

Yeast Biochemical Pathways Tool

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SGD

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About *S. cerevisiae*

- Simplest eukaryotic unicellular organism
- Its power:
 - Model organism to study genetics, cellular processes
 - Several industrial applications

About SGD

Online database for the genomic sequence, genetics and molecular biology of *Saccharomyces cerevisiae*, commonly known as baker's or budding yeast.

**Saccharomyces Genome Database**
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- **Homology & Comparisons**
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- **Function & Expression**
[Protein Info](#), [Function/Junction](#), [Pathways](#), [Expression](#), [Connections](#), and more.
- **GO Resources**
[GO Tutorial](#), [What is GO?](#), [GO Slim Mapper](#), [GO Term Finder](#), and more.
- **Community Info**
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SGD™ is a scientific database of the molecular biology and genetics of the yeast *Saccharomyces cerevisiae*, which is commonly known as baker's or budding yeast.

New and Noteworthy

- **Updated transcription factor binding site data**
The transcription factor binding sites published by [Hartshorn, et al. \(2004\)](#) have been remapped to the current *S. cerevisiae* genes in GBrowse and in the "Regulatory Role" section on the Locus Summary Pages (see [SUM1](#)). In addition, the regulatory map data available from the [ETP site](#). Thanks to Kenzie MacIsaac for providing information to remap the binding sites and new data to SGD.
- **SGD Curation News**
 - [Genome Snapshot](#)
 - New papers added to SGD this week.
 - View [Genome-wide Analysis papers](#) in SGD.
 - Do a [literature search](#).
 - [Table of Gene Summary Paragraphs](#) (new ones highlighted yellow).
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- **Changes to the Systematic Sequence**
As new data become available, SGD curators update the systematic sequence and its annotation. Information regarding sequence in the [Table of Sequence Updates](#) and in the "Locus History" pages of affected features. Files on the SGD [ETP site](#) are updated.
- **Between 2006-04-15 and 2006-05-12**, sequence and/or annotation changes were made affecting 16 features ([UTR4](#), [YEL038W](#), [KKQ8](#), [YKL168C](#), [CAF4](#), [YKR036C](#), [SEN15](#), [YMR059W](#), [ZIM17](#), [YNI310C](#), [SPS19](#), [YNI202W](#), [MCA1](#), [YOR197W](#), [CEN1](#), [CEN9](#), and [CEN16](#)). (Posted May 12, 2006)
- **SGD Quarterly Newsletter Available**
SGD has sent out the quarterly newsletter to colleagues designated as contacts in SGD. An [expanded HTML version](#) is also available by email in the future, please use the [SGD Colleague Submission/Update form](#) to let us know. (Posted May 1, 2006)
- **Links to eukaryotic Orthology (YOGY) tool added**
Links to eukaryotic Orthology (YOGY), a tool to view orthologous proteins from eukaryotic organisms (*Homo sapiens*, *Mus musculus*, *Arabidopsis thaliana*, *Drosophila melanogaster*, *Caenorhabditis elegans*, *Plasmodium falciparum*, *Schizosaccharomyces pombe*) have been added to the [Model Organism BLAST Best Hits](#) page and the Comparison Resources pull-down menu on the Locus information from KOGs, Inparanoid, Homologene, OrthoMCL, and manually curated orthologs between *S. cerevisiae* and *S. pombe*. [Pavletti CJ, Morris JA, Wood Y, and Babler J](#) (Wellcome Trust Sanger Institute, Cambridge, UK). (Posted April 19, 2006)
- Previous New and Noteworthy items are listed in [What's New in SGD in 2006?](#)

URA2/YJL130C Summary

Summary | Locus History | Literature | Gene Ontology | Phenotype | Interactions | Expression | Protein


[Alternative single page format](#)

URA2 BASIC INFORMATION [[View References](#)]

Standard Name	URA2
Systematic Name	YJL130C
Feature Type	ORF, Verified
Description	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP (1, 2, 3, 4, 5 and see Summary Paragraph)
GO Annotations	URA2 GO evidence and references
Molecular Function	<ul style="list-style-type: none">• aspartate carbamoyltransferase activity (IDA)• carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity (IDA)
Biological Process	<ul style="list-style-type: none">• de novo pyrimidine base biosynthesis (TAS)• glutamine metabolism (IDA)• pyrimidine base biosynthesis (IDA)
Cellular Component	<ul style="list-style-type: none">• cytoplasm (IDA)• integral to membrane (IDA)• mitochondrion (IDA)
Pathways	<ul style="list-style-type: none">• de novo biosynthesis of pyrimidine ribonucleotides• superpathway of histidine, purine, and pyrimidine biosynthesis
Name Description	URAcil requiring 5, 7
Gene Product	aspartate transcarbamylase carbamoyl phosphate synthetase (CPSase) glutamine amidotransferase
Mutant Phenotype	URA2 Phenotype details and references Order mutant strains used in the systematic deletion project
Systematic deletion	• viable
Free text	• uracil requiring
Interactions	URA2 All Interactions details and references
Physical Interactions	URA2 Physical Interactions details and references
Affinity Capture-MS	There are 43 total Affinity Capture-MS interactions
Genetic Interactions	URA2 Genetic Interactions details and references
Synthetic Rescue	There are 3 total Synthetic Rescue interactions resulting in the following phenotype: wildtype
Sequence Information	ChrX:172286 to 165642 ORF Map GBrowse <i>Note: this feature is encoded on the Crick strand.</i>

URA2 RESOURCES

Click on map for expanded view
SGD ORF map | GBrowse



- **Literature**
Literature Guide | [View](#)
- **Retrieve Sequences**
Genomic DNA | [View](#)
- **Sequence Analysis Tools**
BLASTP | [View](#)
- **Protein Info & Structure**
Protein Info | [View](#)
- **Localization Resources**
CFP DB at UCSF | [View](#)
- **Interactions**
BioGRID (Toronto) | [View](#)
- **Phenotype Resources**
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6604 protein coding genes

<http://www.yeastgenome.org>

Building Yeast Biochemical Pathways

- Used GO Function ontology annotations
 - EC2GO mapping
- Gene product or Description field information
 - Matches 'ase', manual mapping
- Initial build done with 731 genes
- We have 6604 protein coding genes in the database

Summary

Total number of genes: 731

EC # matches: 635

Function name matches: 17
(no E.C. available)

Failed matches: 79
(many turned out to be protein kinases, tRNA modification, or ergosterol biosynthesis genes)

Pathways Predicted: 125

Reactions mapped: 652

□ Initial Cleanup after Build

- Resolve ambiguous EC numbers
- Fill in missing reactions
- Delete pathways that don't occur in yeast
- Add pathways unique to yeast
- Contribute new pathways to MetaCyc

Curation

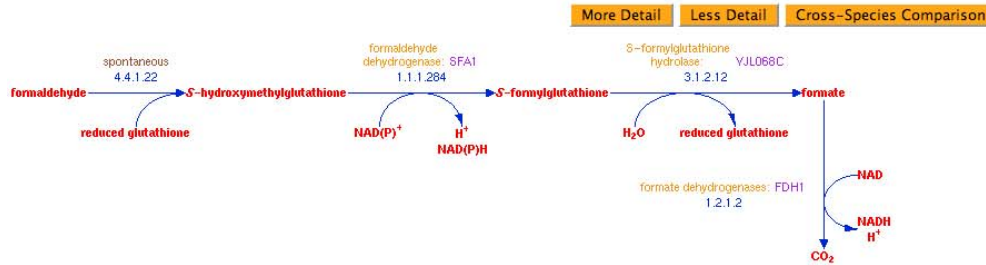
- Types of pathway information captured:
 - References
 - Summary paragraph
 - Evidence code
 - Reactions; EC numbers
 - Genes and gene product references
- Compound IDs from KEGG, CheBI, PubChem

Current Statistics: 154 pathways, 460 genes

Available for download from our FTP site

Curated Pathway

S. cerevisiae Pathway: formaldehyde oxidation II (glutathione-dependent)



Locations of Mapped Genes:



Synonyms: formaldehyde oxidation II (GSH-dependent)

Superclasses: [Degradation/Utilization/Assimilation](#) -> [C1 Compounds](#)

Comment:

Formaldehyde is formed by oxidative demethylation reactions in many plants and methylotrophic organisms, but *Saccharomyces cerevisiae* is a nonmethylotrophic yeast and cannot metabolize methanol to formaldehyde. However, *S. cerevisiae* is exposed to exogenous formaldehyde from plant material or in polluted air and water. Concentrations of formaldehyde of 1mM or higher are cytostatic or cytotoxic to haploid wild-type cells.

Any free formaldehyde in vivo spontaneously reacts with glutathione to form S-hydroxymethylglutathione [[Achkor03](#)], [[Grey96](#)], [[Degrassi99](#)]. The level of enzymes involved in the degradation of formaldehyde, such as Sfa1p and Yj1068p, determine the level of formaldehyde toxicity, and cells overproducing Sfa1p are resistant to formaldehyde and null mutants in either *sfa1* or *yj1068c* are hypersensitive to formaldehyde. Sfa1p is induced in response to chemicals such as formaldehyde (FA), ethanol and methyl methanesulphonate, and Yj1068p is also induced in response to chemical stresses [[Wehner93](#)], [[Grey96](#)], [[Degrassi99](#)], [[Wehner93a](#)], [[GompelKlei89](#)], [[Jelinsky99](#)], [[Schaus01](#)].


Formate dehydrogenase is encoded by FDH1/YOR388C and FDH2. In some strain backgrounds of *S. cerevisiae*, FDH2 is encoded by a continuous open reading frame comprised of YPL275W and YPL276W. However, in the systematic sequence of S288C, FDH2 is represented by these two separate open reading frames due to an in frame stop codon [[Overkamp02](#)].

References

- [Achkor03](#): Achkor H, Diaz M, Fernandez MR, Biosca JA, Pares X, Martinez MC (2003). "Enhanced formaldehyde detoxification by overexpression of glutathione-dependent formaldehyde dehydrogenase from *Arabidopsis*." *Plant Physiol* 132(4):2248-55. PMID: 12913179
- [Degrassi99](#): Degrassi G, Uotila L, Kilma R, Venturi V (1999). "Purification and properties of an esterase from the yeast *Saccharomyces cerevisiae* and identification of the encoding gene." *Appl Environ Microbiol* 65(8):3470-2. PMID: 10427036
- [GompelKlei89](#): Gompel-Klein P, Mack M, Brendel M (1989). "Molecular characterization of the two genes SNQ and SFA that confer hyperresistance to 4-nitroquinoline-N-oxide and formaldehyde in *Saccharomyces cerevisiae*." *Curr Genet* 16(2):65-74. PMID: 2557161
- [Grey96](#): Grey M, Schmidt M, Brendel M (1996). "Overexpression of ADH1 confers hyper-resistance to formaldehyde in *Saccharomyces cerevisiae*." *Curr Genet* 29(5):437-40. PMID: 8625422
- [Jelinsky99](#): Jelinsky SA, Samson LD (1999). "Global response of *Saccharomyces cerevisiae* to an alkylating agent." *Proc Natl Acad Sci U S A* 96(4):1486-91. PMID: 9990050
- [Overkamp02](#): Overkamp KM, Kotter P, van der Hoek R, Schoondermark-Stolk S, Luttkik MA, van Dijken JP, Pronk JT (2002). "Functional analysis of structural genes for NAD(+)-dependent formate dehydrogenase in *Saccharomyces cerevisiae*." *Yeast* 19(6):509-20. PMID: 11921099

How did we integrate Pathways with other resources?

From the home page, from Quick Search box, from individual locus pages



Saccharomyces Genome Database

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Quick search results



Quick Search:

ergosterol biosyn

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SGD Quick Search Result

[Go to Advanced Search Page](#)

Below are the search results for your query, **ergosterol biosynthesis**. If you would like to broaden your search, you may use one or more wildcard characters (*) to indicate the location(s) where any text will be tolerated in your search term.

Search Results for : **ergosterol biosynthesis**

- 0 Gene names (gene name/alias/ORF name)
- 0 Gene products
- [1 Gene Ontology terms \(GO terms, synonyms\)](#)
- 0 Colleagues (by last name)
- 0 Authors (by last name, first initial)
- [1 Biochemical pathways](#)
- [15 Descriptions](#)
- 0 PubMed ID
- 0 Gene Ontology ID

Yeast Biochemical Pathways



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Yeast Biochemical Pathways

This page offers tools for visualizing biochemical pathways of *Saccharomyces cerevisiae* at SGD.

[Help](#)

- [Main Query Page for Yeast Biochemical Pathways](#)
Main query page for searching Pathways, Reactions, Enzymes by name or EC number, Compounds and more.
- [Metabolic Map](#)
A 'bird's eye' view of *S.cerevisiae* metabolism. (This page could take a moment to load).
- [Expression Viewer](#)
Overlay expression data on the Metabolic map.

Yeast Biochemical Pathways are created using the Pathway tools software developed by Peter Karp and his colleagues at [SRI International](#). The current datasets of pathways at SGD were generated using the Pathway Tool's PathoLogic module, which generates an initial set of pathways by comparing SGD annotations to a reference database ([MetaCyc](#)). Although PathoLogic creates a genome database, this feature is not curated by SGD.

These automatically generated pathways are then manually curated and corrected, based on published *S.cerevisiae* literature. When necessary, yeast-specific biochemical pathways are added. Since the functions of many of the yeast genes are not yet known, many of the pathways could be incomplete or may even contain errors. Manual curation of pathways is an ongoing process at SGD and we welcome feedback from the research community. If you notice any problems or errors, please send a message to [SGD curators](#).

For more information about searching and browsing the Yeast Biochemical Pathways, please read the [help](#) document.

NOTE:

Pathway tools uses a non-standard port (:8555). If you are working behind a firewall, you will not be able to access these pathways at SGD. If this is the case, request your network administrator to open the :8555 port on the firewall.

DOWNLOAD

Yeast Biochemical Pathways datasets can be downloaded from our [ftp site](#).

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From the Locus Summary Pages

URA2/YJL130C Summary

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Molecular Function	<ul style="list-style-type: none">aspartate carbamoyltransferase activity (IDA)carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity (IDA)
Biological Process	<ul style="list-style-type: none">de novo pyrimidine base biosynthesis (TAS)glutamine metabolism (IDA)pyrimidine base biosynthesis (IDA)
Cellular Component	<ul style="list-style-type: none">cytoplasm (IDA)integral to membrane (IDA)mitochondrion (IDA)
Pathways	<ul style="list-style-type: none">de novo biosynthesis of pyrimidine ribonucleotidessuperpathway of histidine, purine, and pyrimidine biosynthesis
Name Description	URAcil requiring 6, 7
Gene Product	aspartate transcarbamylase carbamoyl phosphate synthetase (CPSase) glutamine amidotransferase
Mutant Phenotype	URA2 Phenotype details and references Order mutant strains used in the systematic deletion project
Systematic deletion	<ul style="list-style-type: none">viable
Free text	<ul style="list-style-type: none">uracil requiring
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Sequence Information	ChrX:172286 to 165642 ORF Map GBrowse Note: <i>this feature is encoded on the Crick strand.</i>

URA2 RESOURCES

Click on map for expanded view

SGD ORF map 165000 to 170000

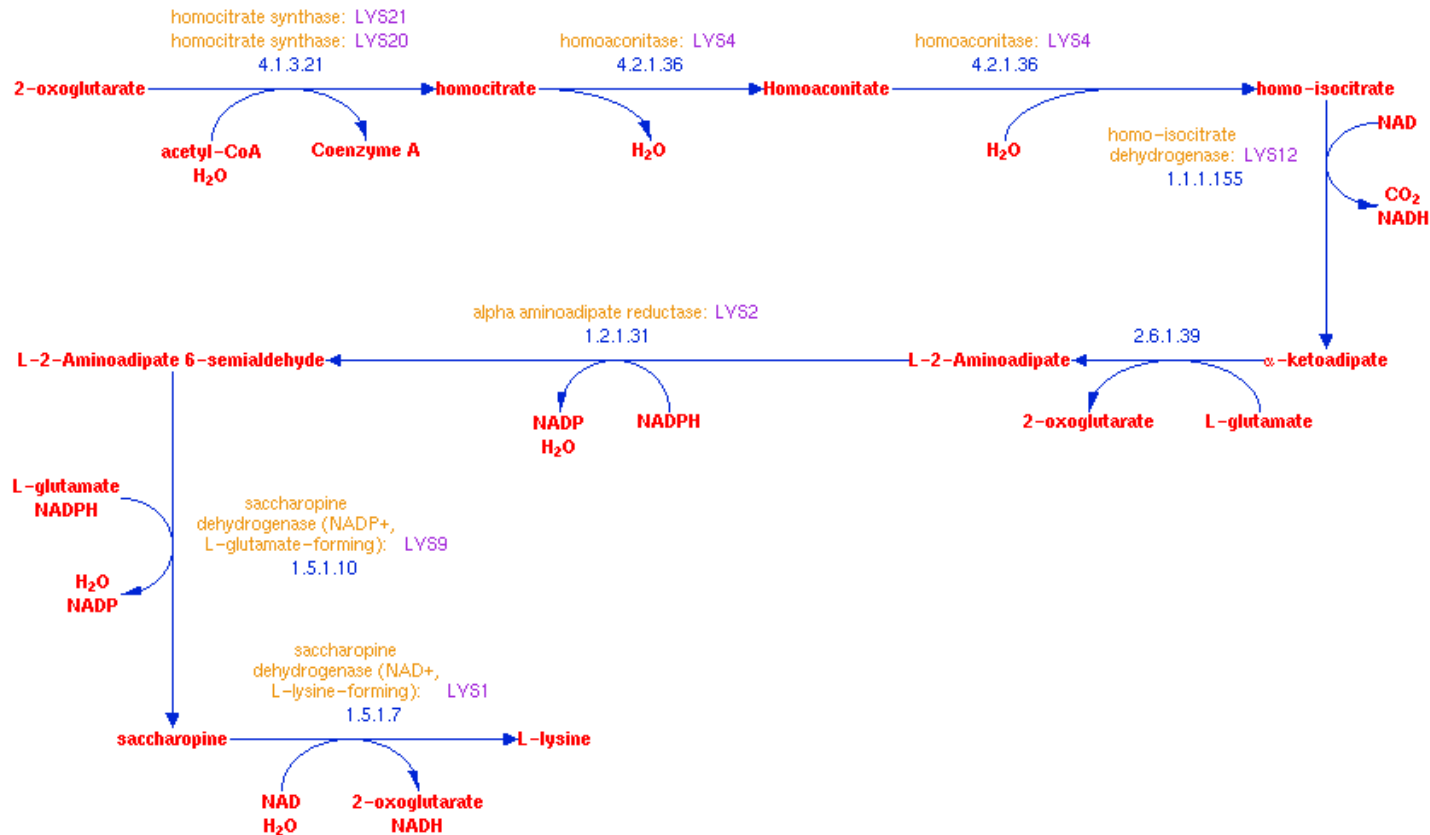
GBrowse chrX 170k

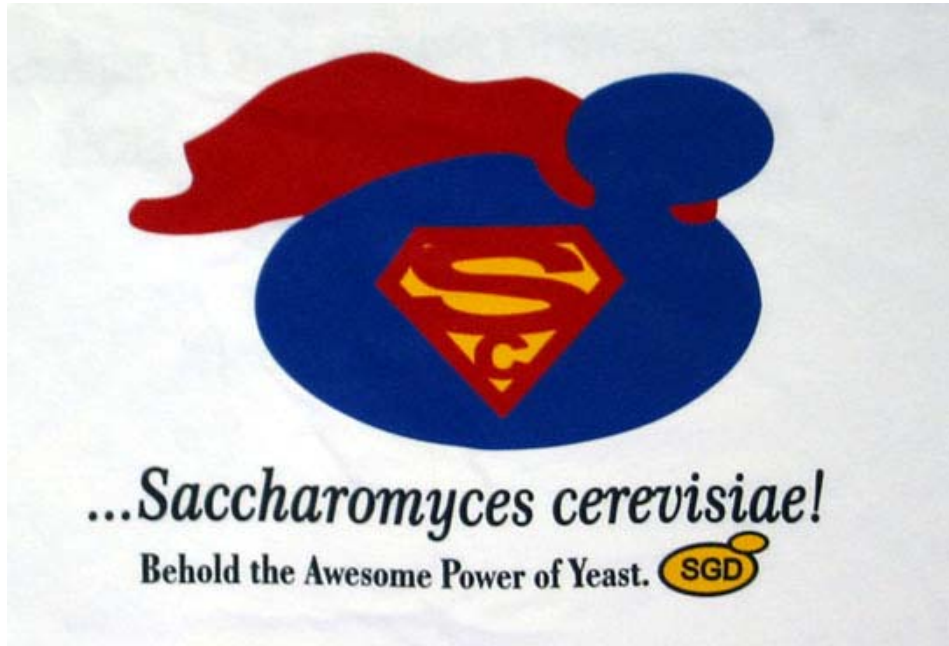
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Chromosomal Features Map
- Comparison Resources**
PSI-BLAST Results

Lysine Biosynthesis - Detailed View

S. cerevisiae Pathway: lysine biosynthesis

More Detail Less Detail Cross-Species Comparison





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