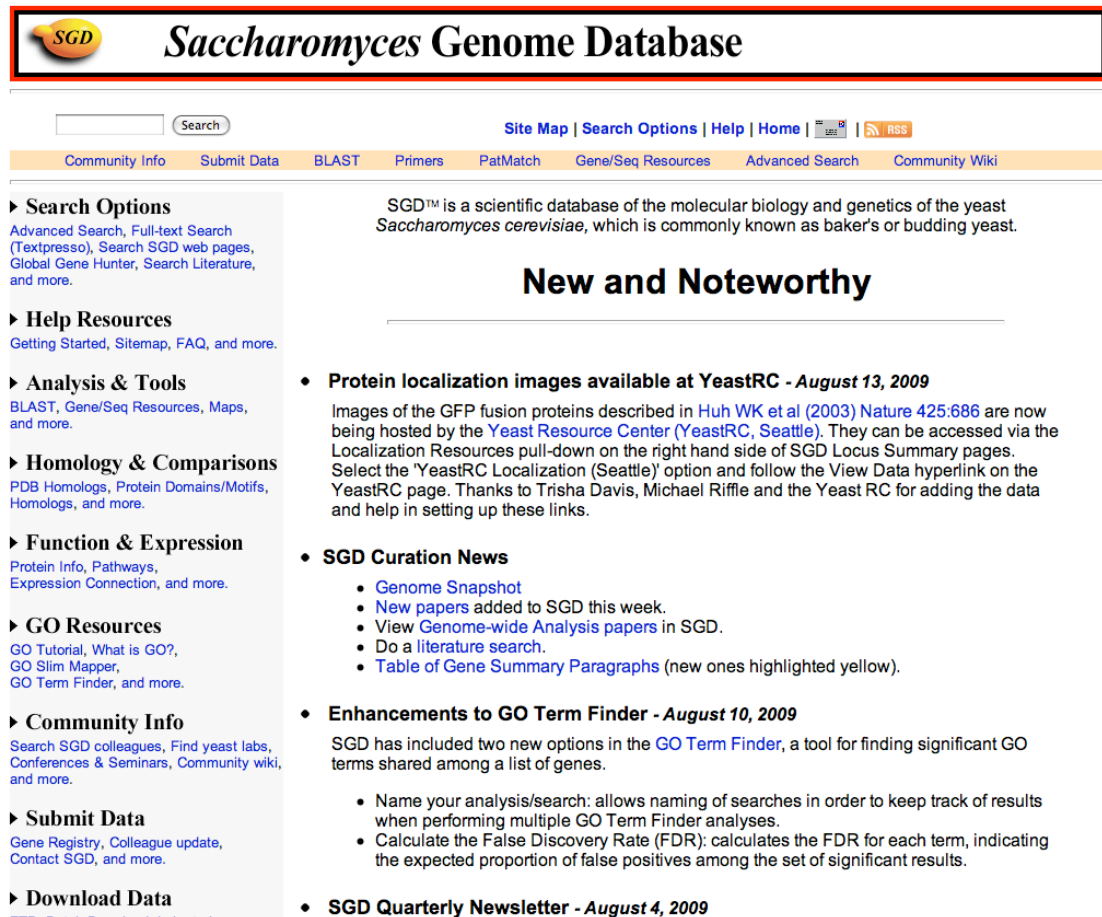




# Curation and Integration of Pathway Tools at the *Saccharomyces* Genome Database



 **Saccharomyces Genome Database**

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Getting Started, Sitemap, FAQ, and more.

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BLAST, Gene/Seq Resources, Maps, and more.

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PDB Homologs, Protein Domains/Motifs, Homologs, and more.

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Protein Info, Pathways, Expression Connection, and more.

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GO Tutorial, What is GO?, GO Slim Mapper, GO Term Finder, and more.

► **Community Info**  
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Gene Registry, Colleague update, Contact SGD, and more.

► **Download Data**  
FTP, Bulk Download, etc.

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

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  - [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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- **SGD Quarterly Newsletter - August 4, 2009**

<http://www.yeastgenome.org/>



# Scientific community



Sequences

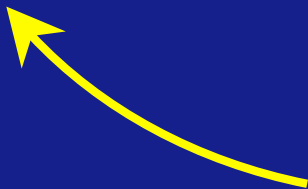
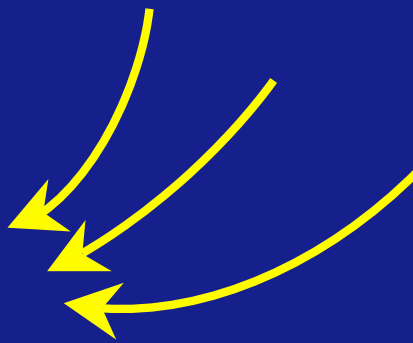
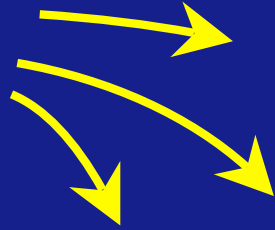
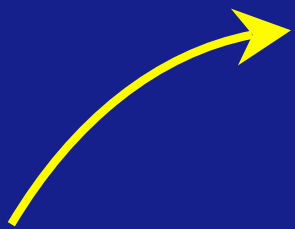
Phenotypes

Interactions

Functional Genomics

Biochemical Pathways

Gene Structures



<http://www.yeastgenome.org/>

**SGD Saccharomyces Genome Database**

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Search

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Tools

News and updates



# Locus Summary Page

Nomenclature



Free text summaries  
of published data



Curated data from  
published literature  
using controlled  
vocabularies



Sequence information



Links to other  
databases



References



**VIP1 BASIC INFORMATION**

Standard Name: VIP1  
Systematic Name: YLR410W  
Feature Type: ORF, Verified  
Description: Inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) kinases: generation of IP7 by Vip1 is important for phosphate signaling; likely involved in cortical actin cytoskeleton function, by analogy with *S. pombe* ortholog *asp1* (1, 2, 3 and see [Summary Paragraph](#))

**VIP1 RESOURCES**

Click on map for expanded view  
SGD ORF map | GBrowse

**Literature**  
Literature Guide (2) | View

**Retrieve Sequences**  
Genomic DNA (2) | View

**Sequence Analysis Tools**  
BLASTP (2) | View

**Protein Info & Structure**  
Protein info (2) | View

**Localization Resources**  
YeastRC Localization Seattle (2) | View

**Interactions**  
BioGRID (Toronto) (2) | View

**Phenotype Resources**  
PROPECY (2) | View

**Maps & Displays**  
Chromosomal Features Map (2) | View

**Comparison Resources**  
PSI-BLAST Results (2) | View

**Functional Analysis**  
Expression Connection Summary (2) | View

Click on histogram for expression summary  
Expression Summary

Number of Experiments vs. Log<sub>2</sub> Ratios

Log<sub>2</sub> Ratio: -4 -3 -2 -1 0 1 2  
Aug 23, 2009

**ADDITIONAL INFORMATION FOR VIP1**

Community wiki	Domains/Motifs	Expression Connection	Gene/Sequence Resources
Global Gene Hunter	Locus History	PDB Homologs	Protein Info
Researchers			

**SUMMARY PARAGRAPH FOR VIP1**

VIP1 encodes one of two yeast inositol pyrophosphate synthases (also known as inositol hexakisphosphate kinases; IP6Ks); the other is encoded by *KCS1*. The inositol pyrophosphates (PP-IPs) produced by *Kcs1p* and/or *Vip1p* serve as high-energy signaling molecules involved in such diverse processes as vacuolar biogenesis, the stress response, DNA repair, cell wall synthesis, telomere maintenance, and phosphate homeostasis (see 4, 5, 6, and references therein).

Both enzymes catalyze the addition of beta-phosphate to the fully phosphorylated six-carbon ring of inositol hexakisphosphate (IP6). However, these enzymes produce different isomers of diphosphoinositol pentakisphosphate (IP7). *Kcs1p* phosphorylates IP6 at the C3 position forming SPP-IP6, and *Vip1p* phosphorylates IP6 at the C4 or C5 position forming 4PP-IP6 or 5PP-IP6, respectively (the exact phosphorylation position has not yet been determined). The different IP7 isomers are biologically relevant: the *Kcs1p* product cannot substitute for the *Vip1p* product during phosphate homeostasis (2). *Kcs1p* and *Vip1p* also work in concert to produce bis-diphosphoinositol tetakisphosphate (PP2-IP4; IP8). *Kcs1p* phosphorylates the *Vip1p* IP7 product 4SPP-IP6, and *Vip1p* phosphorylates the *Kcs1p* IP7 product SPP-IP6 (3).

Inositol pyrophosphate synthases are highly conserved and found across eukaryotes. In humans, three *Kcs1p*-like enzymes (IPK1/IP6K1, IPK2/IP6K2, IPK3/IP6K3) (7, 8) and two *Vip1p*-like enzymes (HISPPD2a/PPiPSK1/VIP1 and PPiPSK2/VIP2) (9, 10) have been identified.

Last updated: 2008-01-22

**REFERENCES CITED ON THIS PAGE** [View Complete Literature Guide for VIP1]

1) Feoktistova A, et al. (1999) Identification and characterization of Schizosaccharomyces pombe *asp1*(+), a gene that interacts with mutations in the Arp2/3 complex and actin. *Genetics* 152(3):895-908

Links to SGD tools  
and other databases



Data from  
high throughput  
experiments

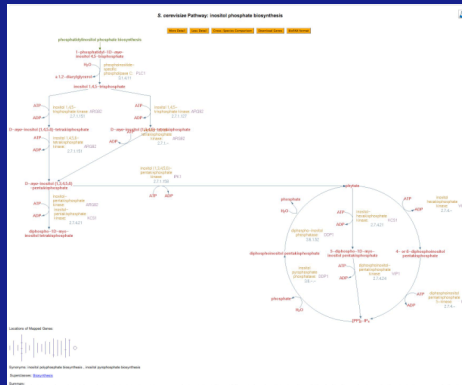




# Creating YeastCyc

(circa 2002)

## MetaCyc (PathoLogic)



+

## Gene Ontology (use GO2EC mapping)

GO Annotations

All **KCS1** GO evidence and references  
View Computational GO annotations for **KCS1**

**Molecular Function**  
Manually curated

- inositol 1,3,4,5,6-pentakisphosphate kinase activity (IDA)
- inositol heptakisphosphate 5-kinase activity (SS)
- inositol heptakisphosphate kinase activity (IDA)
- inositol hexakisphosphate kinase activity (IDA)

**Biological Process**  
Manually curated

- inositol phosphate biosynthetic process (DA, IMP)
- negative regulation of transcription, RNA-mediated (IMP)
- response to drug (IMP)

**Cellular Component**  
High-throughput

- cytoplasm (DA)

**Pathways**

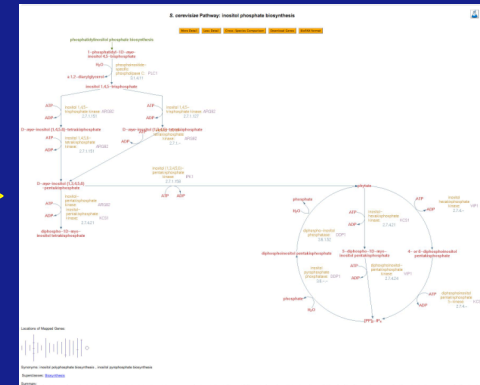
- inositol phosphate biosynthesis

Retrieval Tools

- Retrieve Sequences
  - Genomic DNA
- Sequence Analysis Tools
  - BLASTP
- Protein Info & Structure
  - Protein Info
- Localization Resources
  - GFP DB at UCSF
- Interactions
  - BioGRID (Toronto)
- Phenotype Resources
  - Phenotype



## YeastCyc



# Curation of YeastCyc

Experimental evidence

**S. cerevisiae Pathway: inositol phosphate biosynthesis**

**Locations of Mapped Genes:**

**Synonyms:** inositol polyphosphate biosynthesis, inositol phosphorylate biosynthesis

**Superclasses:** Biosynthesis

**Summary:**  
 Inositol phosphates (IPs) are an important class of signaling molecules that regulate cellular processes such as transcription, mRNA export, DNA repair, chromatin remodeling, glucose-induced calcium signaling, telomere elongation, vacuolar biogenesis, the stress response, cell wall synthesis and phosphate homeostasis (reviewed in [1,204] and [205]).

**References:**

Bennett98, Bennett M, Onrabe SM, Azevedo C, Saikat A (2008). "Inositol polyphosphates: metabolism and signaling." *Cell Mol Life Sci* 636:552-64. PMID: 16429206

Dube92, Dubois C, Scherens B, Vandenbosch F, Ho MM, Messeroux F, Shears SB (2002). "In *Saccharomyces cerevisiae*, the inositol polyphosphate kinase activity of Kcs1p is required for resistance to salt stress, cell wall integrity, and vacuolar morphogenesis." *J Biol Chem* 277(26):23758-63. PMID: 11960013

Flick99, Flick JS, Thoner J (1999). "Genetic and biochemical characterization of a phosphatidylinositol-specific phospholipase C in *Saccharomyces cerevisiae*." *Mol Cell Biol* 19(9):5861-76. PMID: 8395019

Itaya06, Ito H, Nichols J, Wente SR, York JD (2006). "Biochemical and functional characterization of inositol 1,4,4,5,5,6-pentakisphosphate 2-kinase." *J Biol Chem* 281(47):36575-83. PMID: 16950485

Mulvaney07, Mulvaney B, Bai W, Fridy JC, Bastidas SI, Cho JC, Dolina DE, Haystead TA, Ribeiro AA, York JD (2007). "A conserved family of enzymes that phosphorylate inositol hexakisphosphate." *Science* 316(5841):1106-9. PMID: 17412568

Odeon07, Odeon AR, Stambiers A, Wente SR, York JD (2008). "A role for nuclear inositol 1,4,5-tetraphosphate kinase in transcriptional control." *Science* 320(5868):2008-9. PMID: 18720331

Rafany09, Rafany ST, Rogers SW, Carafoli J, Flick JS, Molnar AG, Barnea LD, Shears SB (1999). "The diadenosine hexaphosphate hydrolases from *Schizosaccharomyces pombe* and *Saccharomyces cerevisiae* are homologues of the human dihydroinostol polyphosphate phosphatases. Overexpression of these phosphatases in a *Medicago sativa* strain." *J Biol Chem* 274(21):17246-50. PMID: 10519398

Saikat98, Saikat A, Caffrey JJ, Snyder SH, Shears SB (2000). "Inositol polyphosphate multikinase (Arp81) determines nuclear mRNA export in *Saccharomyces cerevisiae*." *FEBS Lett* 468(1):28-32. PMID: 10955430

Saikat99, Saikat A, Caffrey JJ, Snyder SH, Shears SB (2000). "The inositol hexakisphosphate kinase family: Catalytic flexibility and function in yeast vacuole biogenesis." *J Biol Chem* 275(32):24886-92. PMID: 10827188

Saikat99, Saikat A, Erdmann-Brönner H, Smeeman AM, Tempest P, Snyder SH (1999). "Synthesis of dihydroinostol pentakisphosphate by a newly identified family of higher inositol polyphosphate kinases." *Curr Biol* 9(21):1323-6. PMID: 10574790

York\_York\_JD "Regulation of nuclear processes by inositol polyphosphates." *Biochim Biophys Acta* 1761:60-65. PMID: 10781889

Zhang01, Zhang T, Caffrey JJ, Shears SB (2001). "The transcriptional regulator, Arp82, is a hybrid kinase with both monophosphoinositide and dihydroinostol polyphosphate synthase activity." *FEBS Lett* 494(3):208-12. PMID: 11311242

Curate enzymes, reactions, pathways for *S. cerevisiae*

Free text summaries

References

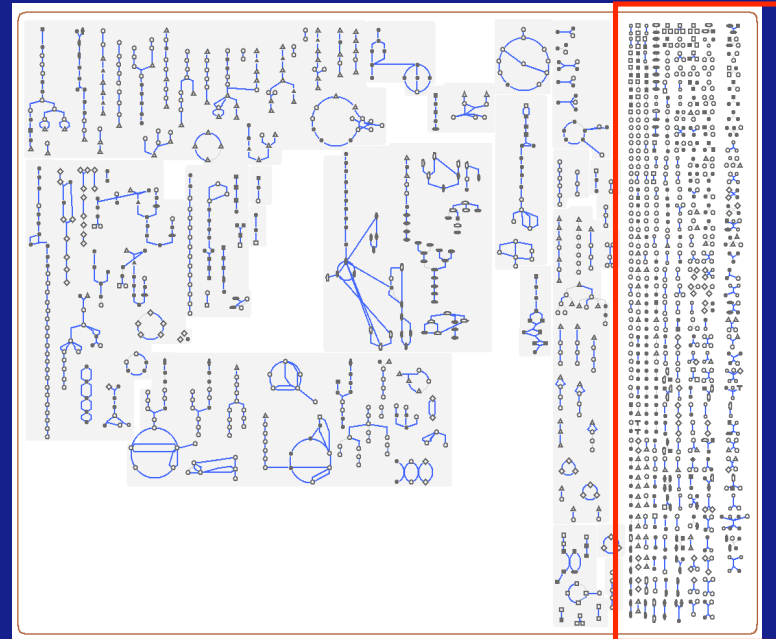


# Curation Status

- All pathways have been manually reviewed
  - \* first pass completed in January 2008
  - \* 140 manually curated pathways as of August 2009
- Addition of fungal-specific pathways
  - \* ergosterol biosynthesis
  - \* chitin (cell wall) biosynthesis
- Continued improvement of pathways as data are published

# Future Curation Plans


- Continued improvement of pathways as data are published
- Reviewing orphan reactions
- Metabolite levels
- Kinetic data



# Searching for Biochemical Pathways

Search





## Saccharomyces Genome Database

Site Map | Search Options | Help | Home | RSS

Community Info | Submit Data | BLAST | Primers | PatMatch | Gene/Seq Resources | Advanced Search | Community Wiki

**Search Options**  
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- SGD Quarterly Newsletter - August 4, 2009**



# Accessing YeastCyc

## SGD Search Result

Search Results for: **inositol** (wildcard character(\*) automatically appended to the end of the query). Expand your search to the full text of yeast literature using [Textpresso](#).

### Curated Gene/Protein Information

- 0 Gene names (standard name/alias/ORF name)
- 28 Descriptions
- 10 Name descriptions
- 0 Gene product aliases
- 35 Paragraphs
- 4 Notes

### Functional Annotations

- 61 Gene product activities (GO Molecular Function)
- 28 Cellular roles or processes (GO Biological Process)
- 0 Protein complexes and locations (GO Cellular Component)
- 1 Biochemical pathways [Expanded Biochemical Pathways Search]
- 0 Phenotypic annotations [Expanded Phenotype Search]

The screenshot displays the SGD query results for 'inositol'. It includes sections for Pathways, Genes, Proteins, and Compounds. A large red arrow points from the 'Biochemical Pathways' section of the search results to the 'inositol phosphate biosynthesis' pathway diagram on the left.

The screenshot shows the SGD search interface. The search bar contains 'inositol' and the results show 3 hits to the 'inositol phosphate biosynthesis' pathway. A large red arrow points from the search results to the pathway diagram on the right.

**S. cerevisiae Pathway: inositol phosphate biosynthesis**

**Legend for Pathway Diagram**

For enzymes there is shown in bold, there is experimental evidence for this enzymatic activity. Location of Mapped Genes.

**Enzymes:** inositol polyphosphate 5-phosphatase, inositol triphosphate 5-phosphatase

**Substrate:** [inositol](#)/IP

**Summary:** Inositol phosphates (IPs) are an important class of signaling molecules that regulate cellular processes such as transcription, mRNA export, DNA repair, chromatin remodeling, glucose-induced calcium signaling, telomere elongation, vacuolar biogenesis, the stress response, cell wall synthesis and phosphate homeostasis (Newman et al., 2004; [SGD:IP]).

The water-soluble IP<sub>6</sub> are derived from the lipid, phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>, PIP<sub>1</sub>, PIP<sub>2</sub>, PIP<sub>3</sub>, PIP<sub>4</sub> hydrolyase PIP<sub>5</sub> to inositol 1,4,5-trisphosphate (IP<sub>3</sub>) and diacylglycerol, missing IP<sub>6</sub> from the membrane [SGD:IP<sub>6</sub>]. IPs are then sequentially phosphorylated to inositol hexakisphosphate (IP<sub>6</sub>) and inositol pentakisphosphate (IP<sub>5</sub>) by the inositol polyphosphate multikinase (IPMK) Argosin [SGD:IP<sub>5</sub>], Gln10 [SGD:IP<sub>6</sub>], and reviewed in [Fus1]. The fully phosphorylated mix of IP<sub>6</sub> is further phosphorylated to the mixed acylated inositol hexakisphosphate perfluorinated phosphatidyl inositol (PIP<sub>2</sub>IP<sub>6</sub>) and its dephosphorylated derivative inositol hexakisphosphate (IP<sub>6</sub>IP<sub>2</sub>, IP<sub>6</sub>IP<sub>1</sub>, IP<sub>6</sub>IP<sub>0</sub>; [SGD:IP<sub>6</sub>IP<sub>2</sub>] reviewed in [Fus1, Fus2] [SGD:IP<sub>6</sub>IP<sub>1</sub>]). Two different forms of PIP<sub>2</sub>IP<sub>6</sub> have been identified, PIP<sub>2</sub>IP<sub>6</sub> synthesized by Kcs1p and 6-*sn*-PIP<sub>2</sub>IP<sub>6</sub> synthesized by Vps1 in the exact phosphorylation position has yet to be determined [Mazzanti]. Kcs1p and Vps1p are believed to work in concert to form PIP<sub>2</sub>IP<sub>6</sub> and the PIP<sub>2</sub>IP<sub>6</sub> product produced by one enzyme is converted to PIP<sub>2</sub>IP<sub>6</sub> by the other enzyme [Mazzanti]. PIP<sub>2</sub>IP<sub>6</sub> was shown to be dephosphorylated to IP<sub>6</sub>IP<sub>2</sub> and IP<sub>6</sub>IP<sub>1</sub> by the phosphatase Shp1p, but the particular isomers are not yet known [Safirina2001].

**Notes:**

Created: 18 Dec 2007 by Kippert C. SGD  
Created: 08 Jun 2008 by Iwatt J. SGD



# Accessing Locus Summaries

SGD Search Result

Your query, **inositol**, returned 3 hit(s) to the following biochemical pathway(s):

Biochemical Pathways	Associated Genes
<a href="#">inositol phosphate biosynthesis</a>	<a href="#">VIP1</a>   <a href="#">KCS1</a>   <a href="#">DDP1</a>   <a href="#">PLC1</a>   <a href="#">IPK1</a>   <a href="#">ARG2</a>

Send a Message to the SGD Curators

S. cerevisiae Pathway: inositol phosphate biosynthesis

Legend for Pathway Diagram: If an enzyme name is shown in bold, there is experimental evidence for this enzymatic activity. Locations of Mapped Genes:

Synonym(s): inositol phosphate biosynthesis, inositol phosphate biosynthesis

Supplements: [BioGRID](#)

Summary: Inositol phosphates (IPs) are an important class of signaling molecules that regulate cellular processes such as transcription, mRNA export, DNA repair, chromatin remodeling, glucose-induced calcium signaling, telomere elongation, vacuolar biogenesis, the stress response, cell wall synthesis and phosphate homeostasis (reviewed in [2,6,7] and [8]).

The water-soluble IP is derived from the lipid phosphatidylinositol 4-phosphate (PIP2, PIP2). PIP2 hydrolyzes to inositol 1,4,5-trisphosphate (IP3) and diacylglycerol, releasing IP3 from the membrane [3,9,10]. IP3 is then sequentially phosphorylated to inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) by the inositol hexakisphosphate synthase (IPK) family [10,11]. IP6 is further phosphorylated to inositol octakisphosphate (IP8) phosphorylated to inositol nonakisphosphate (IP9) and inositol decaoctakisphosphate (IP10) by the inositol octakisphosphate synthase (IOS) [12]. The fully phosphorylated form of IP6 is further phosphorylated by the inositol phosphatase phosphatase (IPP) family [13,14]. Two different forms of IPPs have been identified: SPP-IPP synthesized by Kcs1p and Vsp1p, and VPP-IPP synthesized by Vsp1p for the most phosphorylated position has yet to be determined [13,14]. Kcs1p and Vsp1p are believed to use inositol to form IPPs, but the inositol product produced by one enzyme is converted to IPPs by the other enzyme [13,14]. IPPs were shown to be phosphorylated by IPPs and are IP6 by the phosphatases (SPPs), but the cellular functions are not yet known [15].

Created: 16-Jun-2007 by Susan C. Staggs  
Created: 06-Jun-2009 by Susan C. Staggs

VIP1 Locus Summary

VIP1 BASIC INFORMATION

Standard Name: **vip1**  
Systematic Name: YLR410W  
Feature Type: ORF, Verified  
Description: Inositol hexakisphosphate (IP6) and inositol heptakisphosphate (IP7) kinase. Generation of IP7 by Vsp1p is important for phosphate signaling. Kinase generation of cortical actin cytoskeleton function, by analogy with 6-pombe ortholog *asp1* [1, 2, 3 and see Summary Paragraphs]

GO Annotations: All VIP1 GO evidence and references

Molecular Function: Inositol hexakisphosphate kinase activity (IDA), Inositol heptakisphosphate 1-kinase or 2-kinase activity (GOA), IKOT inositol hexakisphosphate 4-kinase or 6-kinase activity (GOA), Inositol heptakisphosphate 4-kinase or 6-kinase activity (GOA)

Biological Process: Inositol phosphate biosynthesis process (GO)

Cellular Component: High-throughput, cytoplasm (GO)

Pathways: inositol phosphate biosynthesis

Mutant Phenotype: All VIP1 Phenotype details and references

Classical genetics: null, viable

Large-scale survey: null, chromatin/histone/maintenance: decreased, resistance to rapamycin: increased, resistance to wortmannin: increased, viable

Interactions: 83 total interaction(s) for 81 unique gene/proteins

Physical Interactions: Affinity Capture MS: 23, Biochemical Activity: 10

Genetic Interactions: Phenotypic Enhancement: 29, Synthetic Suppression: 12, Synthetic Growth Defect: 10, Synthetic Lethality: 4

Sequence Information: ChrXII:837539 to 840979 | DRP Map | GBrowse

Last Update: Coordinates: 2006-07-09 | Sequence: 1996-07-31

Subfeature details: Relative Coordinates: Most Recent Update: CDS: 1,2441 | 837536-840979 | 2006-07-09 | 1996-07-31

External Links: All Associated Seq | Entrez Gene | Entrez RefSeq Protein | MIPS | UniProtKB

Primary SGDID: 8000004402

ADDITIONAL INFORMATION FOR VIP1

Community xrefs: [Domain/Motifs](#) | [Expression Connection](#) | [Gene/Sequence Resources](#)

Global Gene Hunter: [Locus History](#) | [FDB Homology](#) | [Protein Info](#)

Researchers: [BioGRID](#) | [BioGRID](#) | [BioGRID](#) | [BioGRID](#)

SUMMARY PARAGRAPHS for VIP1

VIP1 encodes one of two yeast inositol pyrophosphate synthases (also known as inositol hexakisphosphate kinases; IPKs); the other is encoded by *IKC1*. The inositol pyrophosphates (IPs) produced by Kcs1p and/or Vsp1p serve as high-energy signaling molecules involved in such diverse processes as vacuolar biogenesis, the stress response, DNA repair, cell wall synthesis, telomere maintenance, and phosphate homeostasis (see 4, 5, 6, and references therein).

Both enzymes catalyze the addition of beta-phosphate to the fully phosphorylated six-carbon ring of inositol hexakisphosphate (IP6). However, these enzymes produce different species of phosphoinositide pentakisphosphate (IP5): Kcs1p phosphorylates IP6 at the C5 position forming SPP-IP5, and Vsp1p phosphorylates IP6 at the C4 or C3 position forming VPP-IP5 or IPP-IP5, respectively. The exact phosphorylation position has not been determined. The different IP7 isomers are biologically relevant: the Kcs1p product cannot substitute for the Vsp1p product during phosphate homeostasis [2]. Kcs1p and Vsp1p also work in concert to produce bis-cationic inositol hexakisphosphate (IP6-IP6; IP8). Kcs1p phosphorylates the Vsp1p IP7 product 4-IP8, and Vsp1p phosphorylates the Kcs1p IP7 product SPP-IP8 [2].

Inositol pyrophosphate synthases are highly conserved and found across eukaryotes. In humans, three Kcs1p-like enzymes (IPK1/IPK1A, IPK2/IPK2A, IPK3/IPK3A) [7, 8] and two Vsp1p-like enzymes (HSPFD2A/PP1PK1/VIP1 and HSPFD2B/PP1PK2/VIP2) [8, 10] have been identified.

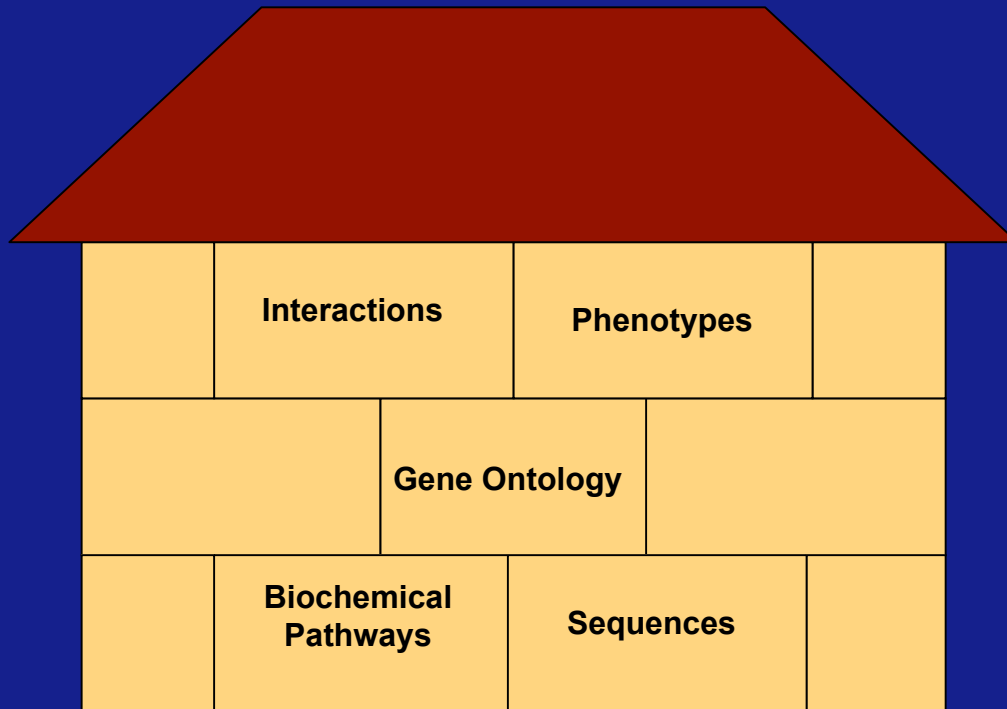
Last updated: 2008-01-22

REFERENCES CITED ON THIS PAGE (View Complete Literature Guide for VIP1)

- 1) Feoktistova A, et al. (1999) Identification and characterization of Schizosaccharomyces pombe *asp1(+)*, a gene that interacts with mutations in the *ARG2* gene and *act1*. *Genetics* 153(3):959-968
- 2) Lee YB, et al. (2007) Isolation of a cyclin-CDK-CDK inhibitor complex by inositol pyrophosphates. *Science* 316(5821):109-12
- 3) Maliga S, et al. (2007) A conserved family of enzymes that phosphorylate inositol pyrophosphates. *Science* 316(5821):106-9
- 4) Bennett M, et al. (2006) Inositol pyrophosphates: metabolism and signaling. *Cell Mol Life Sci* 633(5):552-64
- 5) Onabe B and Saitoh A. (2007) Inositol pyrophosphates get the Vsp1 treatment. *Cell* 126(4):847-9
- 6) Bhandari R, et al. (2007) Inositol pyrophosphates: pyrophosphates. *Cell Metab* 5(5):321-3
- 7) Saitoh A, et al. (2007) Synthesis of phosphoinositide pentakisphosphate by a newly identified family of higher inositol pyrophosphate kinases. *Curr Biol* 17(2):132-6
- 8) Saitoh A, et al. (2001) Identification and characterization of a novel inositol hexakisphosphate kinase. *J Biol Chem* 276(42):39179-85
- 9) Fryd FC, et al. (2007) Cloning and Characterization of Two Human VIP1-like Inositol Hexakisphosphate and Diphosphoinositide Pentakisphosphate Kinases. *J Biol Chem* 282(42):30344-62
- 10) Choi JH, et al. (2007) Purification, sequencing, and molecular identification of a mammalian PP-IP5 kinase that is activated when cells are exposed to hypertonic stress. *J Biol Chem* 282(42):30373-9



# Data Consistency

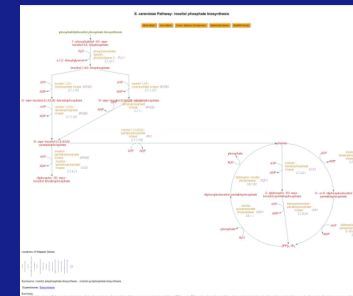
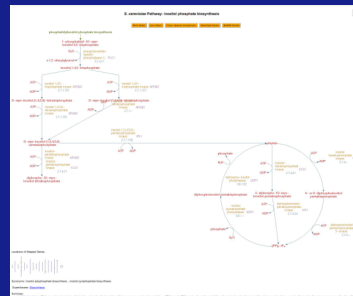


# Consistency with MetaCyc

MetaCyc

YeastCyc

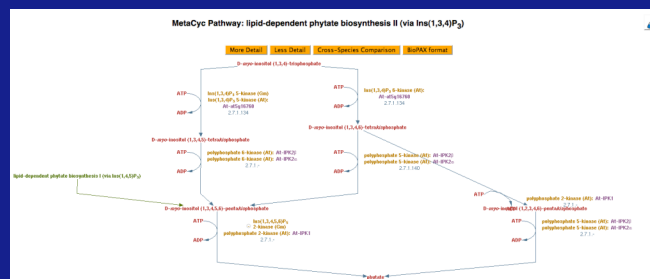
2002



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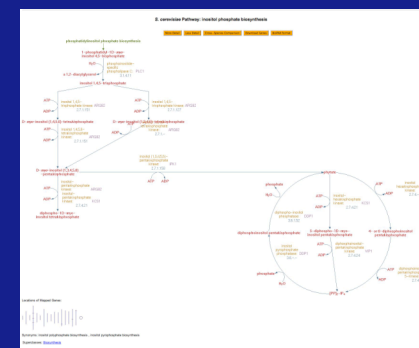


2009



?

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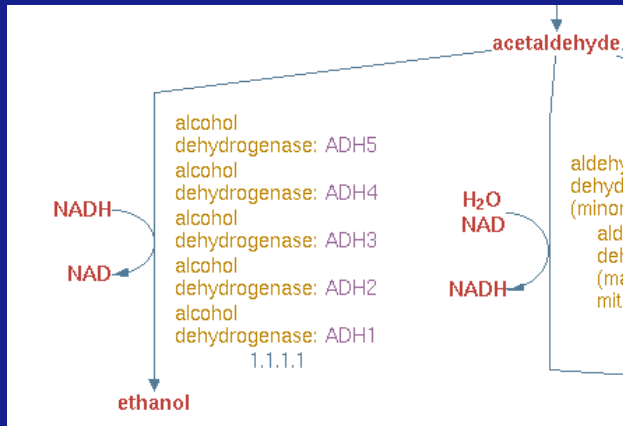


- same IDs for the same pathway and compounds
- syncing pathways
- consistency with other fungal pathways (*C. albicans*)



# Same E.C. Number?

## YeastCyc at SGD



## KEGG

**KEGG Saccharomyces cerevisiae: YOL086C**

Entry	YOL086C	CDS	<i>S.cerevisiae</i>
Gene name	ADH1, ADC1		
Definition	Adh1p [EC:1.1.1.1]		
Orthology	KO: K00001 alcohol dehydrogenase		
Pathway	PATH: sce00010 Glycolysis / Gluconeogenesis PATH: sce00071 Fatty acid metabolism PATH: sce00120 Bile acid biosynthesis PATH: sce00350 Tyrosine metabolism PATH: sce00624 1- and 2-Methylnaphthalene degradation PATH: sce00641 3-Chloroacrylic acid degradation PATH: sce00980 Metabolism of xenobiotics by cytochrome P450		
Class	BRITE hierarchy		
SSDB	<a href="#">Ortholog</a> <a href="#">Paralog</a> <a href="#">Gene cluster</a>		
Motif	Pfam: ADH_N ADH_zinc_N adh_short DapB_N BMC PROSITE: ADH_ZINC <a href="#">Motif</a>		
Other DBs	SGD: S000005446 MIPS: YOL086C NCBI-GI: 6324486 NCBI-GeneID: 854068 UniProt: P00330		

## SGD EC links

Last Update	Genetic position: -86 cM		
Subfeature details	Coordinates: 2006-01-05   Sequence: 1996-07-31		
	Relative Coordinates	Chromosomal Coordinates	Most Recent Updates Coordinates Sequence
	CDS 1..1047	160594..159548	2006-01-05 1996-07-31
	ORF Genomic DNA <input type="button" value="Get Sequence"/>		
External Links	All Associated Seq   E.C.   Entrez Gene   Entrez RefSeq Protein   MIPS   UniProt/Swiss-Prot		
Primary SGDID	S000005446		
<b>ADDITIONAL INFORMATION for ADH1</b>			
Community wiki	Domains/Motifs	Expression Connection	Function Junction
Global Gene Hunter	Locus History	Mapping Data	PDB Homologs
Researchers			

## UniProt

**UniProt** the universal protein resource

Home > Databases > UniProtKB

Notice: This site will be replaced with [beta.uniprot.org](http://beta.uniprot.org). Please

UniProtKB Entry

PIR View

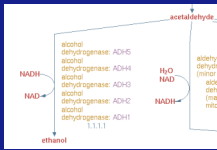
UniProtKB Entry: **P00330**

<b>ENTRY INFORMATION</b>	
ENTRY NAME	ADH1_YEAST <span style="color: red;">New!</span> <a href="#">View this entry in our Beta site</a>
ACCESSION NUMBER	P00330
Integrated into Swiss-Prot on	1986-07-21
Sequence was last modified on	2007-01-23 (Sequence version 4)
Annotations were last modified on	2008-02-05 (Entry version 95)
<b>NAME AND ORIGIN OF THE PROTEIN</b>	
PROTEIN NAME	Alcohol dehydrogenase 1
	EC 1.1.1.1
Synonyms	Alcohol dehydrogenase I YADH-1



# EC Number Agreement

YeastCyc



SGD E.C. links

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

KEGG

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

UniProt

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

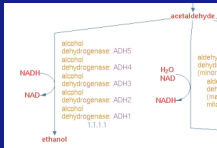
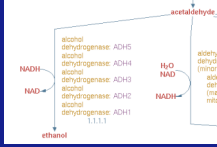
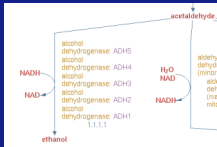
255 genes

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

303 genes



Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Gene	EC	Enzyme Name
ADH1	1.1.1.1	alcohol dehydrogenase (NAD)
ADH2	1.1.1.2	alcohol dehydrogenase (NAD)
ADH3	1.1.1.3	alcohol dehydrogenase (NAD)
ADH4	1.1.1.4	alcohol dehydrogenase (NAD)
ADH5	1.1.1.5	alcohol dehydrogenase (NAD)

Two sources with EC, both agree

847 genes

Discrepancy with one source

269 genes



# Reasons for discrepancies

- Changes to E.C. numbers
  - \* obsoletions
  - \* merges
  - \* new E.C. numbers
- Different philosophies of curation
  - \* assign to only the catalytic subunit
  - \* assign to all subunits of a complex

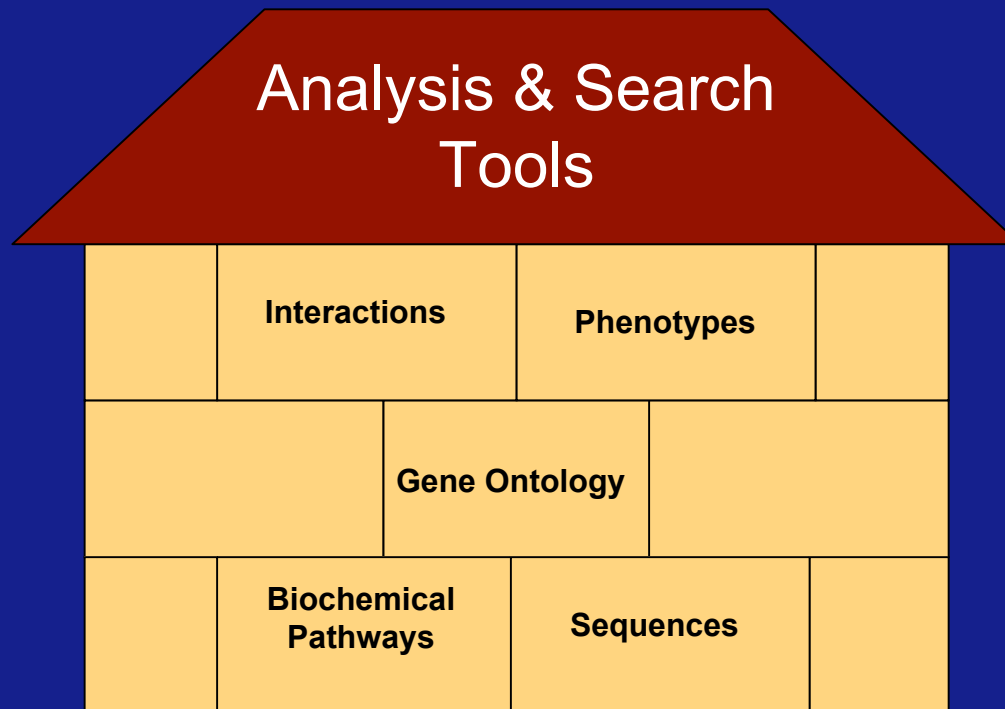
Updated data available at SGD

[http://downloads.yeastgenome.org/chromosomal\\_feature/dbxref.tab](http://downloads.yeastgenome.org/chromosomal_feature/dbxref.tab)





# Data Integration



# Analysis and Search Tools

## Search Tools

This search allows you to retrieve chromosomal features that match the selected criteria. Keyword searches can be performed using the Quick Search box or the Category Search, both located on the Search Options Contents page. The Quick Search box is also located at the top of most SGD pages.

**Advanced Search:**

**Step 1: Select chromosomal feature (required):**

ORF  pseudogene  
 ARS  rRNA  
 X element combinatorial repeats  retrotransposon  
 X element open sequence  snRNA  
 Y' element  snoRNA  
 centromere  rDNA  
 long terminal repeat  telomere  
 ncRNA  telomeric repeat  
 nick in systematic sequence of S288C  transposable element gene  
 not physically mapped  
 Select all chromosomal features

**Step 2: Narrow results (optional):**

**Annotation/sequence properties:**  
Is an ORF that is:  Dubious  Uncharacterized  Verified  Silenced\_gene  Merged  Deleted AND  
The default search excludes Deleted and Merged features. AND  
Contains introns:  Yes  No AND  
Involves frameshift translation:  Yes  No AND  
Is on the following chromosome(s):  AND

**Protein properties:**  
Molecular weight is between  and  daltons AND  
Protein length is between  and  amino acids AND  
pI (calculated) is between  and  AND

**Phenotype properties:**  
Systematic deletion phenotype is:  In viable OR  Viable (choose one) AND

**Interaction properties:**  
Has a physical interaction:  Yes  No AND  
Exhibits a genetic interaction:  Yes  No AND  
Selecting "No" for both options will return features that have no interaction data in SGD.

**Gene Ontology (GO) annotation:**  
Is annotated to the following (GO-Slim terms):  
Base GO terms. If you select multiple GO terms, resulting features must be annotated to all terms you select (i.e. the search uses AND for GO). You can select or deselect multiple GO terms by pressing Control (or Command) while clicking.

**Biological Process terms):**

**Molecular Function terms):**

**Cellular Component terms):**

**Add additional GOIDs here (separated by space or newline):**

**Large-scale expression:**  
Features whose expression:  by  fold (Enter a positive integer greater than or equal to 2) in any of the Expression Connection data sets.

<http://www.yeastgenome.org/cgi-bin/search/featureSearch>

What function or biological role does a list of genes share?

What genes are involved in a particular function or biological role?

## GO Term Finder

**Gene Ontology Term Finder**

The GO Term Finder searches for significant shared GO terms, or parents of those GO terms, used to describe the genes in your list to help you discover what the genes may have in common. To map annotations of a group of genes to more general terms and/or to bin them in broad categories, use the GO Slim Mapper.

**Default Settings:**

- All genes/features that have GO annotations in the database
- Manually curated and High-throughput annotation methods
- Hits with  $p$ -value < 0.01 will be displayed on the results page

**Step 1: Query Set (Your Input)**

Enter Gene/ORF names:  OR Upload a file of Gene/ORF names:  no file selected  
(separated by a return or a space)

**Step 2: Choose Ontology and Set Cutoff**

Process  
 Function  
 Component

Search using default settings or use Step 3, Step 4, and/or Step 5 below to customize your options.

**Optional Step 3: Specify your background set of genes using the options below**

Use default background set (all features in the database that have GO annotations) OR Enter Gene/ORF names:  OR Upload a file of Gene/ORF names:  no file selected  
(separated by a return or a space)

**Customize the gene list in the default or your specific background set (OPTIONAL)**

Feature type:  ORF  ncRNA  not in systematic sequence of S288C  not physically mapped  pseudogene  rRNA  snRNA  snoRNA  transposable\_element\_gene  
ORF Qualifier:  Dubious  Uncharacterized  Verified  
Applicable to Feature type: ORF. Default includes all Qualifiers listed here.

**Optional Step 4: Refine the Annotations used for calculation**

You can use this option with Step 3. Default uses all the options listed here.

Select by Annotation Method:  Manually curated:  yes  no  
 High-throughput:  yes  no

Select by Annotation Source:  SGD  UniProt  HGNC  MGI

Select by Evidence Codes:  IC  IDA  IEP  IGI  IMP  IPI  ISS  NAS  ND  NR  RCA  TAS

**Optional Step 5: Select a p-value cutoff for results**

The default settings display hits with  $p$ -value < 0.01  
Select a different p-value cutoff below:

<http://www.yeastgenome.org/cgi-bin/GO/goTermFinder.pl>



# Analyzing Gene Lists

## Analysis Tools

Gene Ontology Term Finder

This tool will find terms associated with significant GO terms, or groups of them that describe the genes in your list. You can choose which GO terms to use for analysis. You can also choose which GO terms to use for analysis. You can also choose which GO terms to use for analysis.

Default Settings:

1. Gene Ontology Term Finder
2. Gene Ontology Term Finder
3. Gene Ontology Term Finder

Gene Ontology Term Finder

Expression Connection

Similarly Expressed Genes: Effects of glycosylation defects on gene expression in yeast

Scale: 0.0 to 1.0

Click on a color strip to see 20 genes whose expression is similar to that gene

ORF Gene GO Process term GO Function term GO Component term

ORF	Gene	GO Process term	GO Function term	GO Component term
YOL093C	ADH1	metabolic process	alcohol dehydrogenase activity	cytosol
YKL049C	SPC42	metabolic process	cellular structural constituent of cytoskeleton	cellular component
YKL0149C	TSB68	metabolic process	transferase activity	cytosol
YER156C	ATG18	metabolic process	cellular structural constituent of cytoskeleton	cellular component
YER269C	TSB68	metabolic process	transferase activity	cytosol
YKL1000A	-	metabolic process	cellular structural constituent of cytoskeleton	cellular component
YOL021W	RSF1	cell to drug-mediated transport	cellular transporter activity	membrane
YOR193C	PSE1	cell cycle	cell cycle arrest	nucleolus
YER179W	DMC1	cell cycle	nucleosome assembly	cellular component
YOL067C	TSAD3	translation	ribosome biogenesis	cytosol
YLS132C	CSM3	DNA recombination	DNA binding	cytosol
YOR192C	TSAD3	translation	ribosome biogenesis	cytosol
YLS132C	FKH1	regulator of transcription, DNA dependent	DNA binding	nucleus
YOR196C	LRCA	metabolic process	metabolic transporter activity	membrane
YOR244C	RSB1	metabolic process	metabolic transporter activity	membrane
YLS019W	SPY7C	metabolic process	metabolic transporter activity	membrane
YOR197C	-	metabolic process	cellular transporter activity	cellular component
YOR192C	LAT1	metabolic process	cellular transporter activity	membrane

ACHI/YOL63C Physical and Genetic Interactions

Summary Labels Details Interactions Gene Ontology Phenotype Resonance Resonance

This page lists all of the interactions that we have identified for the gene YOL63C.

The following table contains information for each gene. The first column is the interaction type. The second column is the gene symbol. The third column is the gene name. The fourth column is the gene description. The fifth column is the gene accession number. The sixth column is the gene location. The seventh column is the gene coordinates. The eighth column is the gene coordinates. The ninth column is the gene coordinates. The tenth column is the gene coordinates.

Interaction Type	Gene Symbol	Gene Name	Gene Description	Gene Accession	Gene Location	Gene Coordinates	Gene Coordinates	Gene Coordinates	Gene Coordinates
Physical Interaction	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C
Genetic Interaction	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C	YOL63C

## Pathway Omics Viewer

Pathway Omics Viewer

Quick Search: [Text Box] [Search]

Pathway Omics Viewer

This tool displays pathway activity data for a set of genes. The data is presented as a heatmap where each row represents a pathway and each column represents a gene. The color scale ranges from blue (low activity) to red (high activity).

Search a pathway:

Do you want to display details for this pathway?

Do you want to display details for this pathway?

Do you want to display details for this pathway?

## Search Tools

Advanced Search

This search allows you to refine (optional) features that match the selected criteria.

Advanced Search:

- Search by: [Dropdown]
- Search by: [Dropdown]
- Search by: [Dropdown]
- Search by: [Dropdown]

Step 1: Broad Search

Step 2: Narrow results

Advanced Search

Genetic position: 235

Sort by: Systematic Name Col

Analyze gene list: further analyze the gene list displayed above or download information for this list

Further Analysis:	<a href="#">GO Term Finder</a> Find common features of genes in list	<a href="#">GO Slim Mapper</a> Sort genes in list into broad categories	<a href="#">View GO Annotation Summary</a> View all GO terms used to describe genes in list	<a href="#">Expression Connection</a> View expression data for genes in list
Download:	<a href="#">Download All Search Results</a> Download all the data retrieved by the query			<a href="#">Batch Download</a> Download selected information for entire gene list. Available information types include Sequence, Coordinates, GO annotations, Interactions, Phenotype.



# InterMine: More flexible, powerful searches

Input a list of genes



Get a list of genes

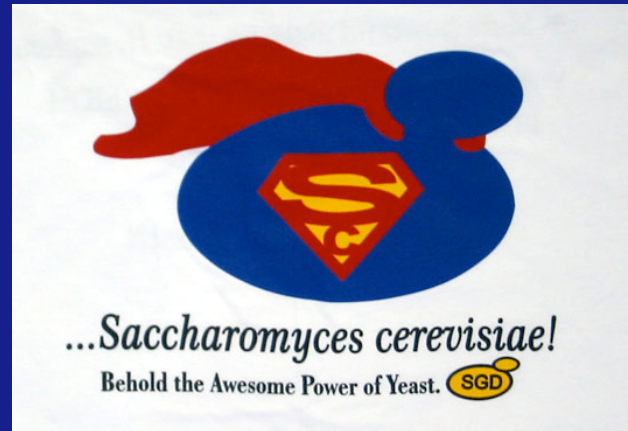
Search or filter your list  
Find homologs in other organisms

# Accessing Data

- publicly available  
<http://www.yeastgenome.org/>
- via FTP  
<http://downloads.yeastgenome.org/>
- Pathway Registry via Pathway tools  
updated monthly



Cindy Krieger, Rama Balakrishnan, Julie Park, Benjamin Vincent, Nastassia Patin



<http://www.yeastgenome.org/>  
[yeast-curator@genome.stanford.edu](mailto:yeast-curator@genome.stanford.edu)



Supported by NIH Human Genome Research Institute