track data' dialog box. The dialog box has a title bar with a close button. It contains three sections: 'Region to save' with two radio buttons ('Visible region - chrVI:46216..63275 (17.06 Kb)' selected and 'Whole reference sequence - chrVI:1..270161 (270.16 Kb)'); 'Format' with three radio buttons ('GFF3' selected, 'BED', and 'Sequin Table'); and 'Filename' with a text input field containing 'Mancera\_2008\_meiotic\_recombination\_hotspots\_V64-chrVI-46216'. At the bottom of the dialog are three buttons: 'Cancel' (with a red X icon), 'View' (with a document icon), and 'Save' (with a floppy disk icon).

# Faceted searching in JBrowse

## Select Tracks

My Tracks

Currently Active

Recently Used

Assay Term Name

19 (no data)

3 CLIP-seq assay

1 CLIP-seq assay (cross-linking immunoprecipitation)

139 ChIP-chip assay

36 ChIP-seq assay

5 Chromatin immunoprecipitation with exonuclease sequencing assay (ChIP-exo)

8 DNA methylation sequencing assay

1 DNA sequence variation detection by tiling array

5 DNA sequencing

1 DNase footprinting assay

3 MNase-seq assay

10 PAR-CLIP

2 PARS

41 RNA-seq assay

8 Serial Analysis of Gene Expression (SAGE)

1 TATL-seq

2 TL-seq

14 micrococcal nuclease digestion followed by high throughput sequencing assay

2 micrococcal nuclease digestion followed by tiling array assay

9 transcription profiling by tiling array assay

2 translation profiling assay

2 whole genome sequencing

Back to browser

Clear

Contains text

PMID

First author

Lab PI

2 translation profiling assay

2 whole genome sequencing assay

Category

10 (no data)

20 DNA replication, recombination and repair

3 RNA catabolism

16 RNA structure

1 Reference sequence

1 carbon utilization

49 chromatin organization

1 chromatin organization | transcription

74 histone modification

14 mRNA processing

1 mitotic cell cycle

17 stress | heat shock | carbon utilization | nutrient utilization | osmotic stress | oxidative stress | phosphorus utilization

77 transcription

16 transcriptional regulation

4 transcriptional regulation | histone modification

2 translation regulation

8 transposons

First author

GBrowse Category


Lab PI


PMID

Strain background

Year

<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H4K12ac_ChIP_chip
<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H3K9ac_ChIP_chip
<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H3K4me3_ChIP_chip
<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H3K4me2_ChIP_chip
<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H3K4me1_ChIP_chip
<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H3K18ac_ChIP_chip
<input type="checkbox"/>	16122352	Liu	Rando, Oliver J.	University of Massachusetts Medical School	ChIP-chip assay	DNA extract	S288C	histone modification	chromatin structure	H3K14ac_ChIP_chip


**ALLIANCE**  
 of GENOME RESOURCES  
 FOUNDING MEMBER


**Saccharomyces**  
 GENOME DATABASE



# Gene expression datasets

SGD *Saccharomyces* GENOME DATABASE

Analyze ▾ Sequence ▾ Function ▾ Literature ▾ Community ▾

Q flocculation

Categories

- References 367
- Genes 44
- Biological Processes 17
- Phenotypes 5
- Downloads 2**
- Observables 1
- Chemicals 1

437 results for "flocculation"

Page 1 of 18

Results 25

Sort By Relevance

**flocculation** Observable

Adhesion and aggregation of cells in liquid culture to produce clumps of cells.

name: **flocculation**

**flocculation** Biological Process

The reversible, non-sexual aggregation of single-celled organisms in suspension to form aggregates of many cells known as flocs.

name: **flocculation**

7 Associated Genes: [Copy to Clipboard](#) [Show All](#)

[◀ Show all categories](#)

## ● Downloads

### Topic

[Transcriptomics](#)

### Data

[Gene expression profile](#)

### Keyword

[flocculation](#)

[fermentation](#)

### Format

[Gene expression report format](#)

### Status

☒ Active

☐ Archived

### Year

2 results for

× "flocculation"

× Download

× Active

Page 1 of 1

Results

Sort By

<

>

25

Relevance ▾

2

### Goossens\_2015\_PMID\_25873380.zip

● Download

Molecular mechanism of flocculation self-recognition in yeast and its role in mating and survival.

2

**description:** Molecular mechanism of **flocculation** self-recognition in yeast and its role in mating and survival.

▼

**keyword:** **flocculation**

2

1

Download

266.7KB

[README](#)

▼

2

### Zeng\_2016\_PMID\_27485516.zip

● Download

Transcriptomes of a xylose-utilizing industrial flocculating *Saccharomyces cerevisiae* strain cultured in media containing different sugar sources

▼

**description:** Transcriptomes of a xylose-utilizing industrial **flocculating** *Saccharomyces cerevisiae* strain cultured in media containing different sugar sources

**keyword:** **flocculation**

▼

Download

99.5KB

[README](#)

# Explore downloadable files

◀ Show all categories

835 results ✕ Download ✕ Active

● Downloads

Topic

- Transcriptomics 3
- Mapping
- Transcription factors and regulatory sites
- Sequence analysis
- Whole genome sequencing

Show more

Data

- Gene expression profile 3
- Sequence
- Sequence coordinates
- Annotation track

Keyword	Status	Year	Format	Download	Size
stress	<input checked="" type="radio"/> Active			<a href="#">Download</a>	4.2M
carbon utilization	<input type="radio"/> Archived				
transcription					
chemical stimulus				<a href="#">Download</a>	557.8
genome variation		2018 6			
		2017 66			
		2016 137			
		2015 89		<a href="#">Download</a>	35.3M
		2014 62			
			Show more		
Gene expression report format					
FASTA					
Alignment format					
Sequence assembly format					

Yassour\_2009\_PMDID\_1920

Transcriptome study

Zhang\_2007\_PMDID\_17351

Study to identify spliced introns

Abbott\_2008\_PMDID\_18676

Raw expression values (CHP data) for tran  
cerevisiae to challenges with lactic acid at

# Finding datasets by publication

Reference: **Capaldi AP, et al. (2008)**

[Abstract](#)

[Expression  
Datasets](#)

Reference: **Capaldi AP, et al. (2008)** Structure and function of a transcriptional network activated by the MAPK Hog1. *Nat Genet* 40(11):1300-6

Abstract

[Reference Help ?](#)

## Expression Datasets 1 dataset for 1 reference

[? Filter table](#)

Dataset	Description	Keywords	Number of Conditions
<a href="#">Structure and Function of a Transcriptional Network Activated by Hog1</a>	Cells regulate gene expression using a complex network of signaling pathways, transcription factors and promoters	osmotic stress, stress, transcription	85
Showing 1 to 1 of 1 entries   10 records per page   « 1 »			

[Download \(.txt\)](#)

# Dataset page

Dataset: **Structure and Function of a Transcriptional Network Activated by Hog1**

Overview

Summary

Conditions

Resources

## Dataset: Structure and Function of a Transcriptional Network Activated by Hog1

**GEO ID:** [GSE12270](#)  
**Reference:** [Capaldi AP, et al. \(2008\)](#)  
**Channels:** 2  
**Conditions:** 85  
**Description:** Cells regulate gene expression using a complex network of promoters  
**Categories:** [osmotic stress](#), [stress](#), [transcription](#)

### Conditions

Filter table	
Condition	GEO ID
hog1D +glucose rep1	GSM308181
hog1D +glucose rep2	GSM308182
hog1D +glucose rep3	GSM308183
hog1D +KCl rep1	GSM308111
hog1D +KCl rep2	GSM308112
hog1D +KCl rep3	GSM308113
hog1D in YEPD rep1	GSM308126
hog1D in YEPD rep2	GSM308127
hog1D in YEPD rep3	GSM308128
hog1D in YEPD rep4	GSM308129
Showing 1 to 10 of 85 entries 10 records per page	
« 1 2 ... 8 9 »	

### Resources

[Download data](#) | [GEO](#) | [GEO supplementary data](#)

# Finding a list of genes

Categories

- References 8,374
- Genes 1,597**
- Biological Processes 358
- Cellular Components 132
- Diseases 59
- Molecular Functions 40
- Downloads 36
- Phenotypes 14
- Observables 10
- Chemicals 4
- Reserved Gene Names 3
- Strains 1

10,628 results for **"mitochondrial"**

Page 1 of 426

Results: 25

Sort By: Relevance

**mitochondrial fusion** ● Biological Process

Merging of two or more mitochondria within a cell to form a single compartment.

**name:** mitochondrial fusion

**description:** Merging of two or more mitochondria within a cell to form a single compartment.

6 Associated Genes: [Copy to Clipboard](#) [Show All](#)

**mitochondrial crista** ● Cellular Component

Any of the inward folds of the mitochondrial inner membrane. Their number, extent, and shape differ in mitochondria from different tissues and organisms. They appear to be devices for increasing the surface

**synonyms:** mitochondrial cristae

**name:** mitochondrial crista

**description:** Any of the inward folds of the mitochondrial inner membrane. Their number, extent, and shape

# ORFs in the mitochondrial envelope

◀ Show all categories

● Genes / Genomic Features

Feature Type

- ORF 354

Molecular Function

- mitochondrial sequence-specific DNA-binding transcription factor activity (direct) 1
- mitochondrial ribosome binding (direct) 1
- mitochondrial RNA polymerase core promoter 1 sequence-specific DNA binding (direct) 1
- transmembrane transporter activity 88
- hydrolase activity 67

Show more

Cellular Component

- mitochondrial envelope 354
- mitochondrial inner membrane (direct) 201

354 results for

× "mitochondrial" × Gene × mitochondrial envelope × ORF

Page 1 of 15 Results Sort By

< > 25 Relevance

≡ List ≡ Wrapped

**MSS2 / YDL107W** ● Gen

Peripherally bound inner membrane protein of the mitochondrial matrix; involved in membrane insertion of C-terminus of Cox2p, interacts genetically and physically with Cox18p

**name description:** *Mitochondrial* Splicing

**cellular component:** *mitochondrial* inner membrane (direct)...*mitochondrial* matrix (direct)...*mitochondrion*...extrinsic component of *mitochondrial* inner membrane (direct)...*mitochondrion*

**description:** Peripherally bound inner membrane protein of the *mitochondrial* matrix; involved in membrane

**biological process:** *mitochondrion* organization...protein insertion into *mitochondrial* inner membrane from matrix side (direct)

**MGE1 / YOR232W** ● Gen

Mitochondrial matrix cochaperone; nucleotide release factor for Ssc1p in protein translocation and folding; also acts as cochaperone for Ssq1p in folding of Fe-S cluster proteins; acts as oxidative sensor to

**description:** *Mitochondrial* matrix cochaperone; nucleotide release factor for Ssc1p in protein

# Making Gene Lists

◀ Show all categories

354 results for × "mitochondrial" × Gene × mitochondrial envelope × ORF

● Genes / Genomic Features

Feature Type ▼

ORF 354

Molecular Function ▼

- mitochondrial sequence-specific DNA-binding transcription factor activity (direct) 1
- mitochondrial ribosome binding (direct) 1
- mitochondrial RNA polymerase core promoter sequence-specific DNA binding (direct) 1
- transmembrane transporter activity 88
- hydrolase activity 67

Show more

Download Analyze List Wrapped

MSS2	MGE1	MPC2	ODC2	ODC1	MTG1
MPC3	MDJ1	MIM1	SOM1	FIS1	MDV1
MRPL32	MPC1	MRS4	MTF1	MDJ2	FMP25
MRS2	MSP1	MSS51	MDM35	MMR1	MDM12
MGM1	MDM31	MMM1	MGR2	MSS1	MME1
MGR3	FMP52	MCY1	MDM38	VMS1	MDM34
MGR1	YME1	MDM32	MDM10	MCR1	MIR1
MTG2	ATM1	YME2	MPM1	FMP30	OXA1
TIM9	TIM8	TOM6	TIM50	MIC27	TOM22
TIM44	TIM22	TIM13	TIM18	MIX14	MIC19



# Analyze Gene Lists

Analyze Search  
Results

Tools

Genes

## Analyze Search Results

### Tools

#### GO Term Finder

Find common GO annotations between genes.

#### GO Slim Mapper

Sort genes into broad categories.

#### SPELL

View expression data.

#### YeastMine

Conduct advanced analysis.

### Genes

 Filter table

Gene  
Name



Description

AAC1

Mitochondrial inner membrane ADP/ATP translocator; exchanges cytosolic ADP for mitochondrially synthesized ATP; phosphorylated; Aac1p is a minor isoform while Pet9p is the major ADP/ATP translocator; relocalizes from mitochondrion to cytoplasm upon DNA replication stress

Mitochondrial inner membrane ADP/ATP translocator; exchanges cytosolic ADP for mitochondrially synthesized ATP; expressed under

# Need help?

Search Tutorial: <http://bit.ly/SGDsearch>

[sgd-helpdesk@lists.stanford.edu](mailto:sgd-helpdesk@lists.stanford.edu)