

Gene Ontology at SGD: GOSlimMapper

ICYGMB 2019

Suzi Aleksander

Gene Ontology overview

GO:0006366 transcription by RNA polymerase II

Gene Ontology overview

GO:0006366 transcription by RNA polymerase II



GO:0072367 regulation of lipid transport by regulation of transcription from RNA polymerase II promoter

Gene Ontology overview

GO:0006366 transcription by RNA polymerase II



GO:0072367 regulation of lipid transport by regulation of transcription from RNA polymerase II promoter



GO:0035968 regulation of **sterol** import by regulation of transcription from RNA polymerase II promoter

Gene Ontology overview

GO:0006366 transcription by RNA polymerase II



GO:0072367 regulation of lipid transport by regulation of transcription from RNA polymerase II promoter



GO:0035968 regulation of **sterol** import by regulation of transcription from RNA polymerase II promoter

Gene Ontology overview

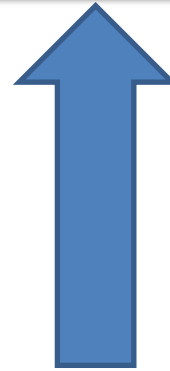
GO:0006366 transcription by RNA polymerase II



GO:0072367 regulation of lipid transport by regulation of transcription from RNA polymerase II promoter

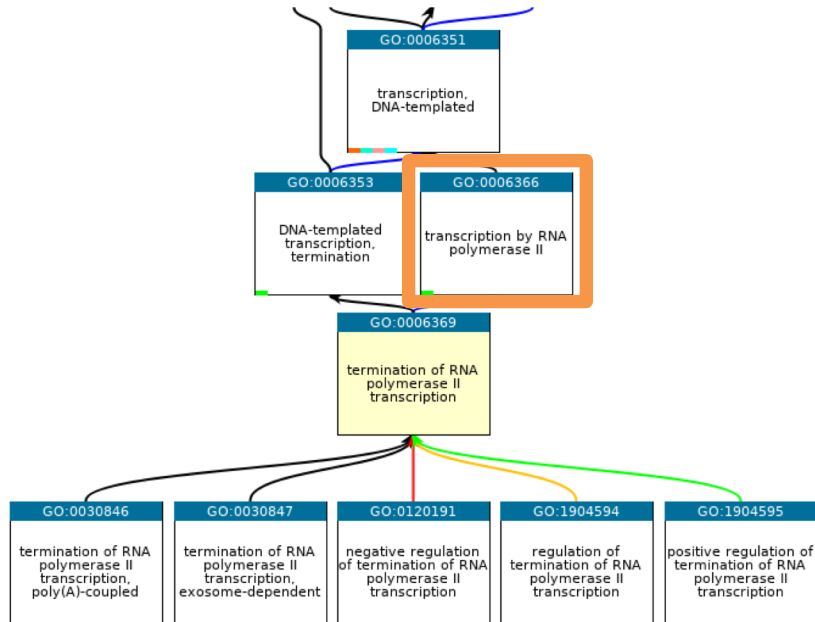


GO:0035968 regulation of **sterol** import by regulation of transcription from RNA polymerase II promoter



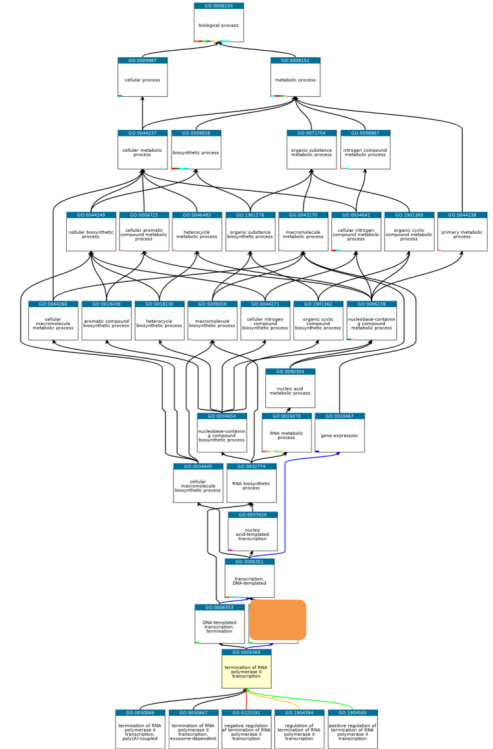
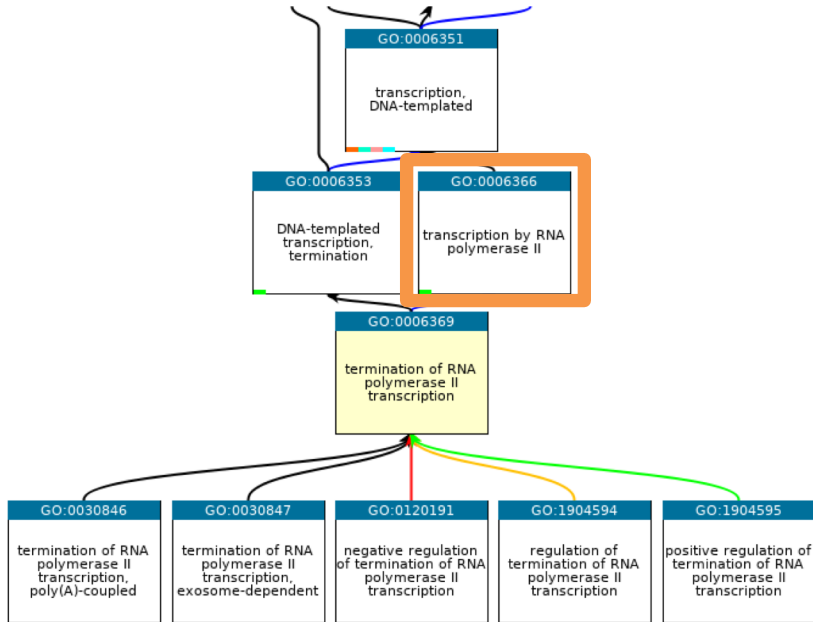
GO:0006369 **termination** of RNA polymerase II transcription

Gene Ontology overview



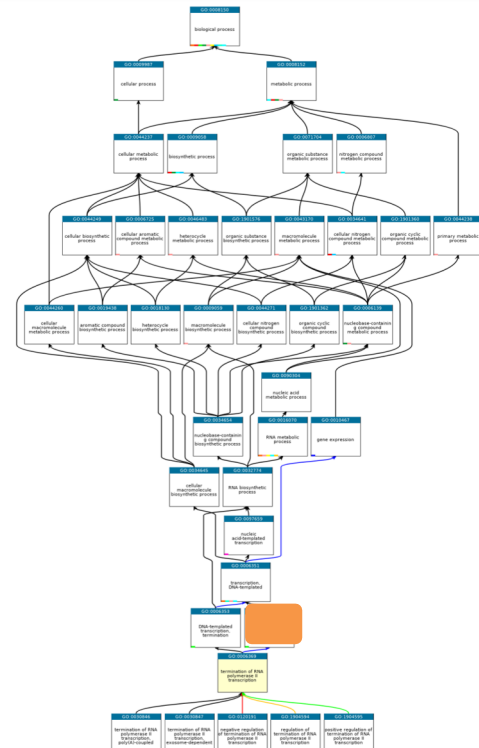
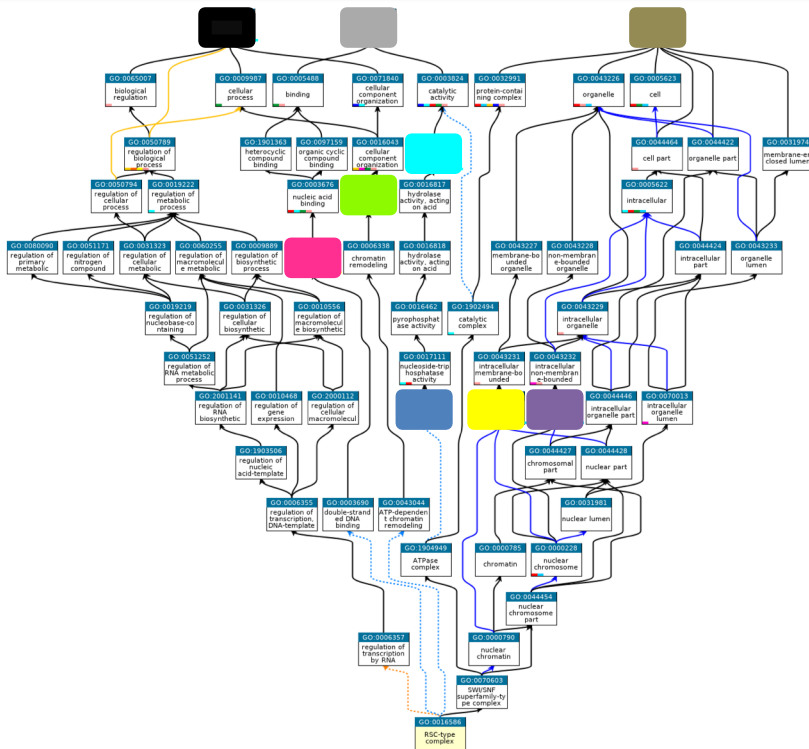
QuickGO - <https://www.ebi.ac.uk/QuickGO>

Gene Ontology overview



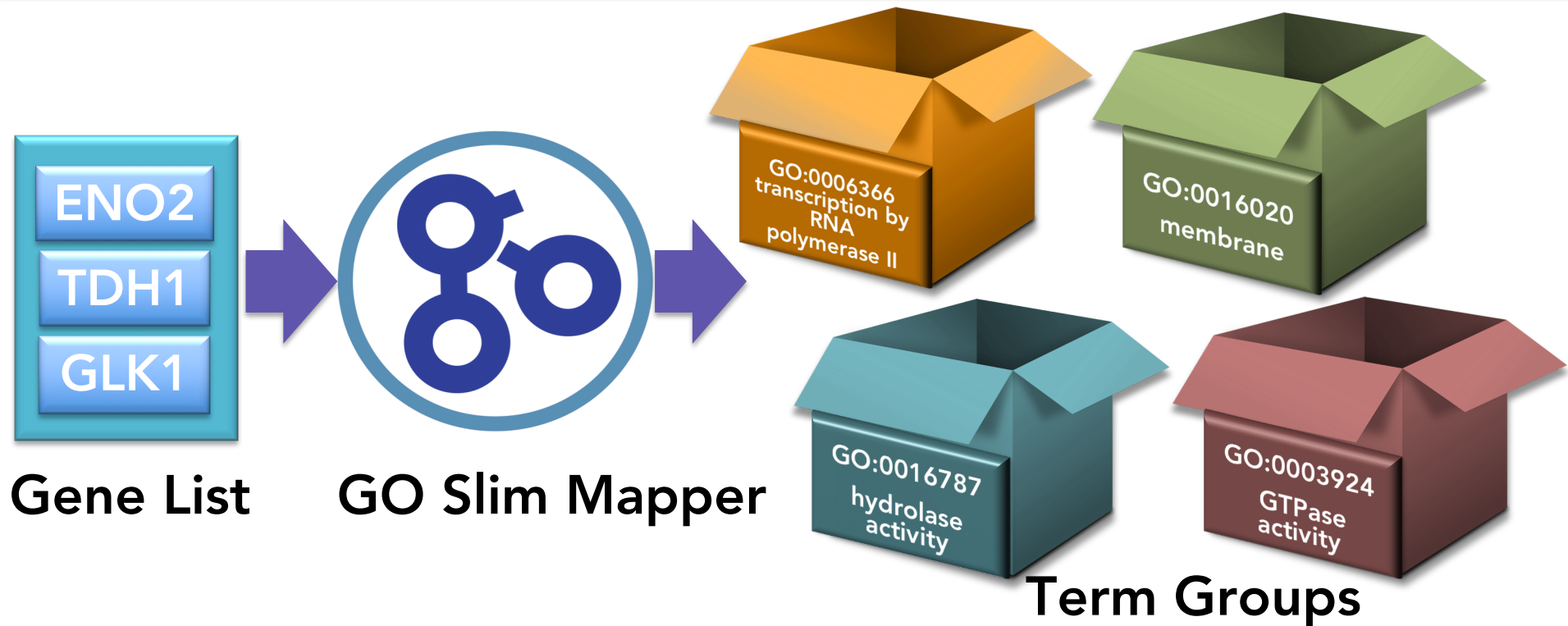
QuickGO - <https://www.ebi.ac.uk/QuickGO>

Gene Ontology overview



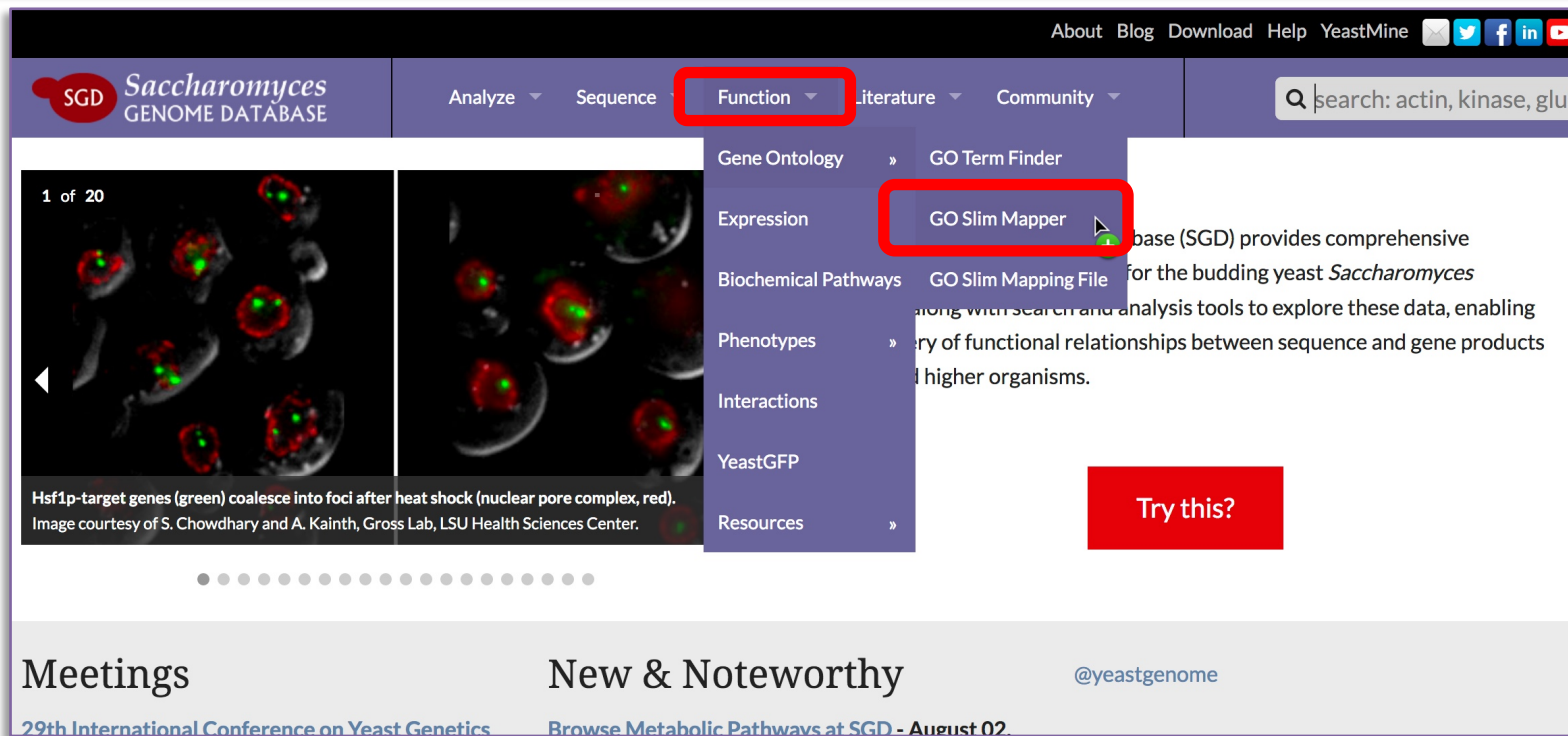
GO Slim Mapper

yeastgenome.org/goSlimMapper



GO Slim Mapper

yeastgenome.org/goSlimMapper



The screenshot shows the SGD (Saccharomyces Genome Database) website. The top navigation bar includes links for About, Blog, Download, Help, and YeastMine, along with social media icons. The main navigation menu has categories: Analyze, Sequence, Function (highlighted with a red box), Literature, and Community. The Function dropdown menu is open, showing options like Gene Ontology, Expression, Biochemical Pathways, Phenotypes, Interactions, YeastGFP, and Resources. The GO Slim Mapper option is highlighted with a red box. A search bar on the right contains the text "search: actin, kinase, glu". Below the navigation bar, there is a section titled "1 of 20" showing a series of images of yeast cells. The first image shows Hsf1p-target genes (green) coalescing into foci after heat shock (nuclear pore complex, red). The text below the images reads: "Hsf1p-target genes (green) coalesce into foci after heat shock (nuclear pore complex, red). Image courtesy of S. Chowdhary and A. Kainth, Gross Lab, LSU Health Sciences Center." To the right of the images, there is a red button labeled "Try this?". At the bottom of the page, there are sections for "Meetings" and "New & Noteworthy". The Meetings section mentions the "29th International Conference on Yeast Genetics". The New & Noteworthy section mentions "Browse Metabolic Pathways at SGD - August 02". The Twitter handle "@yeastgenome" is also visible.

SGD *Saccharomyces* GENOME DATABASE

Analyze Sequence **Function** Literature Community

Search: actin, kinase, glu

Gene Ontology » GO Term Finder

Expression **GO Slim Mapper**

Biochemical Pathways » GO Slim Mapping File

Phenotypes »

Interactions

YeastGFP

Resources »

1 of 20

Hsf1p-target genes (green) coalesce into foci after heat shock (nuclear pore complex, red).
Image courtesy of S. Chowdhary and A. Kainth, Gross Lab, LSU Health Sciences Center.

Try this?

Meetings

New & Noteworthy

@yeastgenome

29th International Conference on Yeast Genetics

Browse Metabolic Pathways at SGD - August 02.

GO Slim Mapper

yeastgenome.org/goSlimMapper

Summary Sequence Protein Gene Ontology Phenotype Interactions Regulation Expression Literature

YLR287C

Locus Overview

Sequence

Protein

Gene Ontology

Phenotype

Interaction

YLR287C

Systematic Name: YLR287C

SGD ID: SGD:S000004277

Feature Type: ORF, Uncharacterized

Description: Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR287C is not an essential gene ^{1 2}

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

Query Set (Your Input)

Enter Gene/ORF names (separated by a return or a space):

BUB3 YMR038C CSM3 CTF4 DIA2 EST1 MAD1 MAD2 NPL3 NPT1 SMT3 TOF1

Note: If you have a big gene list (> 100), save it as a file and upload it below.

OR Upload a file of Gene/ORF names (.txt or .tab format):

No file selected.

Specify your Slim Terms

Choose a GO Set:

Yeast GO-Slim: process

Refine your list of GO Slim Terms:

Select or unselect multiple datasets by pressing the Control (PC) or Command (Mac) key while clicking. Selecting a category will select all datasets in that category.

☒ SELECT ALL Terms from Yeast GO-Slim: process

☐ DNA recombination ; GO:0006310

☐ DNA repair ; GO:0006281

☐ DNA replication ; GO:0006260

☐ DNA-templated transcription, elongation ; GO:0006354

☐ DNA-templated transcription, initiation ; GO:0006353

BUB3
CSM3
CTF4
DIA2
EST1
MAD1
MAD2
NPL3
NPT1
SMT3
TOF1
YMR038C

Query Set (Your Input)

Enter Gene/ORF names (separated by a return or a space):

BUB3 YMR038C CSM3 CTF4 DIA2 EST1 MAD1 MAD2 NPL3 NPT1 SMT3 TOF1

Note: If you have a big gene list (> 100), save it as a file and upload it below.

OR Upload a file of Gene/ORF names (.txt or .tab format):

Browse...

No file selected.

Specify your Slim Terms

Choose a GO Set:

Yeast GO-Slim: process

Refine your list of GO Slim Terms:

Select or unselect multiple datasets by pressing the Control (PC) or Command (Mac) key while clicking. Selecting a category label selects all datasets in that category.

SELECT ALL Terms from Yeast GO-Slim: process

DNA recombination ; GO:0006310

DNA repair ; GO:0006281

DNA replication ; GO:0006260

DNA-templated transcription, elongation ; GO:0006354

DNA-templated transcription, initiation ; GO:0006353

Submit Form

Reset Form

Query Set (Your Input)

Enter Gene/ORF names (separated by a return or a space):

BUB3 YMR038C CSM3 CTF4 DIA2 EST1 MAD1 MAD2 NPL3 NPT1 SMT3 TOF1

Note: If you have a big gene list (> 100), save it as a file and upload it below.

OR Upload a file of Gene/ORF names (.txt or .tab format):

No file selected.

Specify your Slim Terms

Choose a GO Set:

Yeast GO-Slim: process

Refine your list of GO Slim Terms:

Select or unselect multiple datasets by pressing the Control (PC) or Command (Mac) key while clicking. Selecting a category label selects all datasets in that category.

SELECT ALL Terms from Yeast GO-Slim: process

DNA recombination ; GO:0006018

DNA repair ; GO:0006281

DNA replication ; GO:0006260

DNA-templated transcription, elongation ; GO:0006354

DNA-templated transcription, initiation ; GO:0006353

Submit Form

Reset Form

Search Results

Save Options: [HTML Table](#) | [Plain Text](#) | [Tab-delimited](#) | [Your Input List of Genes](#) | [Your GO Slim List](#)

GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
mitotic cell cycle (GO:0000278)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	377 of 6440 annotated genes, 5.85%
chromosome segregation (GO:0007059)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	213 of 6440 annotated genes, 3.31%
organelle fission (GO:0048285)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	271 of 6440 annotated genes, 4.21%
regulation of cell cycle (GO:0051726)	BUB3, CSM3, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	294 of 6440 annotated genes, 4.57%
protein modification by small protein conjugation or removal (GO:0070647)	BUB3, DIA2, MAD2, SMT3	4 of 12 genes, 33.33%	220 of 6440 annotated genes, 3.42%
DNA replication (GO:0006260)	CSM3, CTF4, DIA2, TOF1	4 of 12 genes, 33.33%	147 of 6440 annotated genes, 2.28%
regulation of organelle organization (GO:0033043)	BUB3, EST1, MAD1, MAD2	4 of 12 genes, 33.33%	332 of 6440 annotated genes, 5.16%
DNA repair (GO:0006281)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	301 of 6440 annotated genes, 4.67%
cellular response to DNA damage stimulus (GO:0006974)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	236 of 6440 annotated genes, 3.66%
meiotic cell cycle (GO:0051321)	CSM3, TOF1	2 of 12 genes, 16.67%	321 of 6440 annotated genes, 4.98%
regulation of protein modification process (GO:0031399)	BUB3, MAD2	2 of 12 genes, 16.67%	214 of 6440 annotated genes, 3.32%
chromatin organization (GO:0006325)	DIA2, NPT1	2 of 12 genes, 16.67%	310 of 6440 annotated genes, 4.81%

Search Results

Save Options: [HTML Table](#) | [Plain Text](#) | [Tab-delimited](#) | [Your Input List of Genes](#) | [Your GO Slim List](#)

GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
mitotic cell cycle (GO:0000278)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	377 of 6440 annotated genes, 5.85%
chromosome segregation (GO:0007059)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	213 of 6440 annotated genes, 3.31%
organelle fission (GO:0048285)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	271 of 6440 annotated genes, 4.21%
regulation of cell cycle (GO:0051726)	BUB3, CSM3, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	294 of 6440 annotated genes, 4.57%
protein modification by small protein conjugation or removal (GO:0070647)	BUB3, DIA2, MAD2, SMT3	4 of 12 genes, 33.33%	220 of 6440 annotated genes, 3.42%
DNA replication (GO:0006260)	CSM3, CTF4, DIA2, TOF1	4 of 12 genes, 33.33%	147 of 6440 annotated genes, 2.28%
regulation of organelle organization (GO:0033043)	BUB3, EST1, MAD1, MAD2	4 of 12 genes, 33.33%	332 of 6440 annotated genes, 5.16%
DNA repair (GO:0006281)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	301 of 6440 annotated genes, 4.67%
cellular response to DNA damage stimulus (GO:0006974)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	236 of 6440 annotated genes, 3.66%
meiotic cell cycle (GO:0051321)	CSM3, TOF1	2 of 12 genes, 16.67%	321 of 6440 annotated genes, 4.98%
regulation of protein modification process (GO:0031399)	BUB3, MAD2	2 of 12 genes, 16.67%	214 of 6440 annotated genes, 3.32%
chromatin organization (GO:0006325)	DIA2, NPT1	2 of 12 genes, 16.67%	310 of 6440 annotated genes, 4.81%

Search Results

Save Options: [HTML Table](#) | [Plain Text](#) | [Tab-delimited](#) | [Your Input List of Genes](#) | [Your GO Slim List](#)

GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
mitotic cell cycle (GO:0000278)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	377 of 6440 annotated genes, 5.85%
chromosome segregation (GO:0007059)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	213 of 6440 annotated genes, 3.31%
organelle fission (GO:0048285)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	271 of 6440 annotated genes, 4.21%
regulation of cell cycle (GO:0051726)	BUB3, CSM3, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	294 of 6440 annotated genes, 4.57%
protein modification by small protein conjugation or removal (GO:0070647)	BUB3, DIA2, MAD2, SMT3	4 of 12 genes, 33.33%	220 of 6440 annotated genes, 3.42%
DNA replication (GO:0006260)	CSM3, CTF4, DIA2, TOF1	4 of 12 genes, 33.33%	147 of 6440 annotated genes, 2.28%
regulation of organelle organization (GO:0033043)	BUB3, EST1, MAD1, MAD2	4 of 12 genes, 33.33%	332 of 6440 annotated genes, 5.16%
DNA repair (GO:0006281)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	301 of 6440 annotated genes, 4.67%
cellular response to DNA damage stimulus (GO:0006974)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	236 of 6440 annotated genes, 3.66%
meiotic cell cycle (GO:0051321)	CSM3, TOF1	2 of 12 genes, 16.67%	321 of 6440 annotated genes, 4.98%
regulation of protein modification process (GO:0031399)	BUB3, MAD2	2 of 12 genes, 16.67%	214 of 6440 annotated genes, 3.32%
chromatin organization (GO:0006325)	DIA2, NPT1	2 of 12 genes, 16.67%	310 of 6440 annotated genes, 4.81%

Search Results

Save Options: [HTML Table](#) | [Plain Text](#) | [Tab-delimited](#) | [Your Input List of Genes](#) | [Your GO Slim List](#)

GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
mitotic cell cycle (GO:0000278)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	377 of 6440 annotated genes, 5.85%
chromosome segregation (GO:0007059)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	213 of 6440 annotated genes, 3.31%
organelle fission (GO:0048285)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	271 of 6440 annotated genes, 4.21%
regulation of cell cycle (GO:0051726)	BUB3, CSM3, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	294 of 6440 annotated genes, 4.57%
protein modification by small protein conjugation or removal (GO:0070647)	BUB3, DIA2, MAD2, SMT3	4 of 12 genes, 33.33%	220 of 6440 annotated genes, 3.42%
DNA replication (GO:0006260)	CSM3, CTF4, DIA2, TOF1	4 of 12 genes, 33.33%	147 of 6440 annotated genes, 2.28%
regulation of organelle organization (GO:0033043)	BUB3, EST1, MAD1, MAD2	4 of 12 genes, 33.33%	332 of 6440 annotated genes, 5.16%
DNA repair (GO:0006281)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	301 of 6440 annotated genes, 4.67%
cellular response to DNA damage stimulus (GO:0006974)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	236 of 6440 annotated genes, 3.66%
meiotic cell cycle (GO:0051321)	CSM3, TOF1	2 of 12 genes, 16.67%	321 of 6440 annotated genes, 4.98%
regulation of protein modification process (GO:0031399)	BUB3, MAD2	2 of 12 genes, 16.67%	214 of 6440 annotated genes, 3.32%
chromatin organization (GO:0006325)	DIA2, NPT1	2 of 12 genes, 16.67%	310 of 6440 annotated genes, 4.81%

Search Results

Save Options: [HTML Table](#) | [Plain Text](#) | [Tab-delimited](#) | [Your Input List of Genes](#) | [Your GO Slim List](#)

GO Terms from the biological process Ontology			
GO Term (GO ID)	Genes Annotated to the GO Term	GO Term Usage in Gene List	Genome Frequency of Use
mitotic cell cycle (GO:0000278)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	377 of 6440 annotated genes, 5.85%
chromosome segregation (GO:0007059)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	213 of 6440 annotated genes, 3.31%
organelle fission (GO:0048285)	BUB3, CSM3, CTF4, MAD1, MAD2, TOF1	6 of 12 genes, 50.00%	271 of 6440 annotated genes, 4.21%
regulation of cell cycle (GO:0051726)	BUB3, CSM3, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	294 of 6440 annotated genes, 4.57%
protein modification by small protein conjugation or removal (GO:0070647)	BUB3, DIA2, MAD2, SMT3	4 of 12 genes, 33.33%	220 of 6440 annotated genes, 3.42%
DNA replication (GO:0006260)	CSM3, CTF4, DIA2, TOF1	4 of 12 genes, 33.33%	147 of 6440 annotated genes, 2.28%
regulation of organelle organization (GO:0033043)	BUB3, EST1, MAD1, MAD2	4 of 12 genes, 33.33%	332 of 6440 annotated genes, 5.16%
DNA repair (GO:0006281)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	301 of 6440 annotated genes, 4.67%
cellular response to DNA damage stimulus (GO:0006974)	CSM3, CTF4, TOF1	3 of 12 genes, 25.00%	236 of 6440 annotated genes, 3.66%
meiotic cell cycle (GO:0051321)	CSM3, TOF1	2 of 12 genes, 16.67%	321 of 6440 annotated genes, 4.98%
regulation of protein modification process (GO:0031399)	BUB3, MAD2	2 of 12 genes, 16.67%	214 of 6440 annotated genes, 3.32%
chromatin organization (GO:0006325)	DIA2, NPT1	2 of 12 genes, 16.67%	310 of 6440 annotated genes, 4.81%

yeastgenome.org/goTermFinder



Thank you!

SGD Website

yeastgenome.org

Questions/Comments

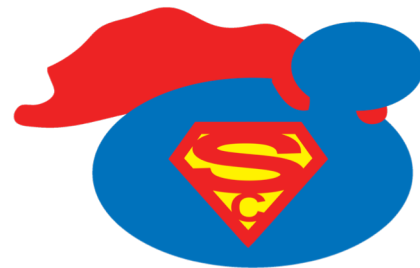
sgd-helpdesk@lists.stanford.edu

YouTube Channel

youtube.com/SaccharomycesGenomeDatabase

Download this presentation

bit.ly/ICYGMB2019



@ yeastgenome



Saccharomyces
GENOME DATABASE