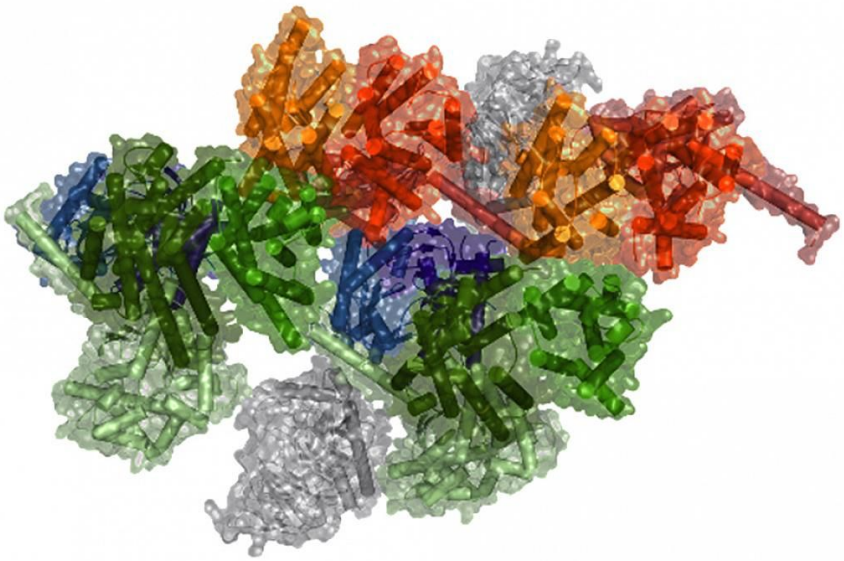
Macromolecular Complex and Chemical Pages at SGD

ICYGMB 2019, Gothenburg, Sweden

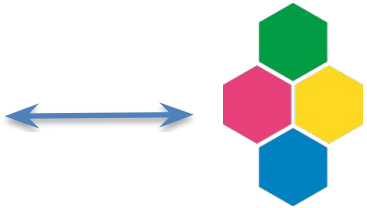
August 2019

What is a macromolecular complex?



From NIH Image Gallery

Collaboration



Complex Portal

Complete complexome of 589 curated complexes

Finding curated complexes

SGD Saccharomyces GENOME DATABASE

MENU search: actin, kinase, glucose

Categories

References	100,416
Biological Processes	24,861
Colleagues	12,438
Molecular Functions	11,300
Diseases	8,926
Genes	8,623
Downloads	8,491
Cellular Components	3,744
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Phenotypes	638
Complexes	589
Observables	205
Strains	56
Resources	50
Reserved Gene Names	16

181,416 results

Page 1 of 7,257 | Results 25 | Sort By Relevance

Reference

Jiang JC, et al. (2019) Dual roles of mitochondrial fusion gene FZO1 in yeast age asymmetry and in longevity mediated by a novel ATG32-dependent retrograde response. Biogerontology 20(1):93-107

The replicative lifespan of the yeast Saccharomyces cerevisiae models the aging of stem cells. Age asymmetry between the mother and daughter cells is established during each cell

Show all categories

Complexes

No filters are available for this category.

589 results × Complex

Page 1 of 24 | Results 25 | Sort By Relevance

Complex

cAMP-dependent protein kinase complex variant 2

Inactive form of the cAMP-dependent protein kinase which assembles when cAMP concentrations are low. Exists as a tetramer composed of two catalytic subunits and two

Complex

cAMP-dependent protein kinase complex variant 4

Inactive form of the cAMP-dependent protein kinase which assembles when cAMP

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

MAD1 / YGL086W

Locus Overview
Sequence
Protein
Gene Ontology
Complex
Phenotype
Interaction
Regulation

MAD1 / YGL086W Overview

Standard Name:	MAD1 [1]
Systematic Name:	YGL086W
SGD ID:	SGD:S000003054
Feature Type:	ORF , Verified
Description:	Coiled-coil protein involved in spindle-assembly checkp Pse1p (aka Kap121p) upon spindle assembly checkpoint activation which leads to inhibition of anaphase promoti dosage imbalance between MAD1 and MAD2 leads to c
Name Description:	Mitotic Arrest-Deficient [1 2]
Comparative Info:	Integrated model organism details available at the Allian

Complex

- Mitotic checkpoint complex, MAD1-MAD2-BUB1-BUB3 subcomplex
- Mitotic spindle assembly checkpoint Mad1-Mad2 complex

Phenotype

Summary: Non-essential gene; null mutant has chromosome instability defect and shows reduced spore germination; in large scale studies null mutant is resistant to caf hydroxyurea and MMS, but sensitive to DMSO

https://www.yeastgenome.org/search?q=&is_quick=true

https://www.yeastgenome.org/locus/S000003054

Macromolecular complex pages

Complex: Mitotic checkpoint complex, MAD1-MAD2-BUB1-BUB3 subcomplex

- Overview
- Complex Diagram
- Subunits
- Gene Ontology
- Shared Annotations
- References

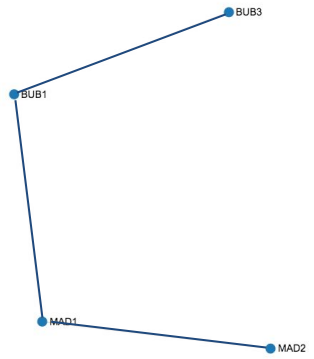
Complex: Mitotic checkpoint complex, MAD1-MAD2-BUB1-BUB3 subcomplex

Curated by: SGD
ComplexAc: CPX-3212
Systematic Name: MAD1:MAD2:BUB1:BUB3
Aliases: Mad2p-Mad1p-Bub1p-Bub3p

This complex forms during mitosis, as a result of the activation of the spindle checkpoint. BUB3 and BUB1 are associated through the cell cycle, however, the addition of MAD1 is cell cycle dependent. The formation of a stable complex requires the functions of MAD2, BUB3, and MPS1. In addition, a highly conserved Arg-Leu-Lys motif at 653-655 of MAD1 is required for the formation of a complete complex.

Complex Diagram

protein · small molecule · subcomplex · other subunit — SGD 2019-03-18



Maximum Number of Nodes
50 150

Download (.png)

Subunits

Filter table

Subunit	Description	Stoichiometry
BUB1	Protein kinase involved in the cell cycle checkpoint into anaphase	1
BUB3	Kinetochore checkpoint WD40 repeat protein	1
MAD1	Coiled-coil protein involved in spindle-assembly checkpoint	1
MAD2	Component of the spindle-assembly checkpoint complex	1

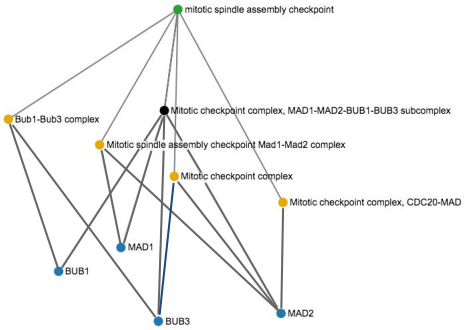
Gene Ontology

Biological Process: • mitotic spindle assembly checkpoin

Cellular Component: • kinetochore

Shared Annotations

FOCUS · GO · subunit · complex — SGD 2019-03-18



All · GO Terms · Subunits

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https://www.yeastgenome.org/complex/CPX-3212

Chemical Pages

Previous chemical page

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SGD Saccharomyces GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glucose

Chemical: methyl methanesulfonate

Overview

Phenotype Annotations

Chemical: methyl methanesulfonate

Chemical Name: methyl methanesulfonate

Chebi ID: CHEBI:25255

Phenotype Annotations 1962 entries for 25 phenotypes

Filter table

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
CHK1	apoptosis: decreased	heterozygous diploid	null	S288C	0.001% methyl methanesulfonate	**Details:** decreased apoptosis in response to MMS treatment	de Clare M and Oliver SG (2013) PMID:23531409
MAD1	apoptosis: decreased	heterozygous diploid	null	S288C	0.001% methyl methanesulfonate	**Details:** decreased apoptosis in response to MMS treatment	de Clare M and Oliver SG (2013) PMID:23531409

https://www.yeastgenome.org/chemical/CHEBI:25255

Expanded chemical pages

Chemical: methyl methanesulfonate

- Overview
- Phenotype Annotations
- Gene Ontology Annotations
- Resources

Chemical: methyl methanesulfonate

Chemical Name: methyl methanesulfonate
Chebi ID: CHEBI:25255
Definition: A methanesulfonate ester resulting from the formal condensation of methanesulfonic acid with metha
Synonyms: as-Dimethyl sulfite; CB1540; Methanesulfonic acid methyl ester; Methyl mesylate; methyl methanesul MMS

Phenotype Annotations (1962 entries for 25 phenotypes)

Filter table

Gene	Phenotype	Experiment	Mutant	Strain	Chemical	Details	Reference
CHK1	apoptosis: decreased						

Gene Ontology Annotations (2 entries for 1 gene)

Filter table

Gene	Qualifier	Gene Ontology Term	Annotation Extension	Evidence	Source	Assigned On	Reference
SGE1		xenobiotic transmembrane transporter activity	has input methyl methanesulfonate	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795
SGE1		transmembrane transport	has input methyl methanesulfonate	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795

Showing 1 to 2 of 2 entries 10 records per page « 1 »

Download (.txt) Analyze

Resources

RHEA | PubChem

Back to Top

https://www.yeastgenome.org/chemical/CHEBI:25255

Chemical: magnesium(2+)

- Overview
- Phenotype Annotations
- Gene Ontology Annotations
- Complexes
- Resources

Chemical: magnesium(2+)

Chemical Name: magnesium(2+)
Chebi ID: CHEBI:18420
Synonyms: magnesium(2+); magnesium(2+) ion; magnesium cation; magnesium, doubly charg cation; MAGNESIUM ION; magnesium, ion (Mg(2+)); Mg(2+); Mg2+

Phenotype Annotations (10 entries for 3 phenotypes)

Complexes

- Nuclear/nucleolar exosome complex, DIS3-RRP6 variant
- Deoxyribonuclease complex MUS81-MMS4
- Cytoplasmic exosome complex, DIS3 variant
- DNA-directed RNA polymerase II complex
- DNA-directed RNA polymerase III complex
- Mitochondrial Succinate - CoA ligase [ADP-forming] complex
- Acetolactate synthase complex
- DNA-directed RNA Polymerase I complex
- Ccr4-Not complex
- Cleavage and polyadenylation specificity factor complex

Resources

RHEA | PubChem

https://www.yeastgenome.org/chemical/CHEBI:18420

Phenotype to chemical connection

CHK1 / YBR274W

Phenotype Overview

Annotations

CHK1 / YBR274W Phenotype

Phenotype Help

Summary: Non-essential gene; null mutant shows abnormal cell cycle arrest following DNA damage and greatly increased rate of gross chromosomal rearrangements; null mutation confers sensitivity to selenomethionine, selenite and bleomycin; overexpression leads to slow growth

Annotations

17 entries for 14 phenotypes

Filter table

Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
resistance to chemicals: decreased	classical genetics	null	S288C	4 ug/ml bleomycin		Omidi K, et al. (2014) PMID:24498054
resistance to chemicals: increased	classical genetics	null	S288C	200 ug/ml 4-aminofolic acid		Dornfeld K (2013) PMID:23645753
vacuolar morphology: abnormal	systematic mutation set	null	S288C	0.4 M sodium chloride	**Details:** small defect in vacuolar fragmentation	Michaillat L and Mayer A (2013) PMID:23383298
apoptosis: decreased	heterozygous diploid	null	S288C	0.001% methyl methanesulfonate	**Details:** decreased apoptosis in response to MMS treatment	de Clare M and Oliver SG (2013) PMID:23531409

https://www.yeastgenome.org/locus/S000000478/phenotype

Phenotype: apoptosis: decreased

Overview

Annotations

Phenotype: apoptosis: decreased

Observable: apoptosis

Qualifier: decreased

Reference: de Clare M and Oliver SG (2013)

Abstract

Phenotype Annotations

Reference: **de Clare M and Oliver SG (2013)** Copy-number variation of cancer-gene orthologs is sufficient to induce cancer-like symptoms in Saccharomyces cerevisiae. *BMC Biol* 11:24

Abstract

Reference Help

Annotations

40 entries for 34 genes

Filter table

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
NUC1	apoptosis: decreased	classical genetics	null	S288C	40 mM acetic acid	**Treatment:** SC glycerol	Büttner S, et al. (2007) PMID:17244531
MCA1	apoptosis: decreased	classical genetics	null	S288C	30 uM cadmium nitrate	**Media:** glucose treated	Nargund AM, et al. (2008) PMID:18463984
CYC3	apoptosis: decreased	classical genetics	null	S288C	15 uM gefitinib	**Details:** gefitinib induced apoptosis is mitochondrial dependent	Wu J, et al. (2011) PMID:21468577
AIF1	apoptosis: decreased	classical genetics	null	S288C	0.4 mM hydrogen peroxide	**Details:** increased survival rate compared to H2O2 treated wild type cells; similar results after acetic acid treatment	Wissing S, et al. (2004) PMID:15381687

https://www.yeastgenome.org/phenotype/decreased_apoptosis

https://www.yeastgenome.org/reference/S000153073

Gene ontology annotations to chemicals

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

SGE1 / YPR198W

Gene Ontology Overview

Manually Curated

SGE1 / YPR198W Gene Ontology

Gene Ontology Help

Summary: Multidrug transporter of the plasma membrane; also localizes to endoplasmic reticulum

GO Slim Terms: membrane, transmembrane transporter activity, response to chemical

Manually Curated

Date Last Reviewed: 2007-02-05

Biological Process (3 entries for 1 Gene Ontology term)

Filter table

Qualifier	Gene Ontology Term	Annotation Extension	Evidence	Source	Assigned On	Reference
	transmembrane transport	has input crystal violet	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795
	transmembrane transport	has input ethidium bromide	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795
	transmembrane transport	has input methyl methanesulfonate	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795

Showing 1 to 3 of 3 entries | 10 records per page | « 1 »

Download (.txt)

Molecular Function (3 entries for 1 Gene Ontology term)

Filter table

Qualifier	Gene Ontology Term	Annotation Extension	Evidence	Source	Assigned On	Reference
	xenobiotic transmembrane transporter activity	has input crystal violet	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795
	xenobiotic transmembrane transporter activity	has input ethidium bromide	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795
	xenobiotic transmembrane transporter activity	has input methyl methanesulfonate	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795

Showing 1 to 3 of 3 entries | 10 records per page | « 1 »

https://www.yeastgenome.org/locus/S000006402/go

Gene Ontology Term: xenobiotic transmembrane transporter activity

Overview

Ontology Diagram

Annotations

Gene Ontology Term: xenobiotic transmembrane transporter activity

GO ID: GO:0042910

Aspect: Molecular Function

Description:

Synonyms:

View GO Annotations in o

Reference: Ehrenhofer-Murray AE, et al. (1998)

Abstract

Gene Ontology Annotations

Reference: **Ehrenhofer-Murray AE, et al. (1998)** The Sge1 protein of Saccharomyces cerevisiae is a membrane-associated multidrug transporter. *Yeast* 14(1):49-65

Abstract

Reference Help

In this study, we report the further characterization of the Saccharomyces cerevisiae crystal violet-resistance protein Sge1. Sge1 is a highly hydrophobic 59 kDa protein with 14 predicted membrane-

Annotations

Manually Curated (10 entries for 4 genes)

Filter table

Gene	Qualifier	Gene Ontology Term	Annotation Extension	Evidence	Source	Assigned On	Reference
QDR2		xenobiotic transmembrane transporter activity	has input quinidine	IMP	SGD	2019-04-18	Vargas RC, et al. (2004) PMID:15215105
AQR1		xenobiotic transmembrane transporter activity	has input quinidine	IMP	SGD	2019-04-18	Tenreiro S, et al. (2002) PMID:11922628
SGE1		xenobiotic transmembrane transporter activity	has input methyl methanesulfonate	IMP	SGD	2019-04-18	Ehrenhofer-Murray AE, et al. (1998) PMID:9483795
AQR1		xenobiotic transmembrane transporter activity	has input ketoconazole	IMP	SGD	2019-04-18	Tenreiro S, et al. (2002) PMID:11922628

https://www.yeastgenome.org/go/GO:0042910

https://www.yeastgenome.org/reference/S000040717

Thank you!

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yeastgenome.org

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sgd-helpdesk@lists.stanford.edu

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youtube.com/SaccharomycesGenomeDatabase

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