



Comparative Genomics at the *Saccharomyces* Genome Database



Patrick C. Ng, Stacia R. Engel, Robert S. Nash, Edith D. Wong, Marek S. Skrzypek, Suzi Aleksander, Sage T. Hellerstedt, Kevin A. MacPherson, Travis Sheppard, Shuai Weng, Kalpana Karra, Felix Gondwe, Ajay V. Prathivadhida, Gail Binkley, Stuart R. Miyasato, Matt Simison, and J. Michael Cherry

Department of Genetics, Stanford University, Stanford, CA 94305

Saccharomyces cerevisiae, a model organism fundamental to our understanding of eukaryotic cell biology, has long been utilized for the exploration of the biology described by omics technologies. The canonical sequence information for this valuable research data is hosted by the *Saccharomyces* Genome Database (SGD), a publicly available resource with manually and high-throughput curated data regarding function, expression, and interaction of genetic loci and their products. SGD also houses comparative analysis tools to explore homology relationships in humans, model organisms, and species across the fungal clade. In addition, SGD facilitates queries into the genetic and peptide sequence divergence among several strains of *S. cerevisiae*. The curated datasets of fungal homologous proteins and annotated whole genome sequences of *S. cerevisiae* isolates that provide the basis for these tools are available for direct download from SGD. SGD seeks to accumulate sequence data from geographically and ecologically diverse *S. cerevisiae* strains for the benefit of the research community; these are provided by resources such as the 100-Genomes Strains and 1002 Yeast Genomes Project.

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Saccharomyces
GENOME DATABASE

Analyze ▾ Sequence ▾

Download YeastMine

View gene, protein sequence for different strains at each Locus Summary Page

Alternative Reference Strains

CEN.PK - Lab strain constructed by Michael Ciriacy and K.D. Entian

OXF1 Location: JRV01000032.1 5919..9779

Download

Download strain genome annotation files using the SGD elastic search

D273-10B_Stanford_2014_JRYI000000000.zip
Laboratory strain
description: Laboratory strain
Download 13.1MB

W303_MPG_2012_ALAV000000000.zip
Laboratory strain
description: Laboratory strain
Download 12.9MB

BLAST

Query over 50 *S. cerevisiae* strains and 300 fungal species for nucleotide/peptide sequence alignments

Fwd: >> Rev: << Neg P Exponent: < 10 10-50 50-100 100-200 > 200

Mine for fungal and non-fungal homologs, including genes with *H. sapiens* disease context

YeastMine

Human Gene -> Yeast Homolog(s) -> OMIM Disease Phenotype

For a given human gene(s) retrieve associated OMIM disease phenotype(s) and yeast homolog(s).

Gene Standard Name	Gene Name	Homologue Standard Name	Homologue Systematic Name	Diseases	Data Source Name
POMT1	protein-O-mannosyltransferase 1	PMT1	YDL095W	3 Diseases	Panther
POMT1	protein-O-mannosyltransferase 1	PMT2	YAL023C	3 Diseases	Ensembl
POMT1	protein-O-mannosyltransferase 1	PMT2	YAL023C	3 Diseases	Panther
POMT1	protein-O-mannosyltransferase 1	PMT3	YOR021W	3 Diseases	Ensembl
POMT1	protein-O-mannosyltransferase 1	PMT3	YOR021W	3 Diseases	Panther
POMT1	protein-O-mannosyltransferase 1	PMT4	YJR143C	3 Diseases	HomoGene
POMT1	protein-O-mannosyltransferase 1	PMT4	YJR143C	3 Diseases	Panther
POMT1	protein-O-mannosyltransferase 1	PMT4	YJR143C	3 Diseases	Treefam
POMT1	protein-O-mannosyltransferase 1	PMT5	YDL095W	3 Diseases	Panther
POMT1	protein-O-mannosyltransferase 1	PMT6	YGR199W	3 Diseases	Ensembl
POMT1	protein-O-mannosyltransferase 1	PMT6	YGR199W	3 Diseases	Panther
POMT1	protein-O-mannosyltransferase 1	PMT7	YDR037W	3 Diseases	Panther

Display nucleotide and amino acid variations between 12 highly-studied Alternative Reference Strains

Variant Viewer

OXF1 / YKL215C 5-oxoprolinase
Location: Chromosome XI 26827..30687

Find model organism orthologs at www.alliancegenome.org

ALLIANCE of GENOME RESOURCES

Focus gene: OXF1 (Species: *Saccharomyces cerevisiae*)
Gene tree: [PANTHER:PTHR11365_SGD:5000001698.f](#)

Species	Gene symbol	Count	Best	Best reverse	Ensembl	UniProt	NCBI	RefSeq	Protein	Protein	Protein	Protein	Protein	Protein	Protein
<i>Homo sapiens</i>	OPLAH	9 of 10	Yes	Yes											
<i>Mus musculus</i>	Oplah	9 of 10	Yes	Yes											
<i>Rattus norvegicus</i>	Oplah	9 of 9	Yes	Yes											
<i>Danio rerio</i>	oplh	10 of 10	Yes	Yes											
<i>Drosophila melanogaster</i>	CG4752	10 of 10	Yes	Yes											
<i>Caenorhabditis elegans</i>	Y38F2AR.12	10 of 10	Yes	Yes											

