

## Retrieve & Analyze Sets of Genes

### Download Data

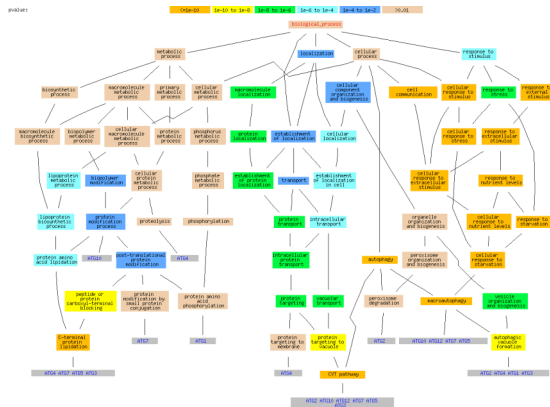
[www.yeastgenome.org/download](http://www.yeastgenome.org/download)

- Download genome-wide data files (use FTP site)
- Gather specific data types for a gene list (use Batch Download)

### GO Term Finder

[www.yeastgenome.org/TermFinder](http://www.yeastgenome.org/TermFinder)

Using a list of genes, find shared functions, processes, or locations.



### GO Slim Mapper

[www.yeastgenome.org/SlimMapper](http://www.yeastgenome.org/SlimMapper)

Map genes to broad functional categories:

- Macromolecular complex: annotated protein complex terms from the Cellular Component ontology
- Super GO-Slim: broad, high level terms
- Yeast GO-Slim: terms that represent the major biological processes, functions, and cellular components in *S. cerevisiae*

## Stay Up to Date with SGD & the Yeast Community

### RSS Feed

[www.yeastgenome.org/RSS](http://www.yeastgenome.org/RSS)

Subscribe to SGD's RSS feed to be alerted about recent changes in SGD.

### SGD Newsletter

[www.yeastgenome.org/newsletters](http://www.yeastgenome.org/newsletters)

Receive our quarterly newsletter by email (sign up via the Colleague Update form) or read it online to learn about the latest developments in SGD.

### SGD Wiki

[www.yeastgenome.org/wiki](http://www.yeastgenome.org/wiki)

Share with the community:

- Gene-specific pages
- Tables of commonly used strains
- Methods
- Reagents
- Career Opportunities



## Quick Resource Guide

July 2008

Find & View Chromosomal Features

Investigate a Gene's Function

View Protein Properties, Structure & Homology

Retrieve & Analyze Sets of Genes

Stay Up to Date with SGD & the Yeast Community

[www.yeastgenome.org](http://www.yeastgenome.org)  
[yeast-curator@yeastgenome.org](mailto:yeast-curator@yeastgenome.org)

# Find & View Chromosomal Features

## SGD Search



Use a keyword to simultaneously search 14 major categories of information in SGD.

## Advanced Search

[www.yeastgenome.org/search](http://www.yeastgenome.org/search)

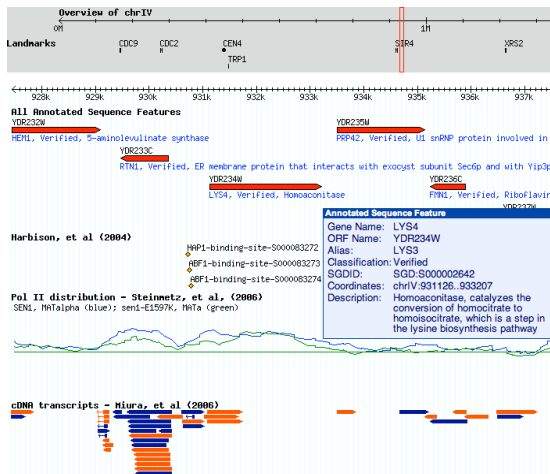
Use multiple search criteria.

- Select features (e.g. ORF, tRNA, etc.)
- Narrow results by sequence & annotations; essentiality; protein properties; function, process, or localization

## GBrowse Genome Browser

[www.yeastgenome.org/gbrowse](http://www.yeastgenome.org/gbrowse)

View the genome with this customizable, dynamic map where annotated features or your own annotations are displayed on multiple "tracks".



# Investigate a Gene's Function

## Phenotypes

[www.yeastgenome.org/phenotypes](http://www.yeastgenome.org/phenotypes)

Find a gene's mutant phenotypes (e.g. *pet8*)

8 Single Mutant Phenotypes for PET8/YNL003C				
Mutant Information	Strain background	Phenotype	Chemical	References
Description: null	S288C	auxotrophy	biotin	Marobbio CM, et al. (2003) Identification and functional reconstitution of yeast mitochondrial carrier for S-adenosylmethionine. <i>EMBO J</i> 22(22):5975-82
Description: null	S288C	respiratory growth rate: absent		Marobbio CM, et al. (2003) Identification and functional reconstitution of yeast mitochondrial carrier for S-adenosylmethionine. <i>EMBO J</i> 22(22):5975-82

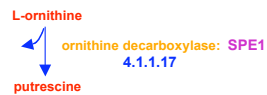
Find genes with a specific mutant phenotype (e.g. affecting *respiratory growth rate*)

Single Mutant Phenotypes for <i>respiratory growth rate</i>				
Gene Name	Mutant Information	Strain background	Phenotype	References
AGC1/YPR021C	Description: null	W303	respiratory growth rate: decreased	Cavero S, et al. (2003) Identification and metabolic role of the mitochondrial aspartate-glutamate transporter in <i>Saccharomyces cerevisiae</i> . <i>Mol Microbiol</i> 50(4):1287-99
AIM11/YER093C-A	Description: null	S288C	respiratory growth rate: decreased	Steinmetz LM, et al. (2002) Systematic screen for human disease genes in yeast. <i>Nat Genet</i> 31(4):400-4

## Biochemical Pathways

[www.yeastgenome.org/pathways](http://www.yeastgenome.org/pathways)

Explore yeast biochemistry with this dynamic display of enzymatic pathways. Browse or search by gene/protein, pathway name, compound, or E.C. number.



## Interactions

[www.yeastgenome.org/interactions](http://www.yeastgenome.org/interactions)

Sort genetic and protein-protein interactions.

Distinct Interactions for PH08/YDR481C						
Feature	Gene	Description	Experiment Type	Type	Action	Reference
YBR200W	BEM1	Protein containing SH3-domains	Co-fractionation	physical interactions	Bait	Xu H and Wickner W (2006) Bem1p is a positive regulator of the homotypic fusion of yeast vacuoles.
YNL009W	LST8	Protein required for the transport of amino acid permease Gao1p from	Co-fractionation	physical interactions	Bait	Arnoova S, et al. (2007) Probing the Membrane Environment of the TOR Kinase Reveals Functional
YOR036W	PEP12	Target membrane receptor	Phenotypic Enhancement	genetic interactions	Bait	Cowles CR, et al. (1997) Novel Golgi to vacuole delivery pathway in yeast: identification of a sorting

# View Protein Properties, Structure & Homology

## Protein Information

[www.yeastgenome.org/protein](http://www.yeastgenome.org/protein)

Find basic information about a protein, links to detailed data and predictions, and protein-specific tools, including:

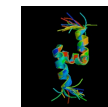
- Sequence
- Protein domains & motifs
- Transmembrane domains
- Signal peptide cleavage sites

## Protein Structure

[www.yeastgenome.org/structures](http://www.yeastgenome.org/structures)

Find yeast & homologous protein structures.

PDB protein structure(s) homologous to RAD54	Homolog Source (per PDB)	Protein Alignment: RAD54 vs. Homolog		
		P-Value	%Identical	%Similar
1z3l (Chain: X) Structure of the swi2/snf2 chromatin remodeling domain of eukaryotic rad54	Danio rerio	3.6e-137	50	23
1z63 (Chain: B, A) Sulfolobus solfataricus swi2/snf2 atpase core in complex with dsdna	Sulfolobus solfataricus	Chain B = 1.1e-37 Chain A = 1.1e-37	28	31



View the structure, sequence, and where it aligns with the yeast protein (e.g. *Rad54p*)

## P-POD

Princeton Protein Orthology Database  
[ortholog.princeton.edu](http://ortholog.princeton.edu)

Find experimentally confirmed orthologs in several species.

