Gene Ontology at SGD: GO Slim Mapper

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

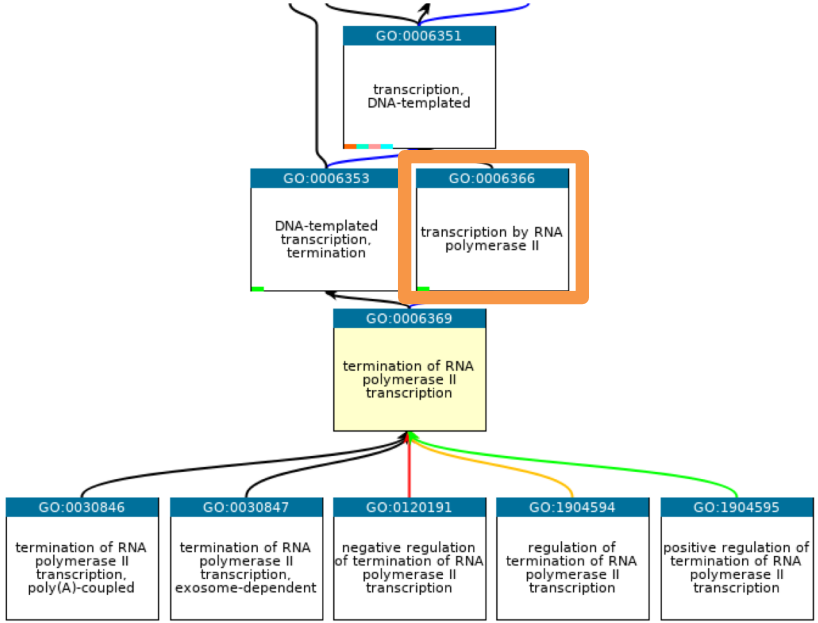
GO:0006366 transcription by RNA polymerase II

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

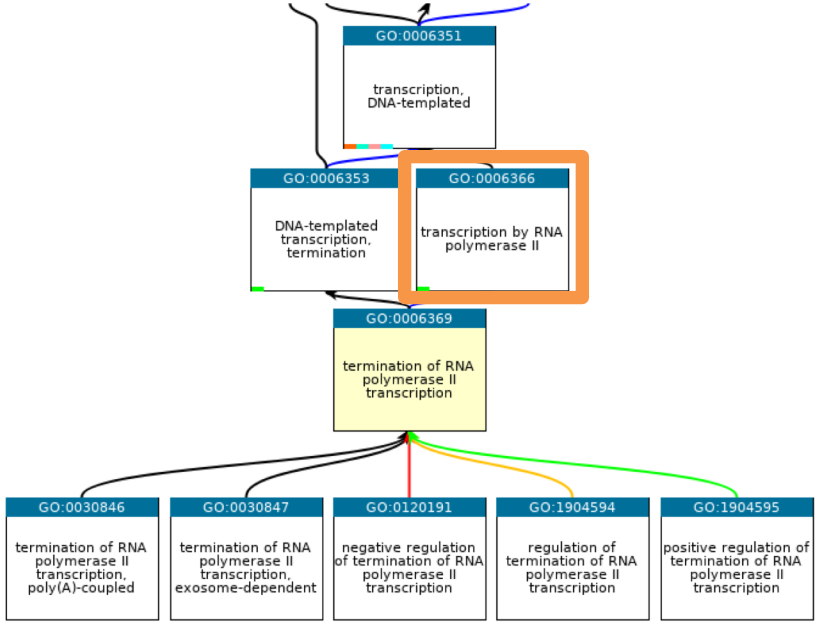
GO:0006369 termination of RNA polymerase II transcription

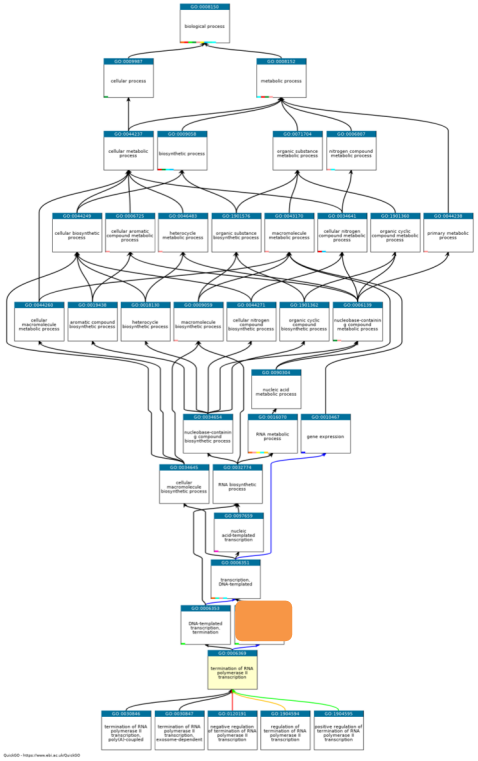
Gene Ontology overview



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

Gene Ontology overview





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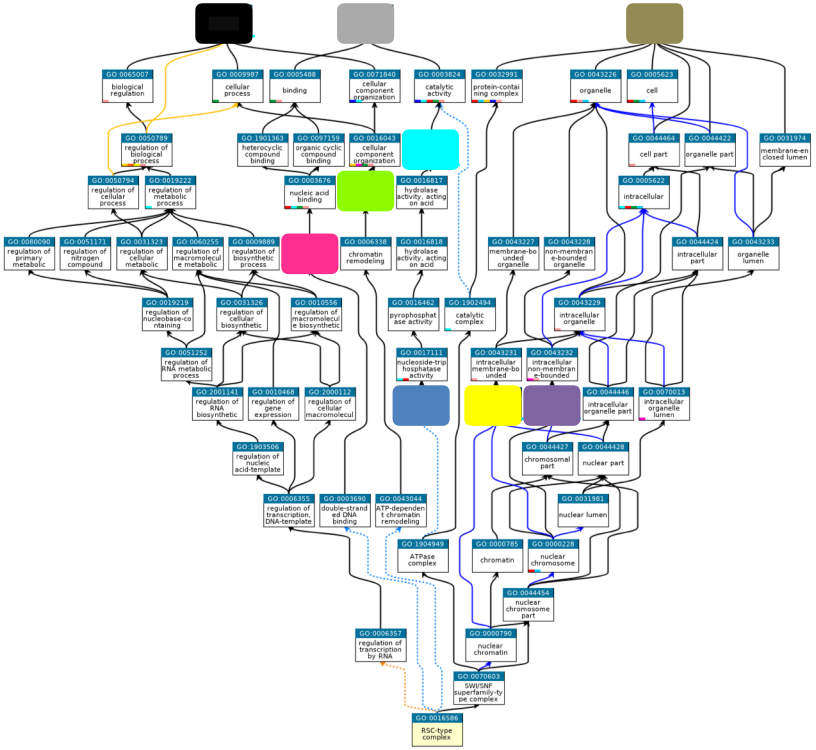

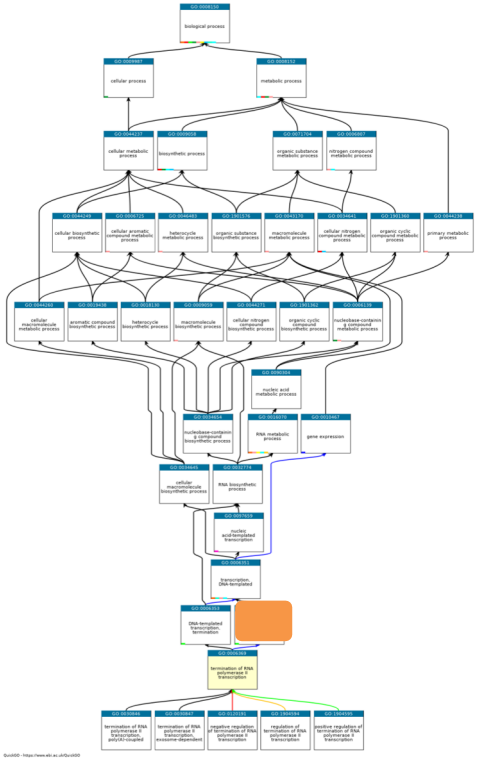

GO Slim Mapper

yeastgenome.org/goSlimMapper

Gene List

GO Slim Mapper

Term Groups

GO Slim Mapper

yeastgenome.org/goSlimMapper

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SGD Saccharomyces GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glu

Gene Ontology »
Expression
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Phenotypes »
Interactions
YeastGFP
Resources »

GO Term Finder
GO Slim Mapper
GO Slim Mapping File

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.

base (SGD) provides comprehensive
for the budding yeast *Saccharomyces*
along with search and analysis tools to explore these data, enabling
ery of functional relationships between sequence and gene products
d higher organisms.

Try this?

Meetings

29th International Conference on Yeast Genetics

New & Noteworthy

Browse Metabolic Pathways at SGD - August 02,

@yeastgenome

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):

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 categ 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

Submit Form | Reset Form

BUB3
CSM3
CTF4
DIA2
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DNA-templated transcription, initiation ; GO:0006352

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%

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GO Term Finder

yeastgenome.org/goTermFinder

Gene List

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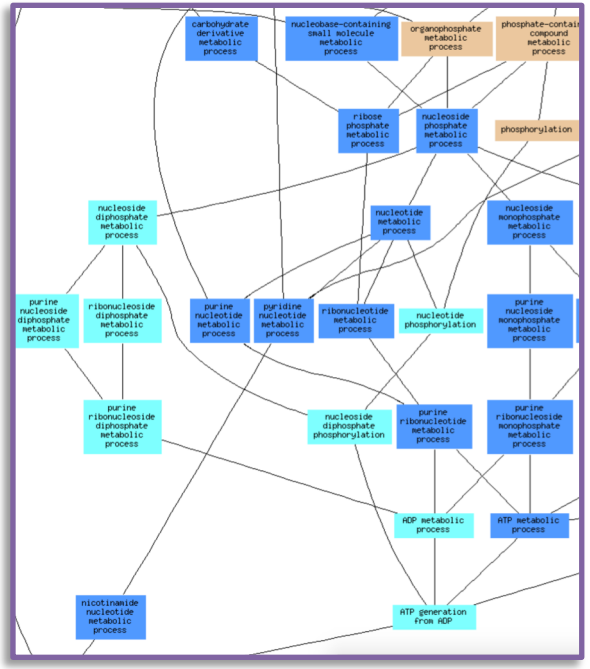

Associated Functions

Thank you!

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