Yeast Genetics Meeting

August 19, 2022


ZFIN
RGD
SGD
MGI
GENEONTOLOGY
Unifying Biology
ALLIANCE
of GENOME RESOURCES
FlyBase
WormBase

SGD Saccharomyces GENOME DATABASE

Analyze | Sequence | Function | Literature | Community

search: actin, kinase, glucose

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

MIP1 / YOR330C

- Locus Overview
- Sequence
- Protein
- Alleles
- Gene Ontology
- Phenotype
- Disease
- Interaction
- Regulation
- Expression
- Literature
- History
- References

MIP1 / YOR330C Overview

Standard Name: MIP1 [1]

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 Polymerase [1]

Comparative Info:

Sequence

Sequence Details

ALLIANCE of GENOME RESOURCES Version: 5.2.1

All search: RPB7, kinase, asthma, liver

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POLG
Homo sapiens
HGNC:9179

- Summary
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- Pathways
- Phenotypes
- Disease Associations
- Alleles and Variants
- Transgenic Alleles
- Models
- Sequence Feature Viewer
- Expression
- Molecular Interactions
- Genetic Interactions

GENE

POLG

Species	*Homo sapiens*
Symbol	POLG
Name	DNA polymerase gamma, catalytic subunit
Synonyms	dna polymerase gamma DNA polymerase subunit gamma-1 Show All 23
Biotype	protein coding gene
Automated Description	Enables several functions, including 3'-5' exonuclease activity; DNA-directed DNA polymerase activity; and protease binding activity. Involved in mitochondrial DNA replication. Acts upstream of or within base-excision repair, gap-filling. Located in extracellular space; mitochondrial nucleoid; and nucleolus. Part of gamma DNA polymerase complex. Implicated in several diseases, including mitochondrial DNA depletion syndrome (multiple); mitochondrial myopathy (multiple); neurodegenerative disease (multiple); ovarian disease (multiple); and sensory ataxic neuropathy, dysarthria, and ophthalmoparesis.
RGD Description	Mitochondrial DNA polymerase is heterotrimeric, consisting of a homodimer of accessory subunits plus a catalytic subunit. The protein encoded by this gene is the catalytic subunit of mitochondrial DNA polymerase. The encoded protein contains a polyglutamine tract near its N-terminus that may be polymorphic. Defects in this gene are a cause of progressive external ophthalmoplegia with mitochondrial DNA deletions 1 (PEOA1), sensory ataxic neuropathy dysarthria and ophthalmoparesis (SANDO), Alpers-Huttenlocher syndrome (AHS), and mitochondrial neurogastrointestinal encephalopathy syndrome (MNGIE). Two transcript variants encoding the same protein have been found for this gene. [provided by RefSeq, Jul 2008]
Cross References	ENSEMBL:ENSG00000140521 NCBI_Gene:5428 Show All 5
Additional Information	Literature

Orthology

Saccharomyces GENOME DATABASE

Analyze | Sequence | Function | Literature | Community

search: actin, kinase, glucose

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

MIP1 / YOR330C

- Homology Overview
- Homologs
- Functional Complementation
- Fungal Homologs
- External Identifiers
- Resources

MIP1 / YOR330C Homology

Standard Name: MIP1 [1]

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 Polymerase [1]

Comparative Info:

Homologs

6 entries for 6 homologs

Filter table

Species	Gene ID	Gene name	Source
Caenorhabditis elegans	WB:WBGene00013258	polg-1	Alliance
Danio rerio	ZFIN:ZDB-GENE-060303-1	polg	Alliance
Drosophila melanogaster	FB:FBgn0004406	PolG1	Alliance
Homo sapiens	HGNC:9179	POLG	Alliance
Mus musculus	MGI:1196389	Polg	Alliance
Rattus norvegicus	RGD:620057	Polg	Alliance

Showing 1 to 6 of 6 entries 10 records per page

1

ALLIANCE of GENOME RESOURCES Version: 5.2.1

All search: RPB7, kinase, asthma, liver

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polg

Danio rerio

ZFIN:ZDB-GENE-060303-1

- Summary
- Orthology
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- Pathways
- Phenotypes
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- Alleles and Variants
- Transgenic Alleles
- Models

GENE

polg

Species	*Danio rerio*
Symbol	polg
Name	polymerase (DNA directed), gamma
Synonyms	*None*
Biotype	protein coding gene
Automated Description	Predicted to enable 3'-5' exonuclease activity and DNA-directed DNA polymerase activity. Predicted to be involved in mitochondrial DNA replication. Predicted to act upstream of or within DNA replication. Predicted to be located in mitochondrial nucleoid. Predicted to be part of gamma DNA polymerase complex. Predicted to be active in mitochondrion. Is expressed in exocrine pancreas. Used to study mitochondrial metabolism disease. Human ortholog(s) of this gene implicated in several diseases, including mitochondrial DNA depletion syndrome (multiple); mitochondrial myopathy (multiple); neurodegenerative disease (multiple); ovarian disease (multiple); and sensory ataxic neuropathy, dysarthria, and ophthalmoparesis. Orthologous to human POLG (DNA polymerase gamma, catalytic subunit).
ZFIN Description	*Not Available*
Cross References	ENSEMBL:ENSDARG00000060951 NCBI_Gene:100150924 Show All 3
Additional Information	Literature

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polg

- Summary
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- Orthology
- Citations

GENE

polg

ID	ZDB-GENE-060303-1
Name	*polymerase (DNA directed), gamma*
Symbol	*polg* Nomenclature History
Previous Names	*None*
Type	protein_coding_gene
Location	Chr: 25 Mapping Details/Browsers
Description	Predicted to have 3'-5' exonuclease activity and DNA-directed DNA polymerase activity. Predicted to be involved in mitochondrial DNA replication. Predicted to localize to mitochondrion. Used to study mitochondrial metabolism disease. Human ortholog(s) of this gene implicated in several diseases, including mitochondrial DNA depletion syndrome (multiple); mitochondrial myopathy (multiple); neurodegenerative disease (multiple); ovarian disease (multiple); and sensory ataxic neuropathy, dysarthria, and ophthalmoparesis. Is expressed in exocrine pancreas. Orthologous to human POLG (DNA polymerase gamma, catalytic subunit).
Genome Resources	Alliance (1), Gene:100150924 (1), VEGA:OTTDARG00000035879 (1), Ensembl(GRCz11):ENSDARG00000060951 (2)
Note	None
Comparative Information	

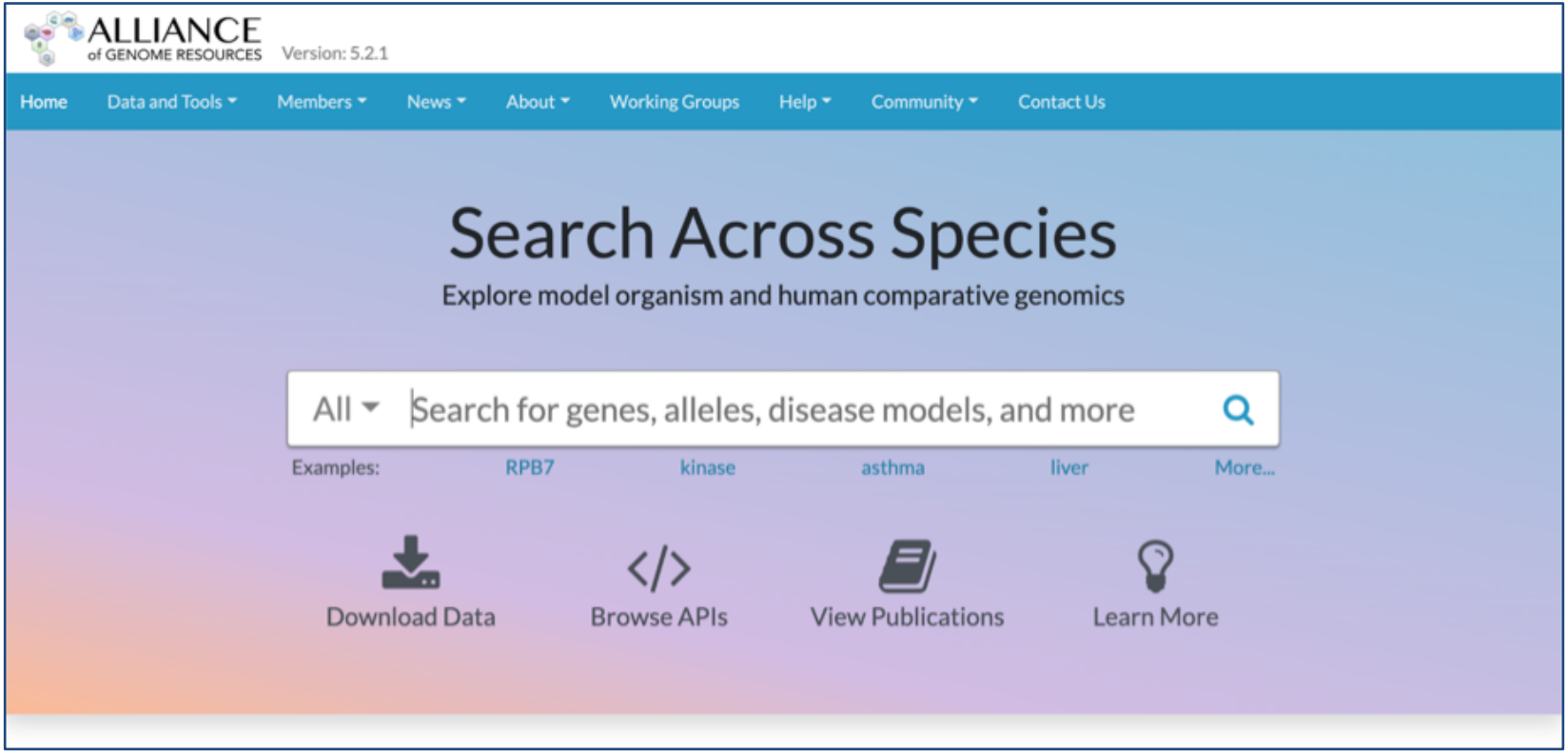
Expression

All Expression Data	8 figures from 7 publications
Cross-Species Comparison	Alliance Bgee
High Throughput Data	GEO (1), Expression Atlas (1) UO scRNA-seq (UCSC browser) (1) Single Cell Expression Atlas (1)
Thisse Expression Data	*No data available*

Wild Type Expression Summary

- Include expression in reporter lines
- Show in situs only

https://zfin.org/ZDB-GENE-060303-1



https://www.alliancegenome.org/

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All search: RPB7, kinase, asthma, liver

Category

Allele/Variant	408,357,361
Gene	312,183
Model	138,027
Gene Ontology	43,701
Disease	10,976
HTP Dataset Index	9,685
	Show More

408,871,933 results

Page 1 of 8,177,439

Sox9 (*Rattus norvegicus*) — Gene

Name: SRY-box transcription factor 9
Synonyms: SRY-box containing gene 9, SRY (sex determining region Y)-box 9, SRY box 9, LOC363699, transcription factor SOX-9, LOC100361122, SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal), SRY
Source: RGD:620474
Biotype: protein coding gene
Disease (5) Allele/Variant (8)

Ace2 (*Mus musculus*) — Gene

Name: angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
Synonyms: RIKEN cDNA 2010305L05 gene, 2010305L05Rik
Source: MGI:1917258
Biotype: protein coding gene
Disease (17) Allele/Variant (1159) Model (26)

TP53 (*Homo sapiens*) — Gene

Name: tumor protein p53
Synonyms: cellular tumor antigen p53, tumor supressor p53, BCC7, transformation-

HTP Dataset Index

Show all Categories

Species

Mus musculus	3,252
Rattus norvegicus	3,120
Saccharomyces cerevisiae	1,435
Caenorhabditis elegans	362
Drosophila melanogaster	11
	Show More

Tags

unclassified	3,219
WT vs. mutant	2,164
genotype	2,090
baseline	1,145
anatomical structure	739
	Show More

Assays

transcript array	3,786
microarray	2,466
RNA-seq	1,786
tiling array	40
proteomic profiling	1
	Show More

9,685 results

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HTP Dataset Index ✖

Solexa sequencing of small RN (SD) rat [dorsal root ganglia]

High-Throughput (HTP) Dataset Index met
ID: GEO:GSE25863
Tags: unclassified
Summary: We applied Solexa sequencing t
root ganglia (DRGs) following sciatic nerve
analysis and Q-PCR verification, 114 novel
which 52 novel miRNAs were first reported
at days 1, 4, 7 and 14 after sciatic nerve res
relating to the role and regulation of miRN
injury and regeneration.

A comparative gene expressio functional Sfp1 knockdown mu strains for five yeast Species in phase

High-Throughput (HTP) Dataset Index met
ID: GEO:GSE119645
Tags: cell morphogenesis
Summary: This data set contains microarra
of several yeast species in the LOG growth
the T=30, 60 or 90 min post glucose repleti
and S. pombe. For S. cerevisiae samples we
both the BY and RM strains of this species.
Sfp1 paralog and data were taken for the W
which Sfp1 was not functioning. This allows

Tissues

nervous system	1,132
hepatobiliary system	869
mesenchyme	774
reproductive system	591
circulatory system	509
	Show More

Sex

male	2,287
unknown	1,586
female	1,041
hermaphrodite	330
pooled	103

which Sfp1 was not functioning. This allows a comparison of the WT and mutant state in each species over several time points in the LOG growth phase. For S. cerevisiae both WT and Sfp1 mutant conditions were studied for both the BY and RM strains, as noted in the description of the samples and in the columns labels of the accompanying data matrix. For C. glabrata and N. Castellii there are two Sfp1 paralog genes, and data was taken for the individual mutant condition of each Sfp1 paralog in each species. These mutant data are noted with _9955 and _682 for the C. glabrata samples, and _719 and _511for the N. castellii samples. These designations indicate mutant conditions for either the CAGL0M09955g or CAGL0D00682g Sfp1 paralogs in C. glabrata, or likewise Scas719.24 or Scas551.1 in N. castellii. In the paper text N. castellii p719, C. glabrata p9995 are refered to as SFP1 and N. castellii p551 and C. glabrata paralog p0682 as SFP1PL.

Expression data from GNMT knockout mice (*Mus musculus*)

HTP Dataset Index

High-Throughput (HTP) Dataset Index metadata provided by MGI
ID: ArrayExpress:E-GEOD-9809, GEO:GSE9809
Tags: sex, WT vs. mutant, age, genotype
Summary: We report that 7 of 7 female Gnmt-/- mice developed hepatocellular carcinoma (HCC), the most common form of liver cancer, at the mean age of 16.1 months. In contrast, only one-third (2/6) of male Gnmt-/- mice had HCC, the remaining had either premature death or liver necrosis. Microarray analysis showed that genes involved in the following pathways were deregulated in different stages of tumorigenesis: S-adenosylmethionine (SAM)-dependent methyltransferases, metabolism, signal transduction, cell proliferation, cell adhesion and immune responses. This study reveals that GNMT plays an important role in the prevention of hapatotumorigenesis through regulating DNA methylaiton and oxidative stress signaling pathways. We postulate that GNMT is a stress-responsive protein and its expression may account for the gender difference of the susceptibility to liver cancer. Keywords: Gnmt knockout Liver tissues from wild-type or Gnmt knockout mice at young ages, developing dysplasia nodules or HCC were used for RNA extraction and hybridization on Affymetrix microarrays. For 11 weeks old mice, total RNA were mixed in equal proportion from 3 mice.

microRNA-seq from forebrain (ENCSR267CQC) (*Mus musculus*)

HTP Dataset Index

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HTP Dataset Index | search: RPB7, kinase, asthma, liver

HTP Dataset Index

Show all Categories

Species

Saccharomyces cerevisiae	1,435

Tags

stress	175
transcription	169
chemical stimulus	149
carbon utilization	117
transcriptional regulation	110
	Show More

Assays

transcript array	935
RNA-seq	352
tiling array	25

1,435 results

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HTP Dataset Index ✖ | Species: *Saccharomyces cerevisiae* ✖

The ATP-dependent chromatin remodeling enzyme Fun30 represses transcription by sliding promoter proximal nucleosomes [array] (*Saccharomyces cerevisiae*) — HTP Dataset Index

High-Throughput (HTP) Dataset Index metadata provided by SGD
ID: GEO:GSE48570
Tags: chromatin organization
Summary: The evolutionarily conserved ATP-dependent chromatin remodeling enzyme Fun30 has recently been shown to play important roles in heterochromatin silencing and DNA repair

SUS1 (*Saccharomyces cerevisiae*) — HTP Dataset Index

High-Throughput (HTP) Dataset Index metadata provided by SGD
ID: GEO:GSE920
Tags: histone modification
Summary: Transcriptome analysis of sus1 mutant in reference to its parental wild type reference

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Search Across Species

Explore model organism and human comparative genomics

All MIP1

Examples:

MIP1 (Sce)	Gene
mip130 (Dme)	Gene
mip120 (Dme)	Gene
mip120<Nterm.UAS.mCherry> (Dme)	Allele/Variant
mip1-G259R (Sce)	Allele/Variant
mip130<Tag:FLAG> (Dme)	Allele/Variant
mip130<1-723+1-36> (Dme)	Allele/Variant
mip1-T809* (Sce)	Allele/Variant
mip1Δ175 (Sce)	Allele/Variant
mip120<GD11805> (Dme)	Allele/Variant

More...

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All | MIP1

Category

- Allele/Variant 186,555
- Gene Ontology 30
- Gene 29
- Disease 22

186,636 results for **MIP1**

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MIP1 (*Saccharomyces cerevisiae*) • Gene

Name: MItochondrial DNA Polymerase
Synonyms: YOR330C
Source: SGD:S000005857
Biotype: protein coding gene
Symbol: *MIP1* (Sce)
Symbol: *MIP1*
Gene Synopsis: in yeast, petites occur more frequently in some lab strains; human ortholog POLG complements yeast *mip1*
Alleles: *mip1-Δ* (Sce)...*mip1-V945R* (Sce)...*mip1-K948R* (Sce)...*MIP1-661T* (Sce)...*mip1Δ216* (Sce)
Disease (22) Allele/Variant (65)

mip130 (*Drosophila melanogaster*) • Gene

Name: Myb-interacting protein 130
Synonyms: Mip130/Twt, Mip130/TWIT, CG3480, twit, TWIT, Twit, Mip130, 86E4.4, EG:86E4.4, twilight
Source: FB:FBgn0023509
Biotype: protein coding gene
Symbol: *mip130* (Dme)
Alleles: *mip130* (Dme)...*mip130* (Dme)...*mip130* (Dme)...*mip130<1-36>* (Dme)...*mip130<1-723>* (Dme)
Symbol: *mip130*
Allele/Variant (101)

mip120 (*Drosophila melanogaster*) • Gene

Name: Myb-interacting protein 120
Synonyms: MIP120, l(3)L4569, Mip120, p120, CG6061
Source: FB:FBgn0033846
Biotype: protein coding gene
Symbol: *mip120* (Dme)
Alleles: *mip120* (Dme)...*mip120* (Dme)...*mip120<67>* (Dme)...*mip120* (Dme)...*mip120<133>*

MIP1

Saccharomyces cerevisiae

SGD:S000005857

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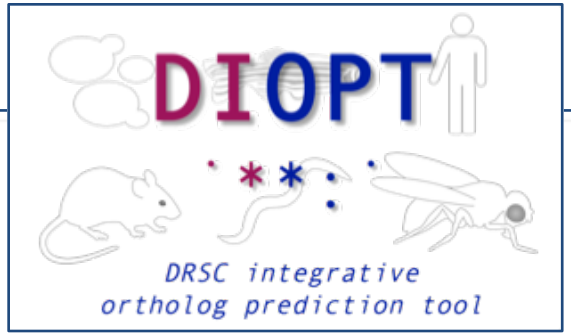
GENE

MIP1

Species	*Saccharomyces cerevisiae*
Symbol	MIP1
Name	MItochondrial DNA Polymerase
Synonyms	YOR330C
Biotype	protein coding gene
Automated Description	Enables 3'-5' exonuclease activity and DNA-directed DNA polymerase activity. Involved in mitochondrial DNA catabolic process and mitochondrial DNA replication. Located in mitochondrion. Used to study Alpers-Huttenlocher syndrome; chronic progressive external ophthalmoplegia; peripheral nervous system disease; and progeria. Human ortholog(s) of this gene implicated in several diseases, including mitochondrial DNA depletion syndrome (multiple); mitochondrial myopathy (multiple); neurodegenerative disease (multiple); ovarian disease (multiple); and sensory ataxic neuropathy, dysarthria, and ophthalmoparesis. 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
Cross References	NCBI_Gene:854508 UniProtKB:P15801
Additional Information	Literature

https://www.alliancegenome.org/gene/SGD:S000005857



MIP1

Saccharomyces cerevisiae
SGD:S000005857

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Stringency: ◉ Stringent ○ Moderate ○ No filter

Additional filters to further constrain the results:

☐ Best Score Only

☐ Best Reverse Score Only

Count: > 0 Species: All Methods: All

Hide additional filters | Reset filters

Species	Gene Symbol	Count	Best	Best Reverse	Method: Ensembl Compara	HGNC	Hieranoid	InParanoid	OMA	OrthoFinder	OrthoInspector	PANTHER	PhylomeDB	SonicParanoid	ZFIN
Homo sapiens	POLG	8 of 9	Yes	Yes	☑	☐	☑	☑	☑	☑	☑	☑	☑	☑	
Mus musculus	Polg	8 of 9	Yes	Yes	☑	☐	☑	☑	☑	☑	☑	☑	☑	☑	
Rattus norvegicus	Polg	6 of 9	Yes	Yes	☐	☐	☐	☑	☑	☑	☑	☑	☑	☑	
Danio rerio	polg	8 of 9	Yes	Yes	☑	☐	☑	☑	☑	☑	☑	☑	☑	☑	
Drosophila melanogaster	PolG1	8 of 9	Yes	Yes	☑	☐	☑	☑	☑	☑	☑	☑	☑	☑	
Caenorhabditis elegans	polg-1	8 of 9	Yes	Yes	☑	☐	☑	☑	☑	☑	☑	☑	☑	☑	

https://www.alliancegenome.org/gene/SGD:S000005857

MIP1

Saccharomyces cerevisiae
SGD:S000005857

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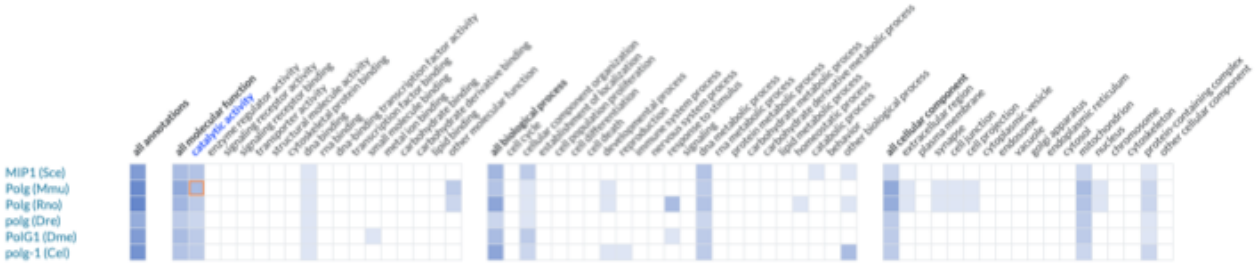
Function - GO Annotations

☑ Compare Ortholog Genes

Stringency: No filter | Species: *Mus musculus* +5 species

☐ Show Functions With At Least One Experimental Evidence



Cell color indicative of annotation volume

Term	Evidence	With/From	Reference
3'-5' exonuclease activity	ISO IBA	UniProtKB:P54098 PANTHER:PTN000030201 UniProtKB:P54098 SGD:S000005857 FB:FBgn0004406	GO_REF:0000096 PMID:21873635
DNA-directed DNA polymerase activity	ISO ISO IBA ISO	UniProtKB:P54098 RGD:620057 PANTHER:PTN000030201 RGD:620057 UniProtKB:Q92076 FB:FBgn0004406 SGD:S000005857 UniProtKB:P54098 UniProtKB:P54098	GO_REF:0000096 GO_REF:0000096 PMID:21873635 PMID:15164064
exonuclease activity	IDA		PMID:15164064

MIP1

Saccharomyces cerevisiae
SGD:S000005857

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Pathways

Reactome Pathway (0) | Reactome Reactions (0) | GO-CAMs (0)

No data available

Phenotypes

Primary Sources SGD

Other Sources *None*

Phenotype Term	Annotation Details	References
abnormal chemical compound accumulation	View	PMID:27693354
abnormal mitochondrial genome maintenance		
abnormal vacuolar morphology		
abnormal vegetative growth	View	PMID:12432101
absent mitochondrial genome maintenance	View	PMID:20883824 PMID:25170845
absent respiratory growth	View	PMID:11907266 PMID:19751518 + Show All 4
absent respiratory metabolism	View	PMID:16491467
decreased acid pH resistance	View	PMID:19220866
decreased cell death	View	PMID:21814286
decreased cell size	View	PMID:12089449

Name	Type	Experimental Condition	Modifier	References
mip1-Δ	Allele	has condition: chemical: alpha-amino acid		PMID:27693354

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MIP1

Saccharomyces cerevisiae
SGD:S000005857

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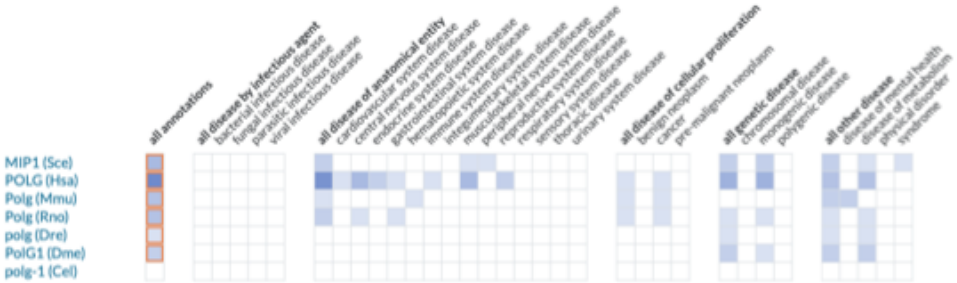
Disease Associations

☑ **Compare Ortholog Genes**

Stringency: Stringent | Species

☐ **Include Negative Annotations** Cases where the expected disease association was NOT found



Cell color indicative of annotation volume

Species	Gene	Association	Disease	Evidence	Source	Based On	References
Homo sapiens	POLG	is implicated in	Alpers-Huttenlocher syndrome	IAGP	RGD, OMIM via RGD		PMID:15689359 PMID:16896309 Show All 5
Homo sapiens	POLG	is implicated in	autosomal dominant progressive external ophthalmoplegia 1	IAGP	OMIM via RGD		RGD:7240710
Homo sapiens	POLG	is implicated in	autosomal recessive progressive external ophthalmoplegia 1	IAGP	OMIM via RGD		RGD:7240710
Homo sapiens	POLG	is implicated in	cardiomyopathy	IMP	RGD		PMID:17310215
Homo sapiens	POLG	is implicated in	cerebellar ataxia	IAGP	RGD		PMID:20803511
Homo sapiens	POLG	is implicated in	chronic progressive external ophthalmoplegia	IAGP	RGD		PMID:11431686 PMID:12565911

MIP1

Saccharomyces cerevisiae
SGD:S000005857

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Alleles and Variants

Genome Location ChrXV:939621..943385 - (3.76 kb)

Assembly Version R64-3-1

940.0k 940.5k 941.0k 941.5k 942.0k 942.5k 943.0k

YOR330C
YOR330C_mRNA

Variant Types and Conse
Only variants associated

Allele/Variant Symbol
mip1-C261R
mip1-R672*
mip1-L260R
mip1-A630T
mip1-V945R
mip1Δ205
mip1Δ279
mip1-G651S
MIP1-R745H
MIP1-661T

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Available Tracks

filter tracks

ALLIANCE of GENOME RESOURCES

- All Genes
- High Throughput Variants
- Reference sequence
- UCSC Conservation

S. cerevisiae (SGD) File View Help

0 100,000 200,000 300,000 400,000 500,000 600,000 700,000 800,000 900,000

chrXV chrXV:937366..945646 (8.28 Kb) Go

7,500 940,000 942,500

All Genes

MIP1
Mitochondrial DNA polymerase gamma

YOR331C
Dubious open readin

SCD5
normal actin organization and endocytosis

VMA4
Subunit E of the V

YOR329W-A
Dubious open reading frame unlikely to encode a functional prot...

High Throughput Variants

ALLIANCE of GENOME RESOURCES Version: 5.2.1

All search: RPB7, kinase, asthma, liver

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mip1-R672*

SGD:S000299821

Allele of MIP1

Saccharomyces cerevisiae

- Summary
- Transgenic Constructs
- Genomic Variant Information
- Variant Molecular Consequences
- Phenotypes
- Disease Associations

ALLELE/VARIANT

mip1-R672*

Species	*Saccharomyces cerevisiae*
Symbol	mip1-R672*
Category	allele
Allele Of Gene	MIP1
Transgenic Constructs	*None*
Synonyms	mip1-Arg672Ter
Description	Corresponds to human POLG variant p.Arg869Ter, implicated in Alpers syndrome
Additional Information	*Not Available*

Transgenic Constructs

No data available

Genomic Variant Information

No data available

Variant Molecular Consequences

No data available

Phenotypes

Phenotype	Annotation Details	Source	References
decreased respiratory growth	View	SGD	PMID:26077851
decreased vegetative growth	View	SGD	PMID:26077851
increased heat sensitivity	View	SGD	PMID:26077851
petite	View	SGD	PMID:26077851

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Disease Associations

No data available

MIP1

Saccharomyces cerevisiae
SGD:S000005857

- Summary
- Orthology
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- Pathways
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- Alleles and Variants
- Transgenic Alleles
- Models
- Sequence Feature Viewer

Sequence Feature Viewer

Genome Location ChrXV:939621...943385 - (3.76 kb)

Assembly Version R64-3-1

940.0k 940.5k 941.0k 941.5k 942.0k 942.5k 943.0k

YOR330C_mRNA (YOR330C)

MIP1

Saccharomyces cerevisiae
SGD:S000005857

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- Expression
- Molecular Interactions
- Genetic Interactions

Expression

Primary Sources SGD; Serial Patterns of Expression Levels Locator (SPELL)

Other Sources GEO; Single Cell Expression Atlas

Compare Ortholog Genes

Stringency: Stringent | Species

all annotations; all anatomical structures: alimentary part of gastrointestinal system, circulatory system, endocrine system, exocrine system, hemolymphoid system, integumentary system, mechanosensory system, musculoskeletal system, nervous system, renal system, reproductive system, respiratory system, sensory system, vestibulo-auditory system, visual system, ectoderm, endoderm, mesoderm, mesenchyme, adipose tissue, appendage, entire exo-endocrine component, anal primordium, pharyngeal arch, other; all stages: embryo stage, post-embryonic, pre-adult, post-juvenile adult stage; all cellular components: extracellular region, plasma membrane, synapse, cell junction, cell projection, cytoplasmic vesicle, endosome, vacuole, golgi apparatus, cytosol, endoplasmic reticulum, mitochondrion, nucleus, chromosome, cytoskeleton, protein-containing complex, other locations

MIP1 (Sce)
Polg (Mmu)
Polg (Rno)
polg (Dre)
PolG1 (Dme)

Cell color indicative of annotation volume; red slash indicates species lacks structure or developmental stage.

Sort by Default

Species	Gene	Location	Stage	Assay	Source	References
Danio rerio	polg	exocrine pancreas	Larval:Day 4	RNA in situ	ZFIN:ZDB-FIG-120807-3	PMID:22465854
Danio rerio	polg	exocrine pancreas	Larval:Day 5	RNA in situ	ZFIN:ZDB-FIG-120807-3	PMID:22465854

MIP1

Saccharomyces cerevisiae
SGD:S000005857

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Molecular Interactions

161 interactor genes based on 197 annotations

Sort by Default

MIP1 Molecule Type	Interactor Gene	Interactor Species	Interactor Molecule Type	Detection Methods	Source	Reference
RNA	CCR4	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:2353546	PMID:29158339
protein	CMR1	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:635063	PMID:22199229
RNA	DHH1	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:2350193	PMID:29158339
protein	HHF1	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:633242	PMID:22199229
protein	HHF1	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:633539	PMID:22199229
protein	HHF2	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:633242	PMID:22199229
protein	HHF2	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:633539	PMID:22199229
protein	HTA1	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:634678	PMID:22199229
protein	HTA2	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:634737	PMID:22199229
protein	HTB1	*Saccharomyces cerevisiae*	protein	affinity chromatography technology	biogrid:634833	PMID:22199229

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Genetic Interactions

Sort by Default

MIP1 Role	MIP1 Genetic Perturbation	Interactor Gene	Interactor Species	Interactor Role	Interactor Genetic Perturbation	Interaction Type	Phenotype Or Trait	Source
unspecified role		AFT1	*Saccharomyces cerevisiae*	unspecified role		negative genetic interaction (sensu BioGRID)	colony size	biogrid:581972
unspecified role		AGP3	*Saccharomyces cerevisiae*	unspecified role		negative genetic interaction (sensu BioGRID)	colony size	biogrid:581556
unspecified role		AIM19	*Saccharomyces cerevisiae*	unspecified role		negative genetic interaction (sensu BioGRID)	colony size	biogrid:583235
unspecified role		AIM36	*Saccharomyces cerevisiae*	unspecified role		negative genetic	colony size	biogrid:586267

Swagger

/openapi | Explore

Alliance of Genome Resources API

/openapi

This is the Alliance Genome Java API for access to the Data

- Allele Search
- Cache Search
- Disease
- Entity Search
- Expression
- Genes
- Homology
- Release Info
- Search
- Search Auto Complete
- Site Map
- Variant Search

Schemas

ALLIANCE of GENOME RESOURCES Version: 5.2.1

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Downloads

- Disease
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- Gene Descriptions
- Molecular Interactions
- Genetic Interactions
- Orthology
- Variants (VCF)
- Variants/Alleles

Downloads

Disease

Description	Download
All disease associations	JSON TSV
Caenorhabditis elegans associations	JSON TSV
Danio rerio associations	JSON TSV
Drosophila melanogaster associations	JSON TSV
Homo sapiens associations	JSON TSV
Mus musculus associations	JSON TSV
Rattus norvegicus associations	JSON TSV
Saccharomyces cerevisiae associations	JSON TSV

ALLIANCE of GENOME RESOURCES AllianceMine

Search and retrieve MODs data with AllianceMine, populated by Alliance of Genome Resources and powered by InterMine. Contact Us | Video Tutorials | Help | Log in

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Search: e.g zen, Q9V4E1 GO

Search

Search AllianceMine. Enter **names**, **identifiers** or **keywords** for genes, ontology terms, authors, etc. (e.g. eve, HIPPO_DROME, glycolysis, hb allele).

e.g. X, Y, Z

SEARCH

Analyse

Enter a **list** of identifiers.

Gene

e.g. CG9151, FBgn0000099, CG3629, TfIIB, Mad, CG1775, CG2262,

advanced

ANALYSE

First Time Here?

AllianceMine integrates many types of data for all the Model Organisms *Fly, Worm, Zebrafish, Yeast, Rat, and Mouse*. You can run flexible queries, export results and analyse lists of data.

TAKE A TOUR

GENOME | DISEASE | FUNCTION | HOMOLOGY | EXPRESSION

Read more

Query for genome:

- Gene → Alleles and its Variants
- Gene → Automated descriptions
- Organism → All genes
- Gene → Alleles
- Chromosomal Region → All genes
- Allele → Identifiers
- Chromosome → Genes of a selected Feature Type
- Gene → Genomic DNA

» More queries

popular templates

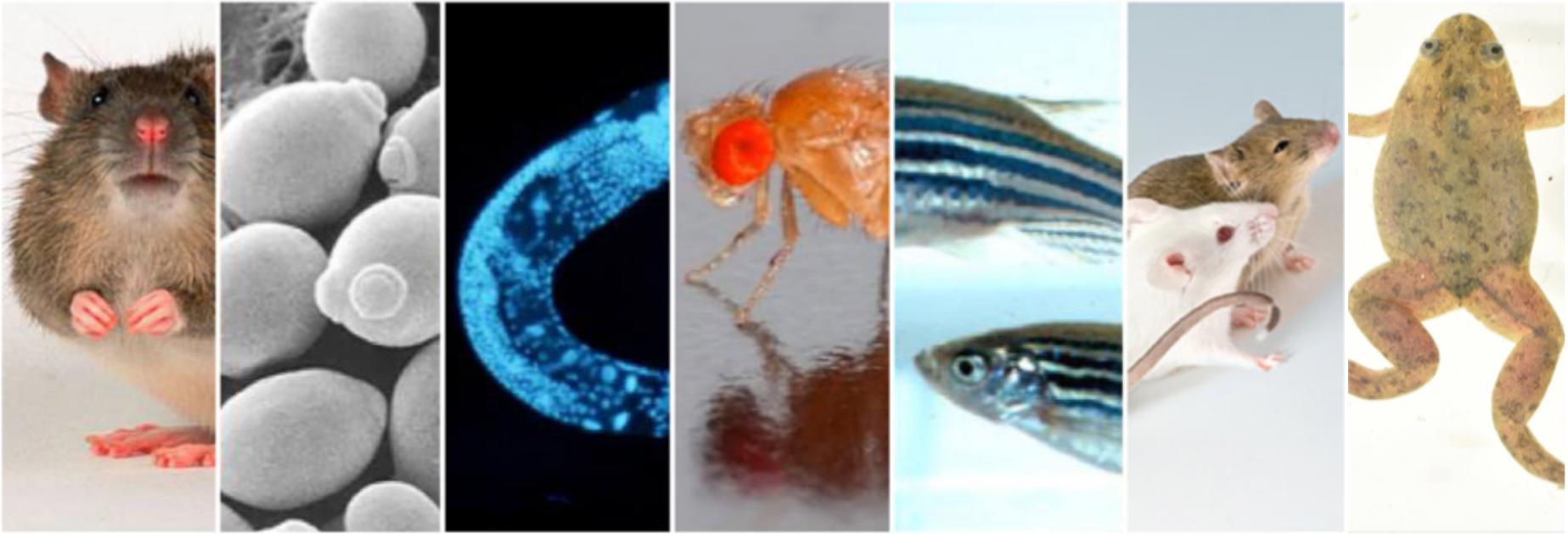
Perl, Python, Ruby and Java API

Access our AllianceMine data via our Application Programming Interface (API) tool. We provide client libraries in the following languages:

News & Updates

23 Apr — BlueGenes 1.0.0 release — We are super excited to announce that BlueGenes 1.0.0 has been officia...

16 Dec — InterMine 4.3.0 release — We are pleased to announce the new InterMine release 4.3.0.It includes...



Xenbase

Leadership Team

Mike Cherry, PhD

Stacia Engel, PhD

Stuart Miyasato

Biocuration Scientists

Suzi Aleksander

Jodi Lew-Smith, PhD

Rob Nash, PhD

Rahi Navelakar, MS

Marek Skrzypek, PhD

Edith Wong, PhD

Scientific Programmers

Kalpana Karra, MS

Shuai Weng, PhD

And all past SGD members