

The yeast research community has long enjoyed the support provided by the *Saccharomyces* Genome Database (SGD), and has flourished because of its existence, making great breakthroughs and technological advances, and contributing countless key insights to the fields of genetics and genomics over the past decades. SGD has recently joined forces with five other model organism databases (MODs) - WormBase, FlyBase, ZFIN, RGD, and MGI - plus the Gene Ontology Consortium (GOC) to form the Alliance of Genome Resources (the Alliance; alliancegenome.org). The Alliance website integrates expertly-curated information on model organisms and the functioning of cellular systems, and enables unified access to comparative genomics and genetics data, facilitating cross-species analyses. The site is undergoing rapid development as we work to harmonize various datatypes across the various organisms. Explore your favorite genes in the Alliance to find information regarding orthology sets, gene expression, gene function, mutant phenotypes, alleles, disease associations and more!

The Alliance is supported by NIH NHGRI U24HG002223-19S1, NIH NHGRI U41HG001315 (SGD), NIH NHGRI P41HG002659 (ZFIN), NIH NHGRI U24HG002223 (WormBase), MRC-UK MR/L001020/1 (WormBase), NIH NHGRI U41HG000739 (FlyBase), NIH NHLBI HL64541 (RGD), NIH NHGRI HG000330 (MGD), and NIH NHGRI U41HG002273 (GOC, which also provides funding to WB, MGD, SGD).

Goal: develop and maintain sustainable genome information resources that facilitate the use of diverse model organisms to understand the genetic and genomic bases of human biology, health, and disease

Yeast, human, and model organism orthologs • Alleles and phenotype variants • Disease associations • Expression

MIP1 / YOR330C

Locus Overview

Sequence

Protein

Gene Ontology

Phenotype

Disease

Interactions

Regulation

Expression

Literature

Summary

MIP1 / YOR330C Overview

Standard Name: MIP1¹

Systematic Name: YOR330C

SGD ID: SGD:S000005857

Feature Type: ORF , Verified

Description: Mitochondrial DNA polymerase gamma; single subunit of mitochondrial DNA polymerase in yeast, in contrast to metazoan complex of catalytic and accessory subunits; polymorphic in yeast, petites occur more frequently in some lab strains; human ortholog POLG complements yeast mip1 mutant; mutations in human POLG associated with Alpers-Huttenlocher syndrome (AHS), progressive external ophthalmoplegia (PEO), parkinsonism, other mitochondrial diseases [2 3 4 5 6 7 8 9](#)

Name Description: Mitochondrial DNA Polymerase¹

Comparative Info: Integrated model organism details available at the [Alliance of Genome Resources](#) website

Sequence

MIP1 Location: [Chromosome XV 939621..943385](#)

Download (.fsa)

View in: JBrowse

Gene Ontology

Summary: Mitochondrial DNA polymerase and 3'-5' exonuclease involved in mitochondrial DNA replication and mitochondrial DNA catabolism during nitrogen starvation

View computational annotations

Molecular Function

Manually Curated:

- 3'-5' exonuclease activity (IDA)

Phenotype

Summary: Non-essential gene; null mutants grow slowly, have abnormal vacuolar morphology, accumulate glycogen, cannot respire or use various nitrogen sources, are sensitive to oxidative stress and desiccation, and have shortened lifespan and small cell size; missense mutants that correspond to human Alpers disease mutations show increased mitochondrial DNA point mutations; heterozygous diploid nulls are haploinsufficient

Classical Genetics

dominant negative:

- mitochondrial genome maintenance: abnormal

Disease

Summary: Yeast MIP1 is homologous to human POLG, and has been used to study chronic progressive external ophthalmoplegia, Alpers syndrome, progeria, and peripheral nervous system disease

Manually Curated

- Alpers syndrome (ISS, IGI)
- chronic progressive external ophthalmoplegia (ISS, IGI)
- peripheral nervous system disease
- progeria (ISS, IGI)

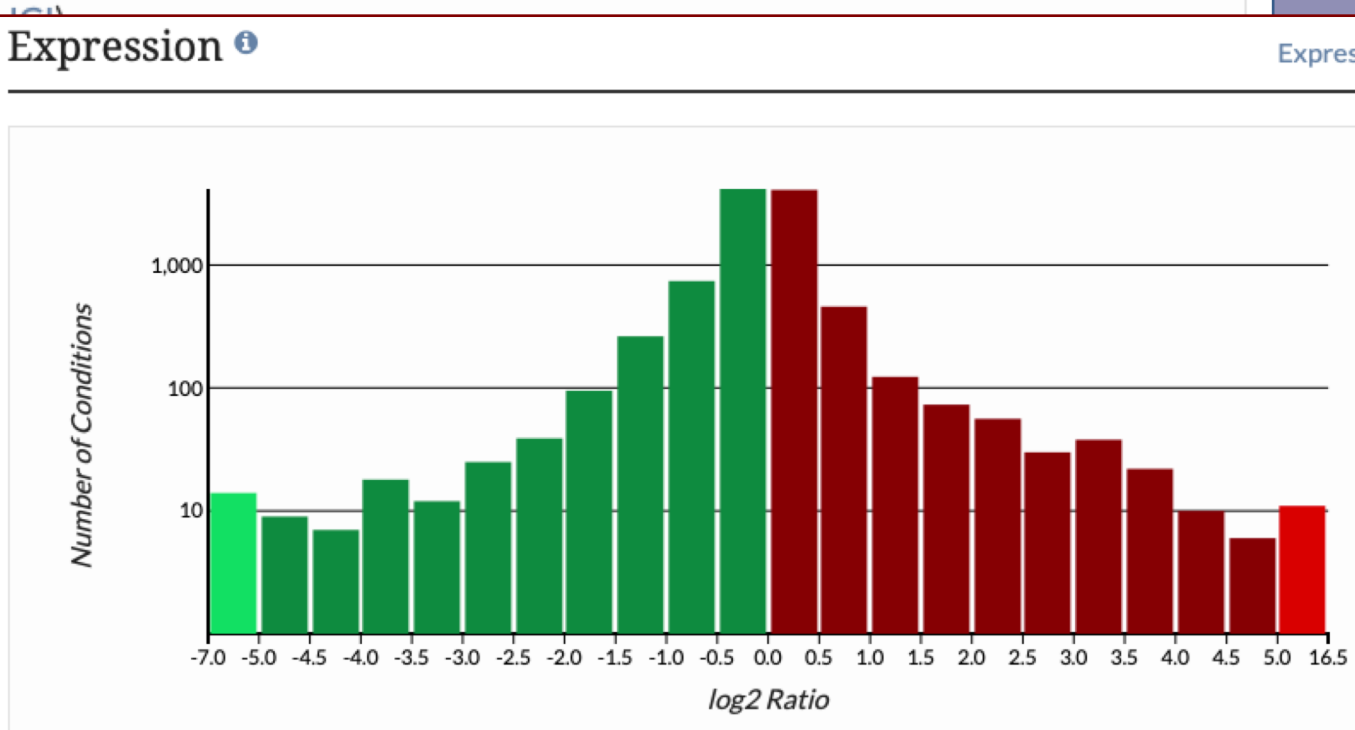
Expression

Number of Conditions

log2 Ratio



Expression data



MIP1

Saccharomyces cerevisiae

SGD:S000005857

Summary

Sequence Feature Viewer

Function - GO Annotations

Orthology

Phenotypes

Disease Associations

Expression

Alleles

Molecular Interactions

Species: Saccharomyces cerevisiae

Symbol: MIP1

Name: Mitochondrial DNA Polymerase

Synonyms: YOR330C

Biotype: protein coding gene

Automated Description: Exhibits 3'-5' exonuclease activity and DNA-directed DNA polymerase activity. Involved in mitochondrial DNA catabolic process and mitochondrial DNA replication. Localizes to the mitochondrion. Used to study Alpers syndrome; chronic progressive external ophthalmoplegia; peripheral nervous system disease; and progeria. Human ortholog(s) of this gene implicated in several diseases, including brain disease (multiple); mitochondrial DNA depletion syndrome (multiple); mitochondrial myopathy (multiple); neurodegenerative disease (multiple); and ovarian disease (multiple). Orthologous to human POLG (DNA polymerase gamma, catalytic subunit).

SGD Description: Mitochondrial DNA polymerase gamma; single subunit of mitochondrial DNA polymerase in yeast, in contrast to metazoan complex of catalytic and accessory subunits; polymorphic in yeast, petites occur more frequently in some lab strains; human ortholog POLG complements yeast mip1 mutant; mutations in human POLG associated with Alpers-Huttenlocher syndrome (AHS), progressive external ophthalmoplegia (PEO), parkinsonism, other mitochondrial diseases

Genomic Resources: [NCBI_Gene:854508](#) [UniProtKB:P15801](#)

Additional Information: [Literature](#)

Sequence Feature Viewer: chrXV:939621..943385 (3.76 kb)
R64-2-1

Function - GO Annotations: All annotations, All molecular function, All biological process, All cellular component

Orthology: Species, Gene symbol, Count, Best, Best reverse, External Compare, HGN, InParanoid, OMA, OrthoFinder, PANTHER, PhyloP, Treefam, ZFIN

Phenotypes: 36 phenotypes based on 36 annotations. Sort by: Default

Disease Associations: Compare to ortholog genes. Stringency: Stringent, Moderate, No filter. POLG (Hsa), Polg (Mmu), Polg (Rno), polg (Dre), tam (Dme), polg-1 (Cel)

Expression: Primary Sources: Serial Patterns of Expression Levels Locator (SPELL), SGD. Other Sources: GEO

Alleles: MIP1 (Sce), Polg (Mmu)

Curated summaries about genes, their functions, disease associations

Yeast, fly, worm, rat, mouse, and human homologs

Phenotypes

Disease associations across species

Expression annotations across species