Yeast Biochemical Pathways Tool

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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.

6604 protein coding genes

http://www.yeastgenome.org
Lysine Biosynthesis from KEGG
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 egosterol 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)

Supertclasses: Degradation/Utilization/Assimilation → C1 Compounds

Comment:

Formaldehyde is formed by oxidative demethylation reactions in many plants and methylophilic organisms, but *Saccharomyces cerevisiae* is a non-methylophilic 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 1ppb or higher are cytostatic or cytotoxic to haploid wild-type cells. Any free formaldehyde in vivo spontaneously reacts with glutathione to form S-hydroxymethylglutathione. The level of enzymes involved in the degradation of formaldehyde, such as Sfo1p and Yj088p, determine the level of formaldehyde toxicity, and cells overproducing Sfo1p are resistant to formaldehyde and null mutants in either Sfo1p or Yj088p are hypersensitive to formaldehyde. Sfo1p is induced in response to chemicals such as formaldehyde (FA), ethanol and methyl mercaptan, and Yj088p is also induced in response to chemical stresses. Formate dehydrogenase is encoded by FDH1/YPD3888C 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 SGD, FDH2 is represented by these two separate open reading frames due to an in-frame stop codon.

References


Degrazia, G., Joo, S., & Thompson, J. (1999). "Molecular characterization of the two genes SNO and SFA that confer hyper-resistance to 4-citroquinoline-N-oxide and formaldehyde in *Saccharomyces cerevisiae*." Curr Genet 26(1):69-74. PMID: 10519461


How did we integrate Pathways with other resources?

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

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/atlas/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

This page offers tools for visualizing biochemical pathways of \textit{Saccharomyces cerevisiae} at SGD.

- **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 \textit{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 \textit{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 curator.

For more information about searching and browsing the Yeast Biochemical Pathways, please read the help document.

**NOTE:**
Pathway tools use 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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 ↑Return to SGD
From the Locus Summary Pages

<table>
<thead>
<tr>
<th>Standard Name</th>
<th>URA2</th>
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<tbody>
<tr>
<td>Systematic Name</td>
<td>YJL130C</td>
</tr>
<tr>
<td>Feature Type</td>
<td>ORF, Verified</td>
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<tr>
<td>Description</td>
<td>Bi-functional carboxymethylase 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)</td>
</tr>
<tr>
<td>GO Annotations</td>
<td><a href="#">URA2 GO evidence and references</a></td>
</tr>
<tr>
<td>Molecular Function</td>
<td>aspartate carbamoyltransferase activity (DA)</td>
</tr>
<tr>
<td>Biological Process</td>
<td>pyrimidine base biosynthesis (DA)</td>
</tr>
<tr>
<td>Cellular Component</td>
<td>cytoplasm (DA)</td>
</tr>
<tr>
<td>Pathways</td>
<td>de novo biosynthesis of pyrimidine ribonucleotides, superpathway of histidine, purine, and pyrimidine biosynthesis</td>
</tr>
<tr>
<td>Gene Product</td>
<td>aspartate transcarbamylase, carbamoyl phosphate synthetase (CPSase), glutamine amidotransferase</td>
</tr>
<tr>
<td>Mutant Phenotype</td>
<td><a href="#">URA2 Phenotype details and references</a></td>
</tr>
<tr>
<td>Systematic deletion</td>
<td>Visible</td>
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<td>Free text</td>
<td>uracil requiring</td>
</tr>
<tr>
<td>Interactions</td>
<td><a href="#">URA2 All Interactions details and references</a></td>
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<tr>
<td>Physical Interactions</td>
<td><a href="#">URA2 Physical Interactions details and references</a></td>
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<tr>
<td>Affinity Capture-MS</td>
<td>There are 43 total Affinity Capture-MS interactions</td>
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<tr>
<td>Genetic Interactions</td>
<td><a href="#">URA2 Genetic Interactions details and references</a></td>
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<tr>
<td>Synthetic Rescue</td>
<td>There are 1 total Synthetic Rescue interactions resulting in the following phenotype: wildtype</td>
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<tr>
<td>Sequence Information</td>
<td><a href="#">ChX:172286 to 165642</a></td>
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</table>
Lysine Biosynthesis - Detailed View

S. cerevisiae Pathway: lysine biosynthesis