



# ALLIANCE of GENOME RESOURCES

GTCGGCAATCCTAAAGATAGCCAAATTATTATTGTGTCAGATACTCAC  
AGCAGTGCAGTGCGATGCCCTGGAGTGTTTGAAATCAGTGAATT  
ATTAATTTAAAAACACAAACAGTGCAACUACAGCGGGGATCTTCATAGA

FlyBase

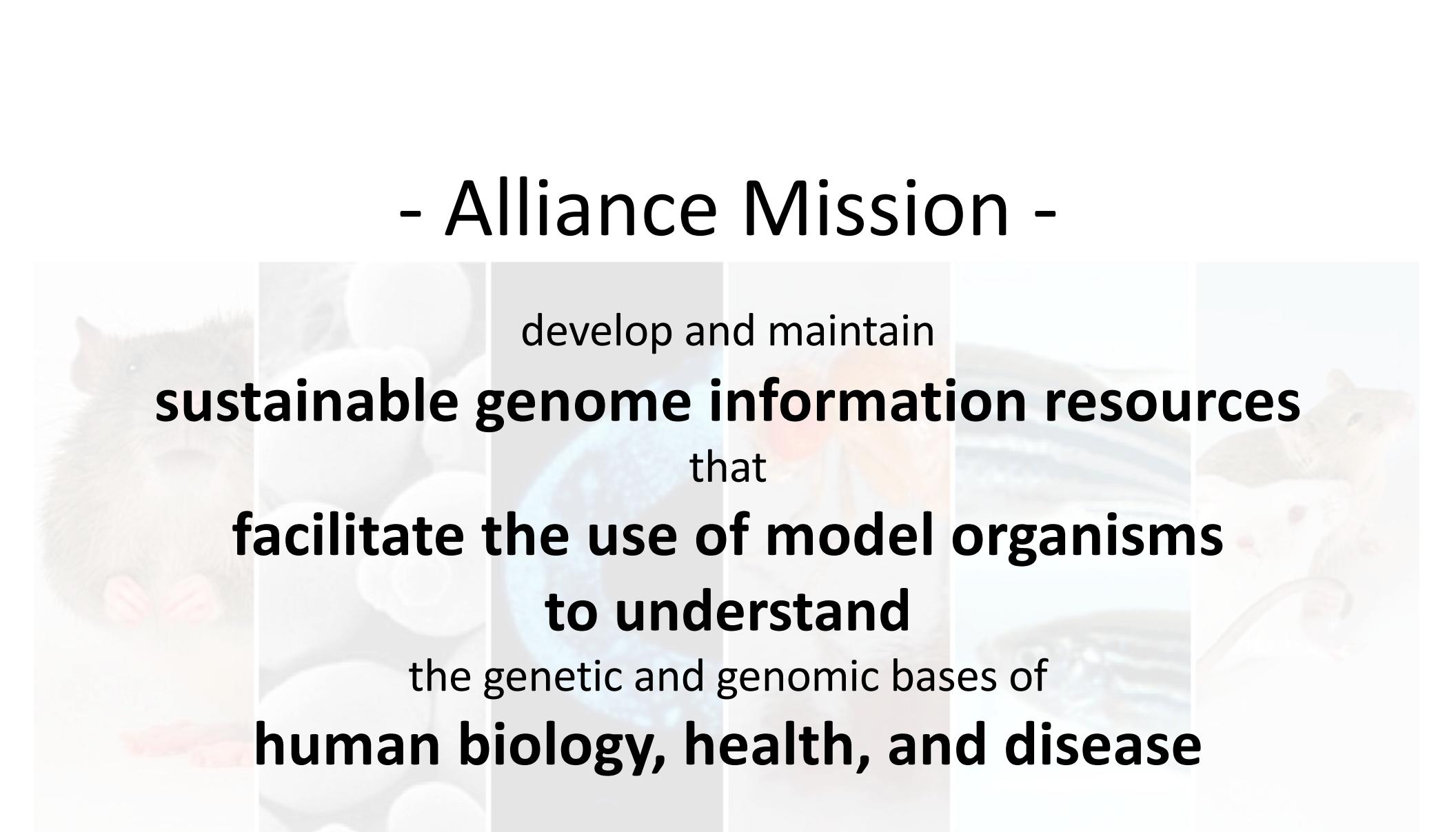


GENEONTOLOGY  
Unifying Biology

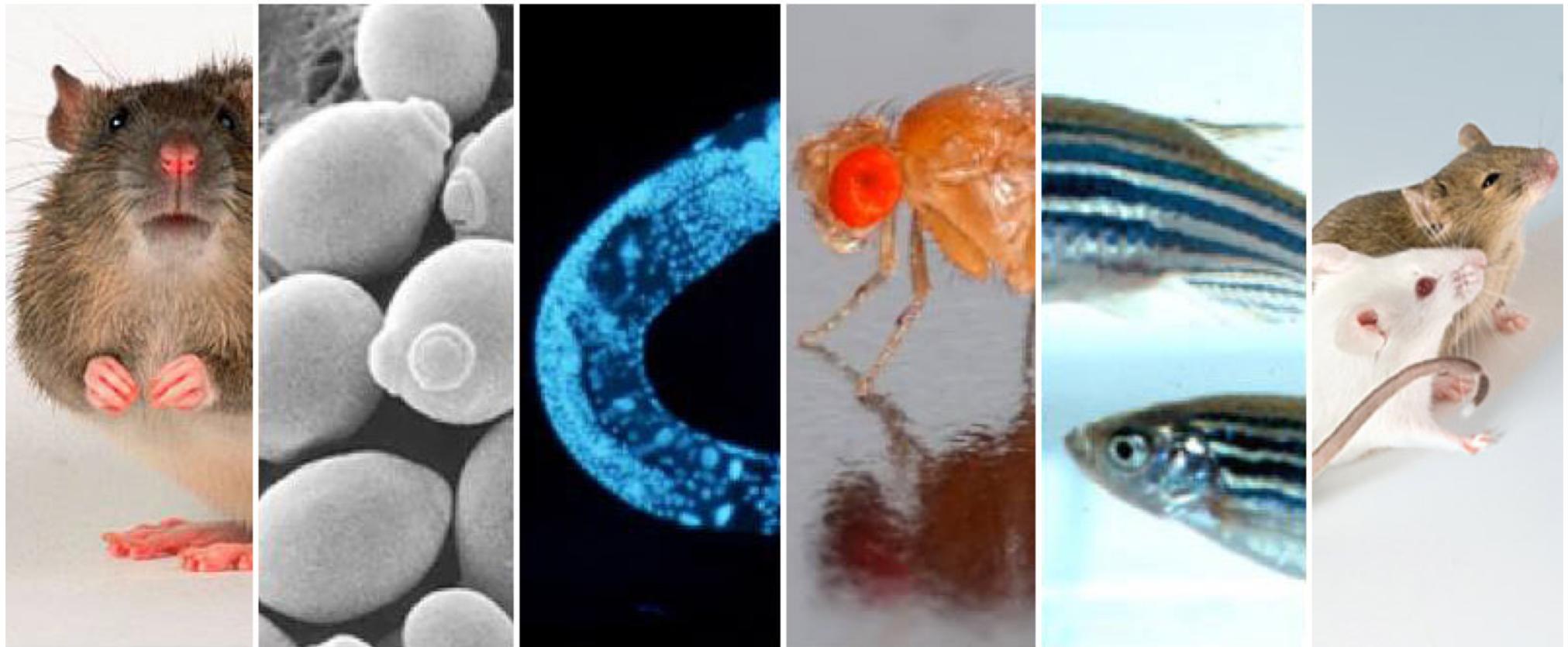
WormBase

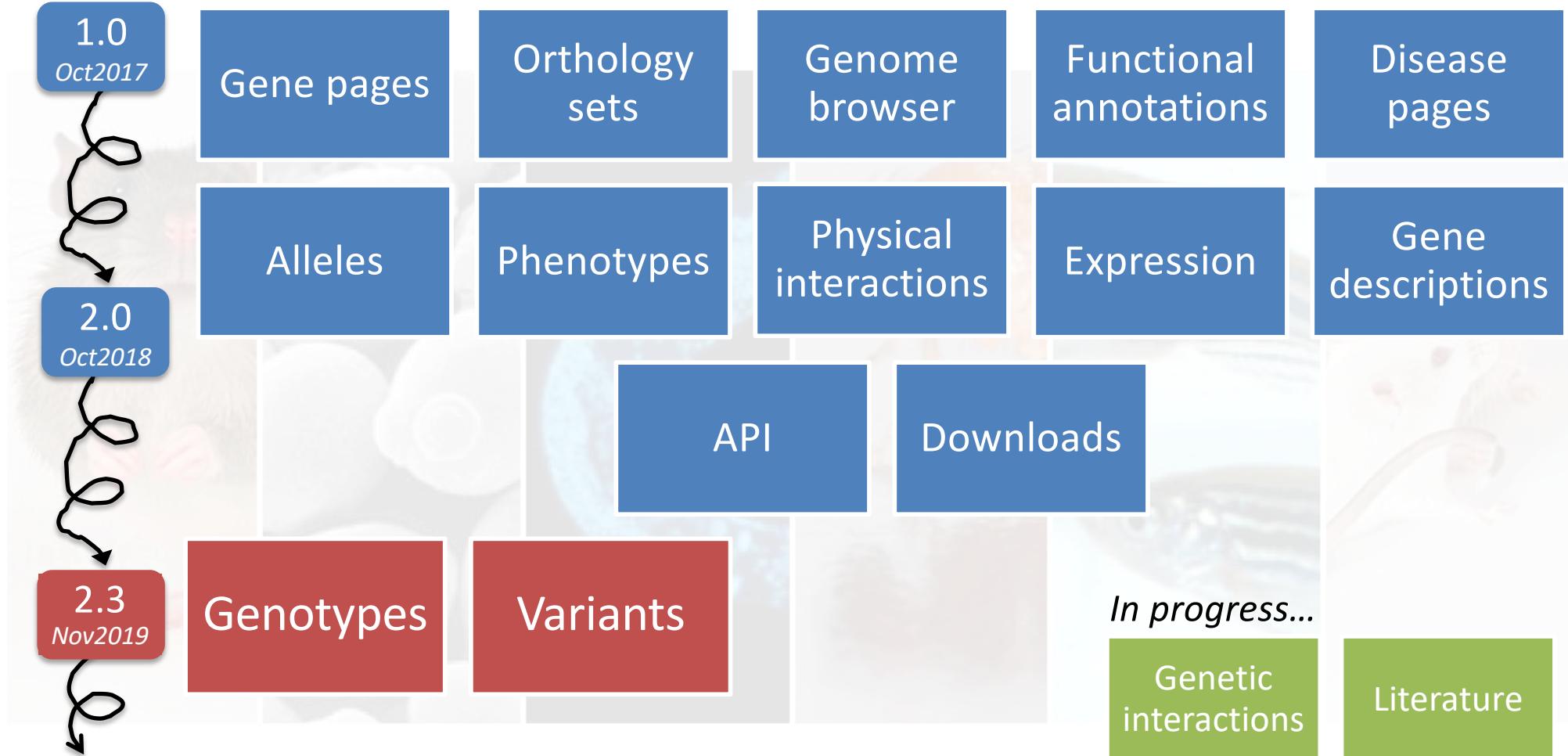


# - Alliance Mission -



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





Questions? Contact Us



**ALLIANCE**  
of GENOME RESOURCES

Release 2.2.0

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# ALLIANCE of GENOME RESOURCES



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## MISSION STATEMENT

The primary mission of the Alliance of Genome Resources (the Alliance) is to develop and maintain sustainable genome information resources that facilitate the use of diverse model organisms in understanding the genetic and genomic basis of human biology, health and disease. This

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MIP1 /  
YOR330CLocus  
Overview

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History

## MIP1 / YOR330C Overview

<b>Standard Name:</b>	MIP1 <a href="#">1</a>
<b>Systematic Name:</b>	YOR330C
<b>SGD ID:</b>	SGD:S000005857
<b>Feature Type:</b>	ORF, Verified
<b>Description:</b>	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 <a href="#">2</a> <a href="#">3</a> <a href="#">4</a> <a href="#">5</a> <a href="#">6</a> <a href="#">7</a> <a href="#">8</a> <a href="#">9</a>
<b>Name Description:</b>	Mitochondrial DNA Polymerase <a href="#">1</a>
<b>Comparative Info:</b>	Integrated model organism details available at the <a href="#">Alliance of Genome Resources</a> website

## Sequence [i](#)

[Sequence Details](#) [Download \(faa\)](#)

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**MIP1** (Saccharomyces cerevi

Name: Mitochondrial DNA Pol

Synonyms: YOR330C

Source: SGD:S000005857

Biotype: protein coding gene

 Symbol: **MIP1** (Sce)

**GeneSynopsis:** more frequently in some lab strains; human ortholog POLG complements yeast **mip1** mutant; mutations in


**mip120** (Drosophila melanogaster)

Name: Myb-interacting protein 120

Synonyms: Not Available

Source: FB:FBgn0033846

Biotype: protein coding

 Symbol: **mip120**(Dme)


**mip120[KG05422]** (Drosophila melanogaster)

ID: FB:FBal0137596

Gene: mip120 (Dme)

Synonyms: Not Available

Diseases: Not Available

 Symbol: **mip120[KG05422]**(Dme)





MIP1

*Saccharomyces  
cerevisiae*

SGD:S000005857

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# MIP1

<b>Species</b>	<i>Saccharomyces cerevisiae</i>
<b>Symbol</b>	MIP1
<b>Name</b>	Mitochondrial DNA Polymerase
<b>Synonyms</b>	YOR330C
<b>Biotype</b>	protein coding gene
<b>Automated Description</b>	Exhibits 3'-5' exonuclease activity and DNA-directed DNA polymerase activity; involved in mitochondrial DNA replication; localizes to the mitochondrion; used to study several diseases, including Alpers syndrome, chronic progressive external ophthalmoplegia, and peripheral nervous system disease.
<b>SGD Description</b>	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
<b>Genomic Resources</b>	<a href="#">NCBI_Gene:854508</a> <a href="#">UniProtKB:P15801</a>
<b>Additional Information</b>	<a href="#">Literature</a>



MIP1

*Saccharomyces cerevisiae*

SGD:S000005857

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## Sequence Feature Viewer

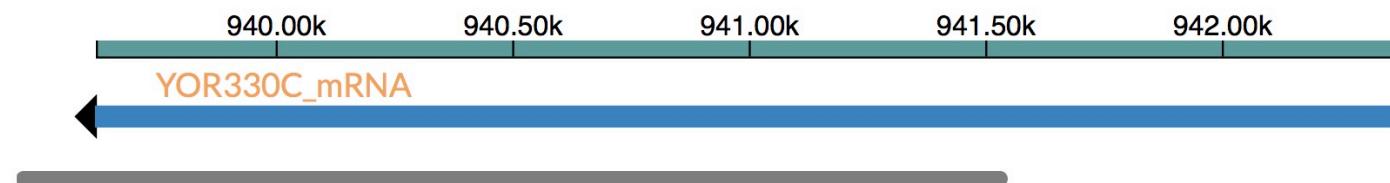
[Linkout to genome browser](#)

Genome location

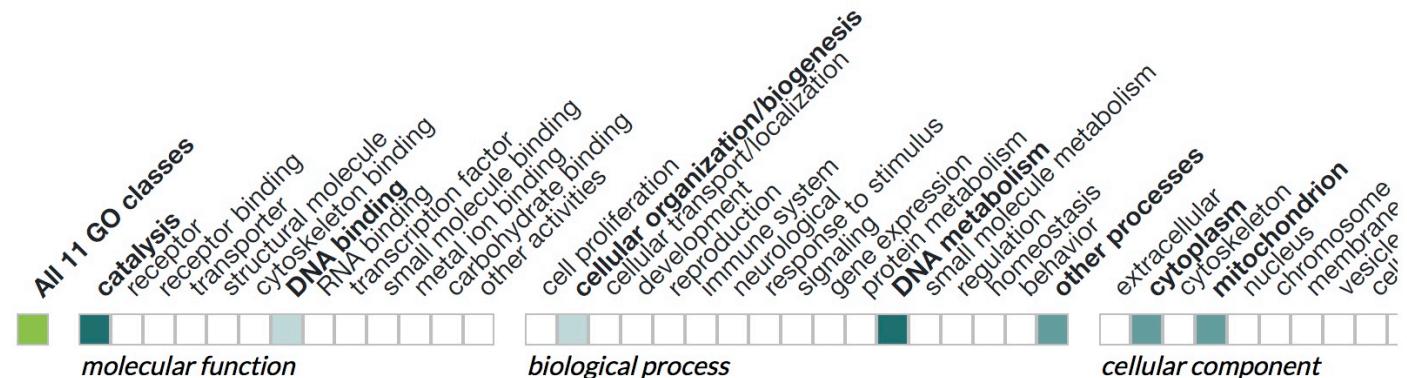
chrXV:939621...943385 (3.76 kb)

Assembly version

R64-2-1



## Function - GO Annotations





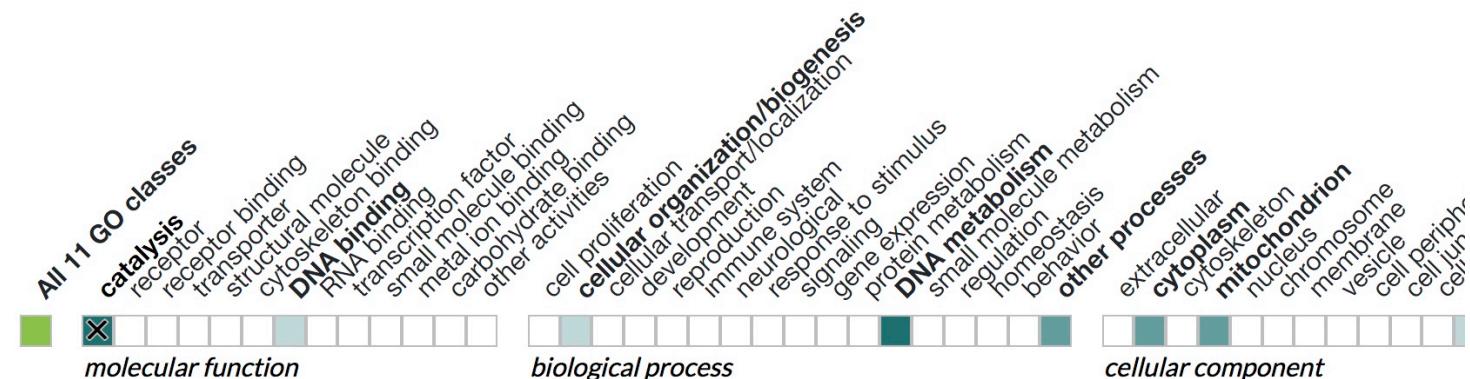
MIP1

*Saccharomyces cerevisiae*

SGD:S000005857

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## Function - GO Annotations

*Saccharomyces cerevisiae*

MIP1 annotations at GO → to catalysis

Term	Evidence	Based on	Reference
3'-5' exonuclease activity	IDA	PANTHER:PTN000030 PMID:21873201, SGD:S000005857	PMID:20601
	IBA		
DNA-directed DNA polymerase activity	IDA	InterPro:IPR001098 InterPro:IPR019760 EC:2.7.7.7	SGD_REF:S000005857 SGD_REF:S000005857 SGD_REF:S000005857
	IEA		



MIP1

*Saccharomyces cerevisiae*

SGD:S000005857 ↗

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## Orthology

Focus gene

MIP1 - (Species: *Saccharomyces cerevisiae*)

Gene tree

PANTHER:PTHR10267 ↗

Stringency:  Stringent filter (default)  Moderate filter  No filter / Show all

Show additional filters

Reset filters

Species	Gene symbol	Count	Best ?	Best reverse ?	Method						
					Ensembl Compara	HGNC	Hieranoid	InParanoid	OMA	OrthoFinder	Orthologs
<i>Homo sapiens</i>	POLG	9 of 10	Yes	Yes	<input checked="" type="checkbox"/>						
<i>Mus musculus</i>	Polg	9 of 10	Yes	Yes	<input checked="" type="checkbox"/>						



MIP1

*Saccharomyces cerevisiae*  
SGD:S000005857 ↗

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## Phenotypes

36 phenotypes based on 36 annotations

Sort by Default ▾

Phenotype Term ▾	Genetic Entity ▾	Genetic Entity Type	References ▾
abnormal chemical compound accumulation		gene	<a href="#">PMID:27693354 ↗</a>
abnormal mitochondrial genome maintenance		gene	<a href="#">PMID:19751518 ↗</a> , <a href="#">PMID:16368709 ↗</a>
abnormal vacuolar morphology		gene	<a href="#">PMID:23383298 ↗</a>
abnormal vegetative growth		gene	<a href="#">PMID:12432101 ↗</a>
absent mitochondrial genome maintenance		gene	<a href="#">PMID:25170845 ↗</a> , <a href="#">PMID:20883824 ↗</a>
absent respiratory growth		gene	<a href="#">PMID:20883824 ↗</a> , <a href="#">PMID:19751518 ↗</a> , <a href="#">PMID:11907266 ↗</a>
absent respiratory metabolism		gene	<a href="#">PMID:16491467 ↗</a>
decreased acid pH resistance		gene	<a href="#">PMID:19220866 ↗</a>
decreased cell death		gene	<a href="#">PMID:21814286 ↗</a>



MIP1

*Saccharomyces cerevisiae*  
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## Disease Associations

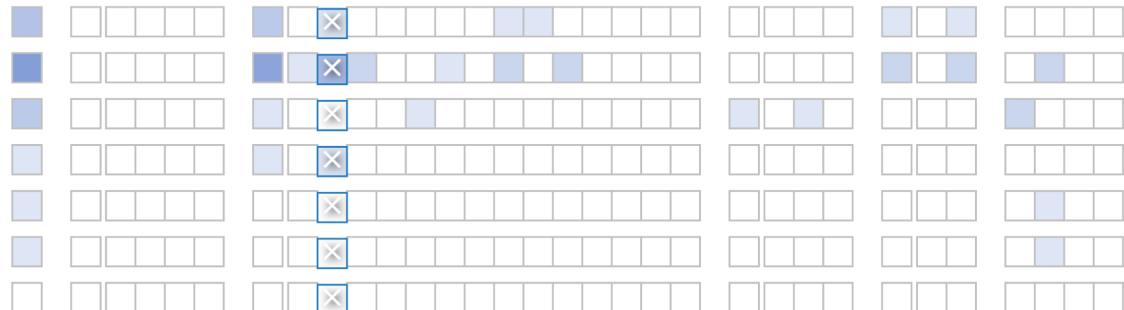
## Compare to ortholog genes

Stringency:  Stringent  Moderate  No filter

POLG (Hsa) × Polg (Mmu) × Polg (Rno) × polg (Dre) × tam (Dme) × polg-1 (Cel) ×

or [Add all](#)

All annotations  
All disease by infectious agent  
bacterial infectious disease  
fungal infectious disease  
parasitic infectious disease  
viral infectious disease  
Cardiovascular system disease  
Central nervous system disease  
Endocrine system disease  
Gastrointestinal system disease  
Hematopoietic system disease  
Immune system disease  
Integumentary system disease  
Musculoskeletal system disease  
Peripheral nervous system disease  
Reproductive system disease  
Sensory system disease  
Thoracic system disease  
Urinary system disease  
All disease of cellular proliferation  
benign neoplasm  
cancer  
pre-malignant neoplasm  
All genetic disease  
chromosomal disease  
monogenic disease  
disease of mental health  
disease of metabolism  
physical disorder





MIP1

Saccharomyces cerevisiae  
SGD:S000005857 [🔗](#)

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## Disease Associations

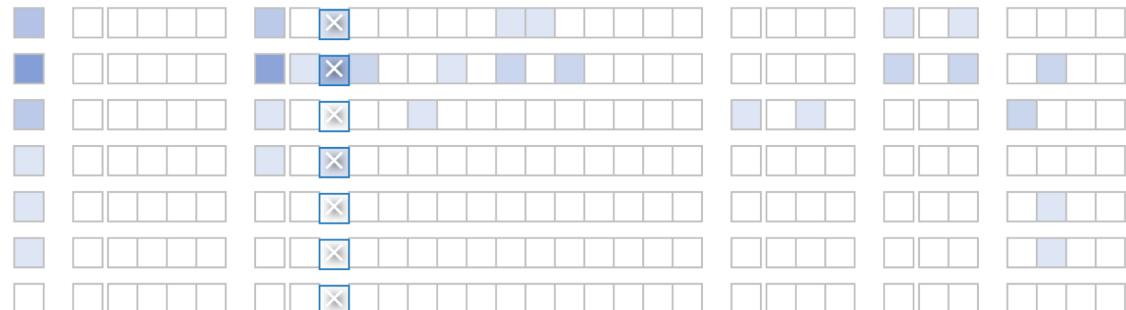
### Compare to ortholog genes

Stringency:  Stringent  Moderate  No filter

POLG (Hsa) [X](#) Polg (Mmu) [X](#) Polg (Rno) [X](#) polg (Dre) [X](#) tam (Dme) [X](#) polg-1 (Cel) [X](#)

[X](#) | [▼](#) or [Add all](#)

All annotations  
All disease by infectious agent  
bacterial infectious disease  
fungal infectious disease  
parasitic infectious disease  
viral infectious disease  
All disease of anatomical entity  
cardiovascular system disease  
central nervous system disease  
endocrine system disease  
gastrointestinal system disease  
hematopoietic system disease  
immune system disease  
integumentary system disease  
musculoskeletal system disease  
peripheral nervous system disease  
respiratory system disease  
sensory system disease  
thoracic disease  
urinary system disease  
All disease of cellular proliferation  
benign neoplasm  
pre-malignant neoplasm  
All genetic disease  
chromosomal disease  
monogenic disease  
disease of mental health  
disease of metabolism  
physical disorder



- MIP1
- POLG
- Polg
- Polg
- polg
- tam
- polg-1



MIP1

*Saccharomyces cerevisiae*  
SGD:S000005857 ↗

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## Compare to ortholog genes

Stringency:  Stringent  Moderate  No filter

POLG (Hsa) ✕ Polg (Mmu) ✕ Polg (Rno) ✕ polg (Dre) ✕ tam (Dme) ✕ polg-1 (Cel) ✕

X

or [Add all](#)

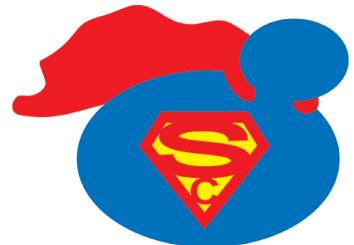
The image features a large, bold, black-outlined yellow arrow pointing from left to right. Inside the arrow, the words "UNDER CONSTRUCTION" are written in a large, bold, black sans-serif font. The arrow is positioned diagonally across the frame. In the upper left corner, there is a small blue hexagon containing a white icon of a cell with internal structures. To the right of the arrow, there is a legend consisting of a grid of colored squares. The colors include light blue, medium blue, grey, and white. Some squares contain small black symbols, such as a checkmark or an 'X'. The overall background is white, and the entire graphic has a clean, modern look.



[alliancegenome.org](http://alliancegenome.org)



# *Saccharomyces* GENOME DATABASE



*Saccharomyces*  
Genome Database  
(SGD)  
[yeastgenome.org](http://yeastgenome.org)

Leadership Team



Mike Cherry, PhD



Stacia Engel, PhD

Senior Biocuration Scientists



Rob Nash, PhD



Edith Wong, PhD



Marek Skrzypek, PhD



Barbara Dunn, PhD



Joanna Argasinska, PhD

Biocuration Scientists



Suzi Aleksander



Kevin MacPherson, MS



Patrick Ng, MS

Software Developers



Shuai Weng, PhD



Kalpana Karra, MS



Felix Gondwe



Sagar Jha, MS

System Administrators (DevOps)



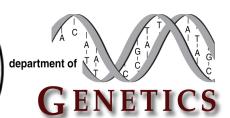
Stuart Miyasato



Matt Simison



Alliance of Genome Resources  
[alliancegenome.org](http://alliancegenome.org)



Department of Genetics,  
Stanford University