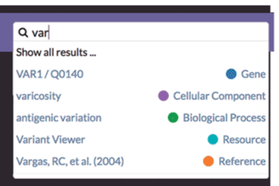
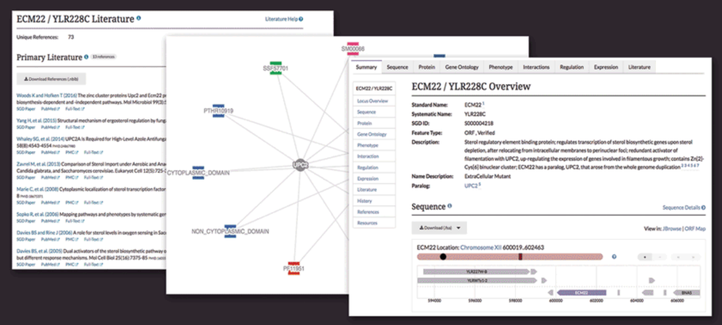


The *Saccharomyces* Genome Database (SGD) is the premier genetics & genomics resource for the budding yeast *S. cerevisiae*.



SGD provides free public access to high quality, expertly-curated information on the budding yeast genome and proteome.

Find your favorite yeast genes through the easy-to-navigate SGD website ***http://yeastgenome.org*** and get informed:

- Protein Function
- Phenotypes
- Genetic Interactions
- Physical Interactions
- Expertly Curated Literature
- Curated Summaries
- Gene Expression
- Protein Localization
- Pathways
- Functional Complementation
- Analysis Tools
- Sequence Search Tools

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Questions, suggestions?
sgd-helpdesk@lists.stanford.edu

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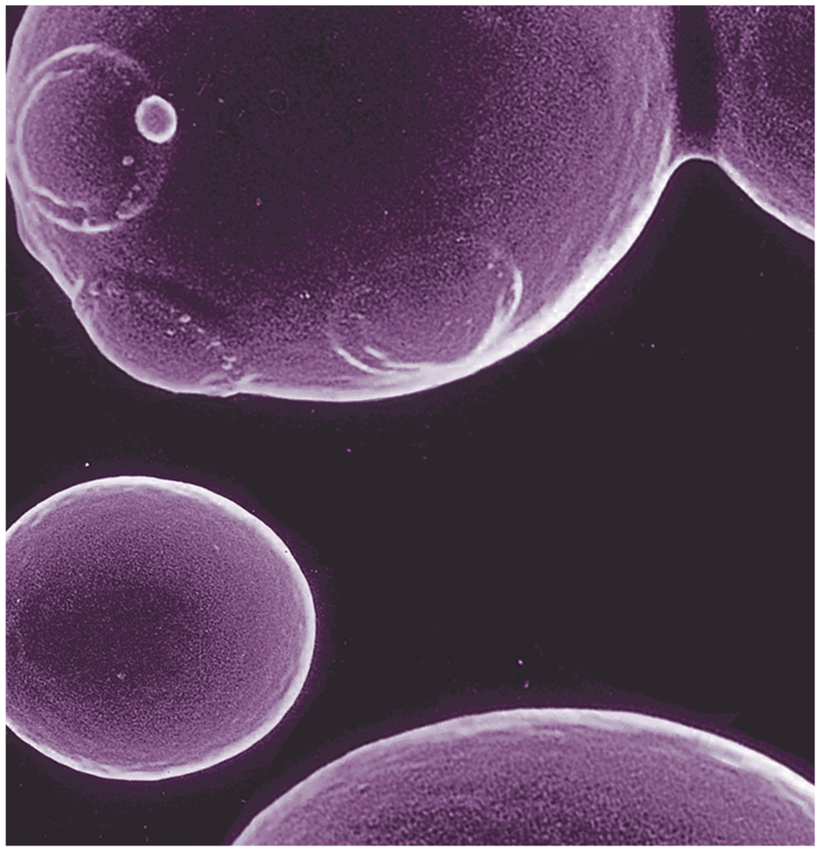
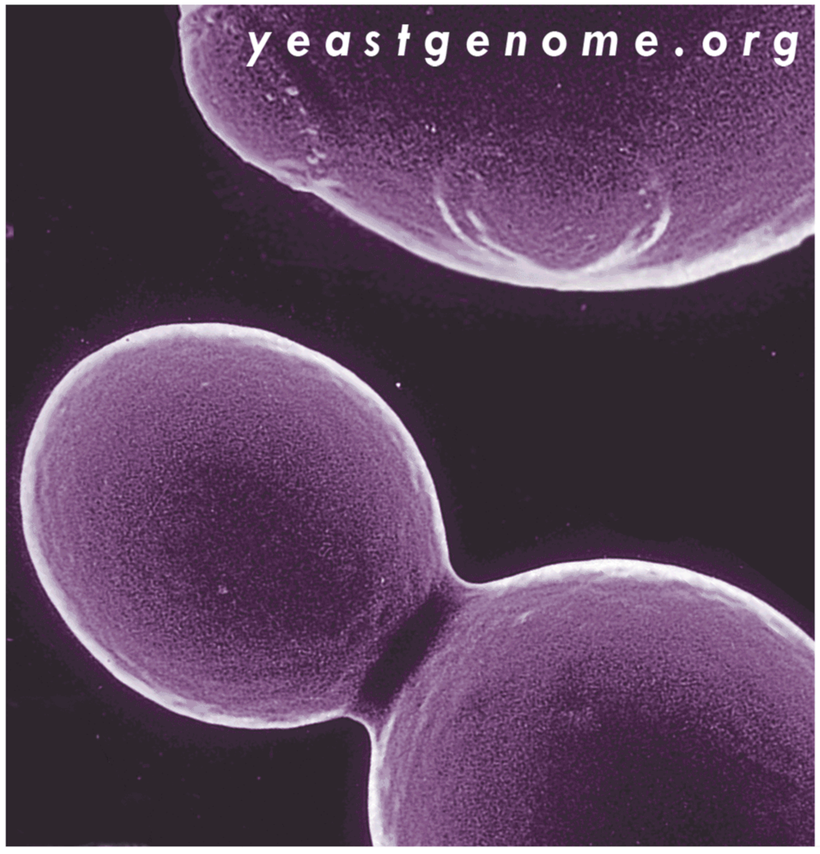


SGD Saccharomyces GENOME DATABASE



Saccharomyces Genome Database • yeastgenome.org • sgd-helpdesk@lists.stanford.edu

SGD Saccharomyces GENOME DATABASE

Analyze | Sequence | Function | Literature | Community

Rich gene summary pages

More data in each tab!

Summary | Sequence | Protein | Gene Ontology | Phenotype | Interactions | Regulation | Expression | Literature

HPT1 / YDR399W Overview

ORF info & description

Standard Name: HPT1 [1]
Systematic Name: YDR399W
SGD ID: S000002807
Aliases: BRA6 [2], HGPRTase [3], HPRT [4]
Feature Type: ORF, Verified
Description: Dimeric hypoxanthine-guanine phosphoribosyltransferase; catalyzes the transfer of the phosphoribosyl portion of 5-phosphoribosyl-alpha-1-pyrophosphate to a purine base (either guanine or hypoxanthine) to form pyrophosphate and a purine nucleotide (either guanosine monophosphate or inosine monophosphate); mutations in the human homolog HPRT1 can cause Lesch-Nyhan syndrome and Kelley-Seegmiller syndrome [3 4 5]
Name Description: Hypoxanthine guanine PhosphoribosylTransferase [6]

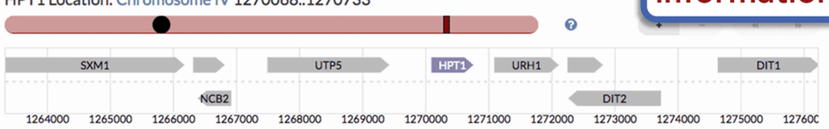
Sequence

Sequence Details

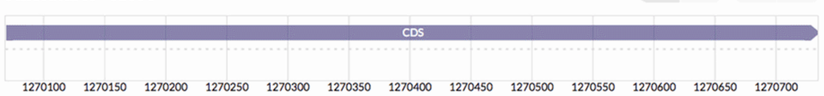
Sequence information

Download (.fsa)

HPT1 Location: Chromosome IV 1270068..1270733



Subfeatures - S288C 1 subfeature



Filter table

Feature	Relative Coordinates	Coordinates	Coord. Version	Seq. Version
CDS	1..666	chrIV:1270068..1270733	2011-02-03	1996-07-31

Protein

Protein Details

Protein information

Length (a.a.): 221
Mol. Weight (Da): 25184.9
Isoelectric Point: 5.40

Gene Ontology

Gene Ontology Details

View computational annotations

Molecular Function
Manually Curated:
- hypoxanthine phosphoribosyltransferase activity (IMP, IDA, IGI)

Biological Process
Manually Curated:
- GMP salvage (IDA, IMP, IGI)
- IMP salvage (IDA)

Cellular Component
High-Throughput:
- cytoplasm (IDA)
- nucleus (IDA)

Molecular functions, biological processes, & cellular components

Pathways

- salvage pathways of guanine, xanthine, and their nucleosides
- salvage pathways of adenine, hypoxanthine, and their nucleosides
- salvage pathways of purines and their nucleosides
- superpathway of purine biosynthesis and salvage pathways

Biochemical pathways

Phenotype

Mutant phenotypes & alleles

Classical Genetics
null:
- resistance to cisplatin: increased

unspecified:
- resistance to 8-azaguanine: decreased
- viable

Large-scale Survey
null:
- alpha-amino acid accumulation: abnormal
- auxotrophy
- resistance to cisplatin: increased
- resistance to mycophenolic acid: decreased
- vacuolar morphology: abnormal
- viable

Interaction

Interaction Details

149 total interactions for 98 unique genes

Physical Interactions
- Affinity Capture-RNA: 4
- Co-crystal Structure: 1
- Co-purification: 1
- Two-hybrid: 1

Genetic Interactions
- Dosage Rescue: 1
- Negative Genetic: 130
- Phenotypic Suppression: 5
- Positive Genetic: 6

Genetic & physical interactions

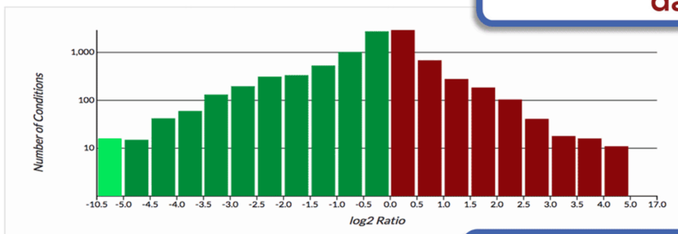
Regulation

Regulation Details

Regulators: 7
Targets: 0

Regulation & expression data

Expression



Detailed gene summaries

Summary Paragraph

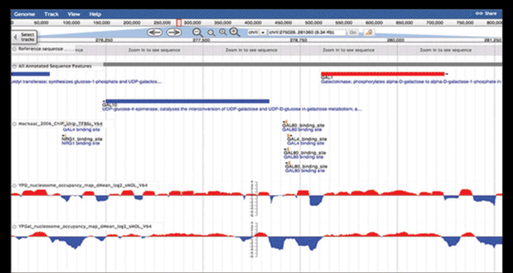
HPT1 encodes hypoxanthine-guanine phosphoribosyltransferase, an enzyme involved in the salvage pathway of purine nucleotide biosynthesis (1). Hpt1p catalyzes the conversion of the purine bases hypoxanthine and guanine to the nucleotides IMP and GMP (5). The enzyme functions as a dimer and can be inhibited *in vitro* by its end-product GMP (4, 6). In hpt1 null mutants, if the de novo pathway of guanine nucleotide biosynthesis is blocked, either through mutation of ade2 or by the addition of mycophenolic acid, cells are unable to grow even with the addition of guanine to the media (1, 2). Null mutants are also resistant to the hypoxanthine/guanine analog 8-azaguanine as well as to the anti-cancer drug cisplatin (1, 7). In humans, partial and complete deficiencies of the HPT1 ortholog HPRT1 (OMIM) are associated with the genetic disorders HPRT-related gout/Kelley-Seegmiller syndrome (OMIM) and Lesch-Nyhan syndrome (OMIM), respectively (2 and references therein).

Search for your favorite yeast genes!

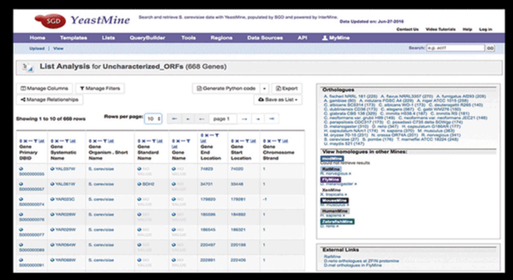
var

Show all results ...

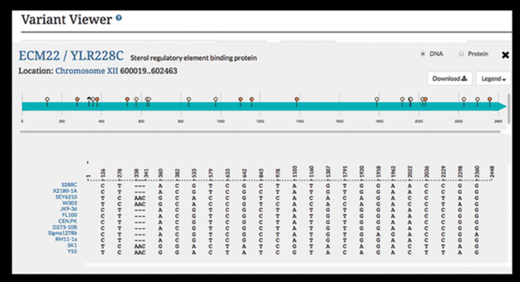
VAR1 / Q0140	Gene
varicosity	Cellular Component
antigenic variation	Biological Process
Variant Viewer	Resource
Vargas, RC, et al. (2004)	Reference



Genome Browser
Explore the yeast genome
yeastgenome.org/browse



SGD: YeastMine
Retrieve and analyze yeast data
yeastmine.yeastgenome.org



Sequence Variant Viewer
Compare *S. cerevisiae* strains
yeastgenome.org/variant-viewer