Gene Ontology at SGD:

GO Slims, Grouping Genes by Function, & Enrichment Analyses

YGM 2022

Suzi Aleksander

Haddaway
what is ?
SINGLES OF THE 90s

USC University of Southern California

Keck School of Medicine of USC

Stanford MEDICINE

School of Medicine

BERKELEY LAB

Bringing Science Solutions to the World

Caltech

EMBL-EBI

NYU Langone Health

UNIVERSITY OF CAMBRIDGE

The Jackson Laboratory

Northwestern Medicine

Feinberg School of Medicine

HARVARD UNIVERSITY

SIB

Swiss Institute of Bioinformatics

UCL

UNIVERSITY OF OREGON

MEDICAL COLLEGE OF WISCONSIN

Phoenix BIOINFORMATICS

TEXAS A&M UNIVERSITY Biology

GO:0055085 transmembrane transport

Description: The process in which a solute is transported across a lipid bilayer, from one side of a membrane to the other.

Synonyms: membrane transport, ATP hydrolysis coupled transmembrane transport

GO:0055085 transmembrane transport

GO:0055085 transmembrane transport

is_a

GO:0034486 **vacuolar** transmembrane transport

GO:0055085 transmembrane transport

is_a

GO:0034486 vacuolar transmembrane transport

is_a

GO:0032974 amino acid transmembrane export from vacuole

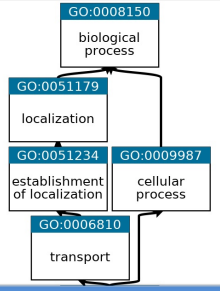
GO:0055085 transmembrane transport

GO:0034486 vacuolar transmembrane transport

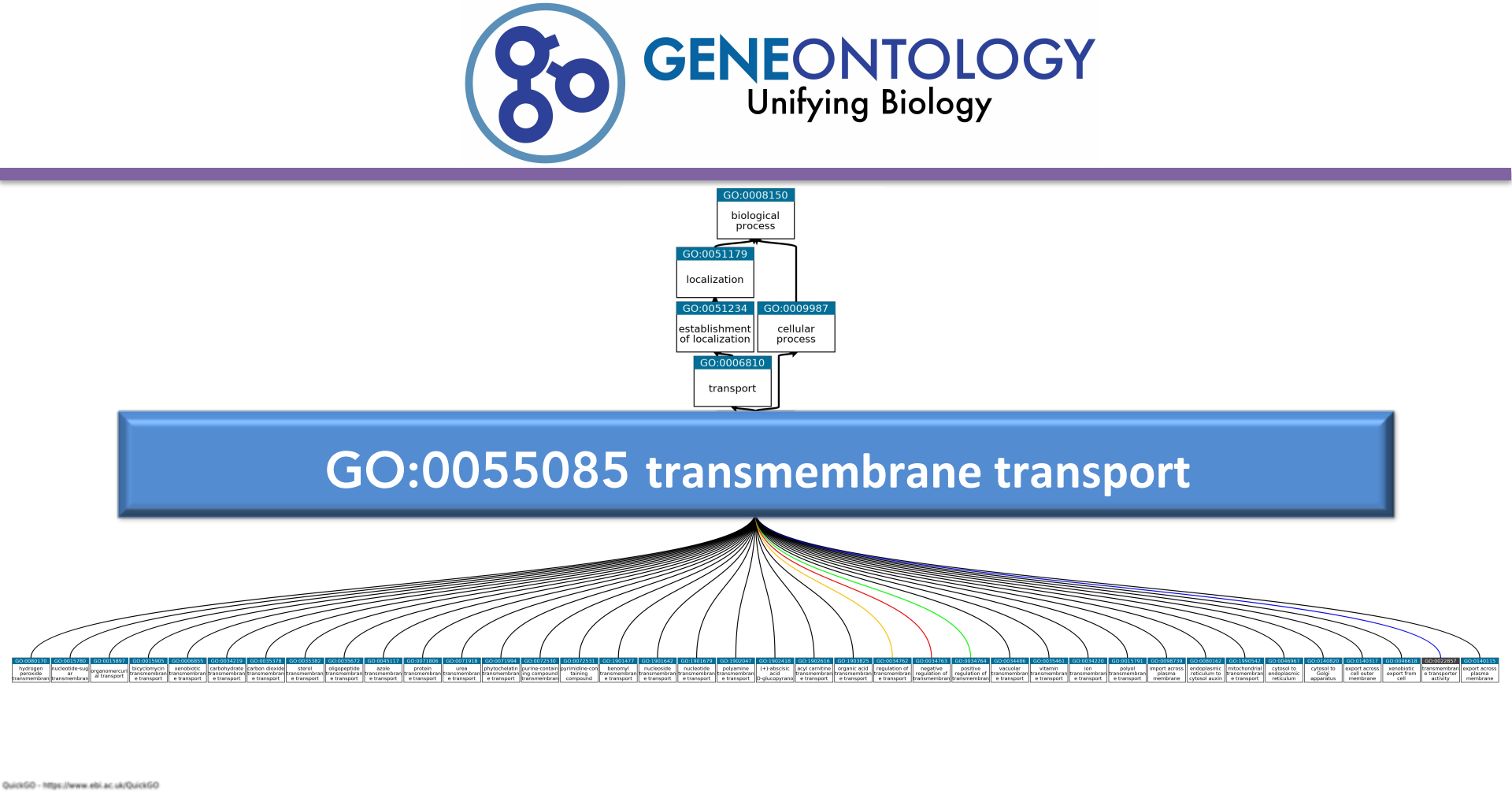
GO:0032974 amino acid transmembrane export from vacuole

is_a

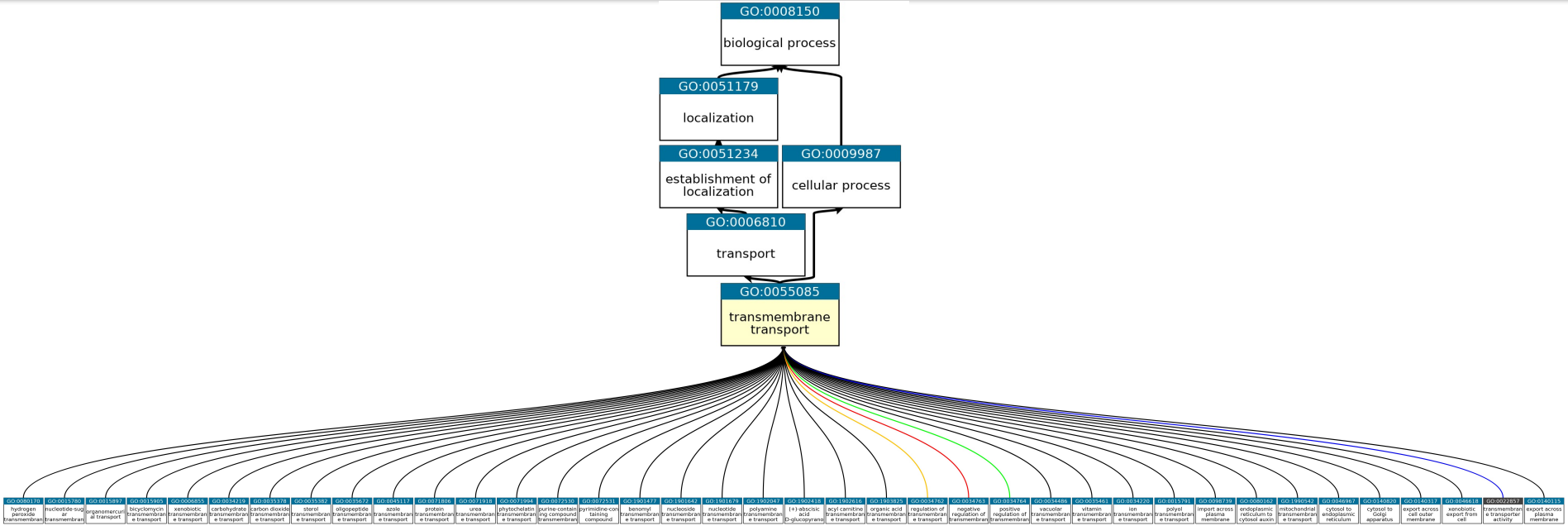
GO:0071806 protein transmembrane transport



GO:0055085 transmembrane transport


GENEONTOLOGY
Unifying Biology
GO:0008150
biological process
GO:0051179
localization
GO:0051234
establishment of localization
GO:0009987
cellular process
GO:0006810
transport
GO:0055085 transmembrane transport
GO:0080120 hydrogen peroxide transmembran
GO:0015780 nucleotide-sugar transmembran
GO:0015897 organomercurial transport
GO:0015905 bicyclomycin transmembran e transport
GO:0006855 xenobiotic transmembran e transport
GO:0034219 carbohydrate transmembran e transport
GO:0015376 carbon dioxide transmembran e transport
GO:0035382 sterol transmembran e transport
GO:0035672 oligopeptide transmembran e transport
GO:0035117 azole transmembran e transport
GO:0015806 protein transmembran e transport
GO:0071918 urea transmembran e transport
GO:0071904 phytochelatin transmembran e transport
GO:0072530 purine-contain ing compound transmembran
GO:0072531 pyrimidine-con taining compound
GO:1901477 benomyl transmembran e transport
GO:1901642 nucleoside transmembran e transport
GO:1901678 nucleotide transmembran e transport
GO:1902047 polyamine transmembran e transport
GO:1902418 (+)-abscisic acid (D-glucopyrano
GO:1902416 acyl carnitine transmembran e transport
GO:1903825 organic acid transmembran e transport
GO:0034762 regulation of transmembran e transport
GO:0034763 negative regulation of transmembran
GO:0034764 positive regulation of transmembra
GO:0034486 vacuolar transmembran e transport
GO:0034461 vitamin transmembran e transport
GO:0034220 ion transmembran e transport
GO:0015791 polyol transmembran e transport
GO:0098739 import across plasma membrane
GO:0080162 endoplasmic reticulum to cytosol auxin
GO:1990542 mitochondrial transmembran e transport
GO:0046967 cytosol to endoplasmic reticulum
GO:0140920 cytosol to Golgi apparatus
GO:0140317 export across cell outer membrane
GO:0046618 xenobiotic export from cell
GO:0022857 transmembran e transporter activity
GO:0140115 export across plasma membrane
QuickGO - https://www.ebi.ac.uk/QuickGO
ALLIANCE of GENOME RESOURCES FOUNDING MEMBER
SGD Saccharomyces GENOME DATABASE

GENEONTOLOGY
Unifying Biology



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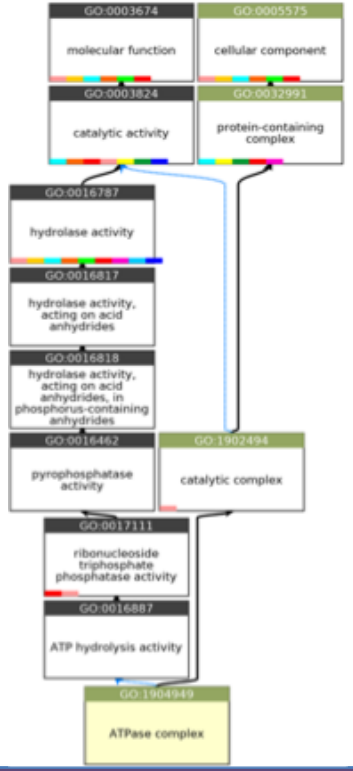

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GENEONTOLOGY
Unifying Biology

Ontology

Property	Value
Valid terms	43558 (Δ = -55)
Obsoleted terms	3770 (Δ = 53)
Merged terms	2405 (Δ = 25)
Biological process terms	28140
Molecular function terms	11238
Cellular component terms	4180

Annotations

Property	Value
Number of annotations	7,483,496
Annotations for biological process	2,817,817
Annotations for molecular function	2,350,202
Annotations for cellular component	2,315,477
Annotations for evidence PHYLO	3,994,712
Annotations for evidence IEA	1,389,615
Annotations for evidence OTHER	861,815
Annotations for evidence EXP	926,168
Annotations for evidence ND	252,154
Annotations for evidence HTP	59,032
Number of annotated scientific publications	171,053

Gene products and species

Property	Value
Annotated gene products	1,480,259
Annotated species	5,213
Annotated species with over 1,000 annotations	185

2022-07-01

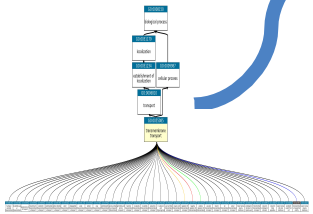
@

SGD

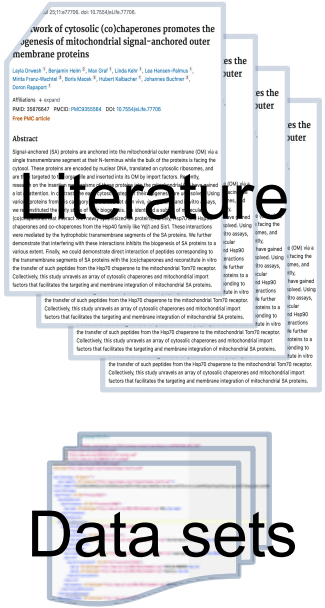
Literature

Data sets

Biocurators



GO @ SGD



Literature

Data sets

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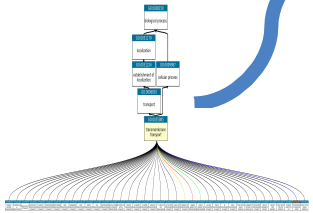
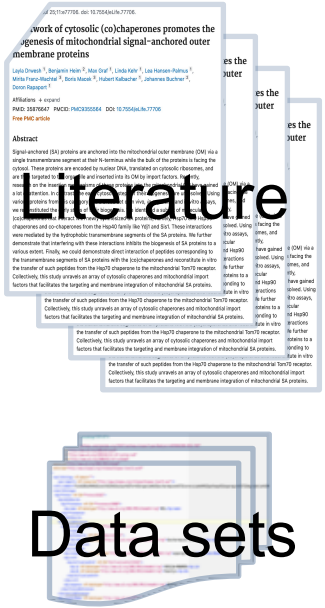


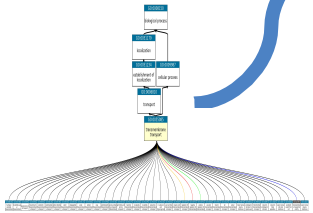
involved in	protein localization	has end location cellular bud scar, has input NBA1	IMP	SGD	2019-10-25	Meitinger F, et al. (2014) PMID:25416945

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

go @ SGD



Biocurators



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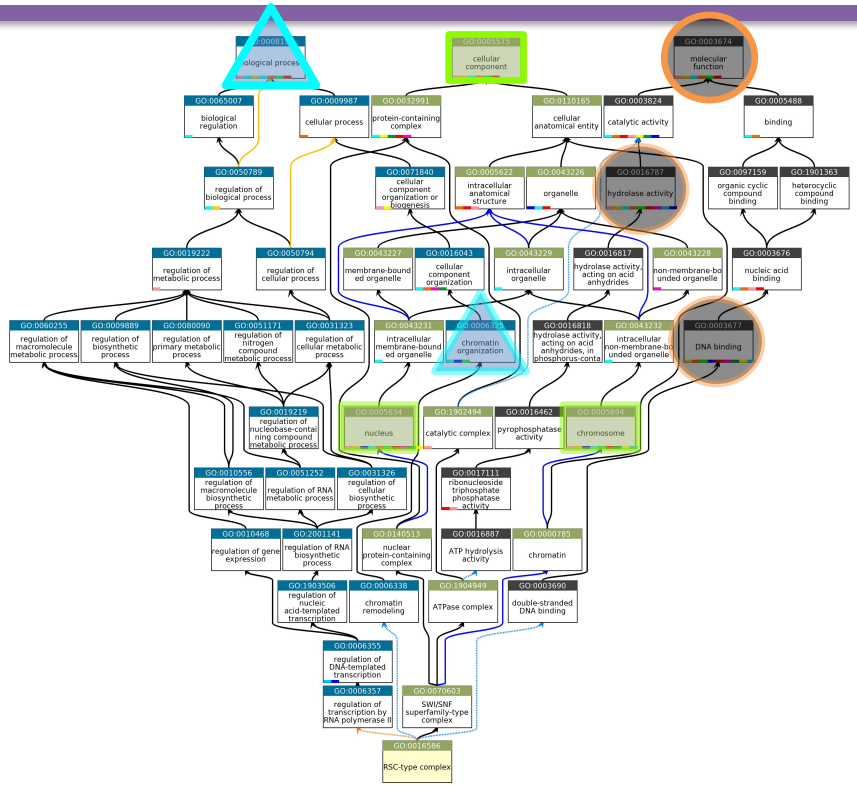
Database

- Nearly 210,000 GO annotations
- 53,330 manually annotated

GENEONTOLOGY

Unifying Biology



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

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

GO Slim Mapper

yeastgenome.org/goSlimMapper

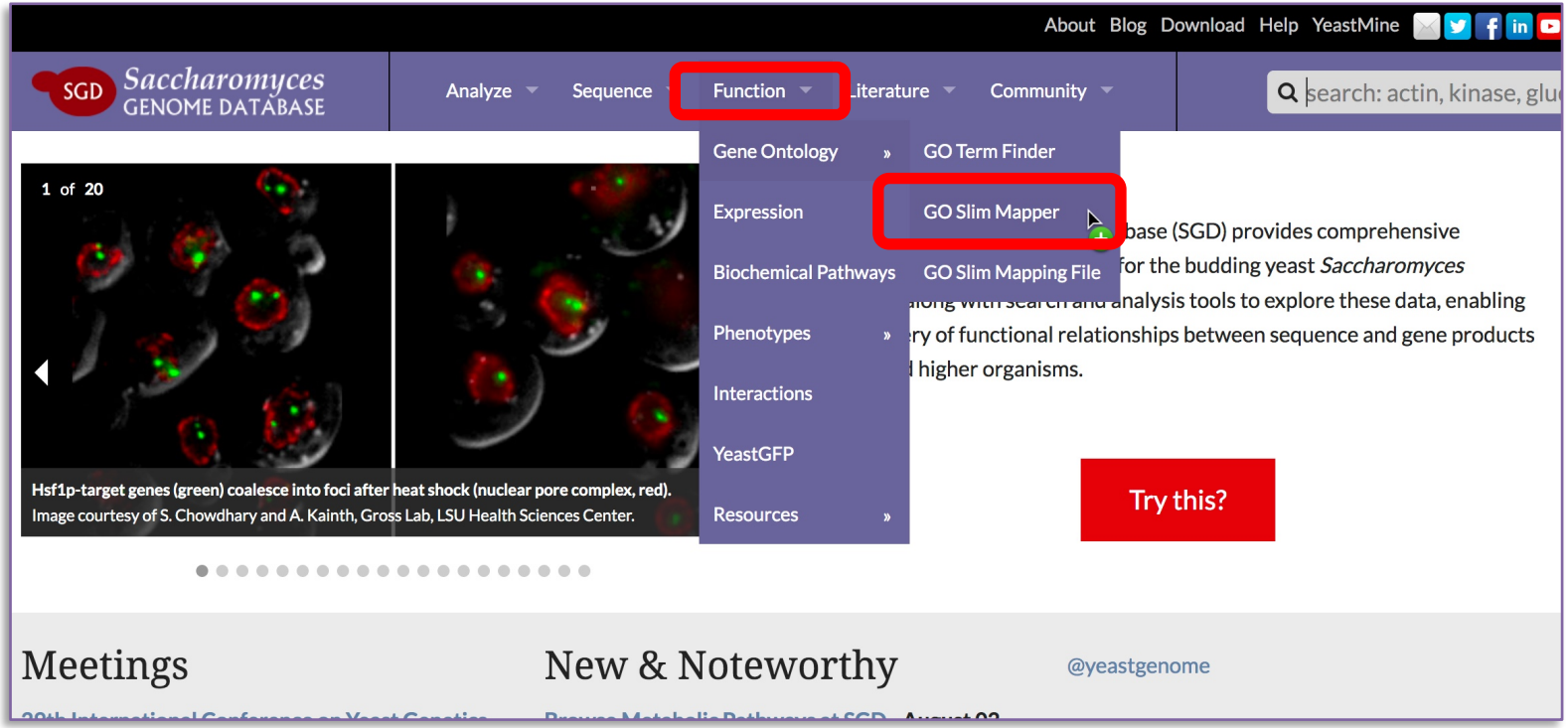
Gene List

GO Slim Mapper

Term Groups

GO Slim Mapper

yeastgenome.org/goSlimMapper



GO Slim Mapper

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
EST1
MAD1
MAD2
NPL3
NPT1
SMT3
TOF1
YMR038C

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DNA replication ; GO:0006260
DNA-templated transcription, elongation ; GO:0006354
DNA-templated transcription, initiation ; GO:0006352

Submit Form | Reset Form

GO Slim Mapper

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%	331 of 6486 annotated genes, 5.10%
chromosome segregation (GO:0007059)	CSM3, CTF4, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	194 of 6486 annotated genes, 2.99%
organelle fission (GO:0048285)	CSM3, CTF4, MAD1, MAD2, TOF1	5 of 12 genes, 41.67%	243 of 6486 annotated genes, 3.75%
regulation of cell cycle (GO:0051726)	BUB3, MAD1, MAD2, TOF1	4 of 12 genes, 33.33%	256 of 6486 annotated genes, 3.95%
DNA replication (GO:0006260)	CSM3, CTF4, DIA2, TOF1	4 of 12 genes, 33.33%	140 of 6486 annotated genes, 2.16%
protein modification by small protein conjugation or removal (GO:0070647)	BUB3, DIA2, MAD2, SMT3	4 of 12 genes, 33.33%	164 of 6486 annotated genes, 2.53%
regulation of DNA metabolic process (GO:0051052)	CSM3, DIA2, EST1, TOF1	4 of 12 genes, 33.33%	119 of 6486 annotated genes, 1.83%
regulation of organelle organization (GO:0033043)	EST1, MAD1, MAD2	3 of 12 genes, 25.00%	237 of 6486 annotated genes, 3.65%
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telomere organization (GO:0032200)	DIA2, EST1, NPT1	3 of 12 genes, 25.00%	134 of 6486 annotated genes, 2.07%
regulation of protein modification process (GO:0031399)	BUB3, MAD2	2 of 12 genes, 16.67%	118 of 6486 annotated genes, 1.82%
chromatin organization (GO:0006325)	DIA2, NPT1	2 of 12 genes, 16.67%	253 of 6486 annotated genes, 3.90%

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GO Term Finder

yeastgenome.org/goTermFinder

Gene List

GO Term Finder

Associated Functions

GO Term Finder

About Blog Download Explore Help YeastMine

SGD Saccharomyces GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glucose

Observable: budding pattern

Overview

Annotations

Observable: budding pattern

Description: The pattern with which buds emerge from a mother cell.

Qualifiers: abnormal

Annotations by mutant type and experiment type

classical genetics large-scale survey

Annot: S288C Annotations: 141 train backgrounds

Annotations 178 entries for 143 genes

Filter table

Gene	Phenotype	Experiment Type	Mutant Information	Strain Background	Chemical	Details	Reference
ACE2	budding pattern: abnormal	classical genetics	null **Allele:** ace2-Δ	W303		**Details:** cells exhibit bipolar budding pattern as opposed to axial; phenotype observed in native W303 background (bud4), but not in W303	Voth WP, et al. (2005) PMID:15947194
BNI1	budding pattern: abnormal	homozygous diploid	null **Allele:** bni1-Δ	Sigma1278b	100 mM hydroxyurea	**Treatment:** HU-induced filamentous growth	Wu X and Jiang YW (2005) PMID:16240455

Showing 1 to 10 of 178 entries 10 records per page

« 1 2 ... 17 18 »

Download (.txt) Analyze Add Annotations to Child Terms

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ALLIANCE of GENOME RESOURCES FOUNDING MEMBER GENETICS Stanford University

GO Term Finder

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SGD Saccharomyces GENOME DATABASE

Analyze Sequence Function Literature Community

search: actin, kinase, glucose

Analyze budding pattern genes

Tools

Genes

Analyze budding pattern genes

Tools

GO Term Finder
Find common GO annotations between genes.

GO Slim Mapper
Sort genes into broad categories.

SPELL
View expression data.

YeastMine
Conduct advanced analysis.

Genes

Filter table

Gene Name	Description
ACE2	Transcription factor required for septum destruction after cytokinesis; part of the RAM network that regulates polarity and morphogenesis; NES phosphorylation by RAM network kinase Cbk1p blocks nuclear exit in mother cells during the M/G1 transition, causing asymmetric localization to daughter cell nuclei, and increased Ace2p activity; phosphorylation by Cdc28p and Pho85p prevents nuclear import during cell cycle phases other than cytokinesis; Spt16p is required for nuclear exclusion during G1
ALG5	UDP-glucose:dolichyl-phosphate glucosyltransferase; involved in asparagine-linked glycosylation in the endoplasmic reticulum; human ortholog ALG5 can partially complement yeast alg5 mutant
ALG6	ER-luminal alpha 1,3 glucosyltransferase; involved in transfer of oligosaccharides from dolichyl pyrophosphate to asparagine residues of proteins during N-linked protein glycosylation; C998T transition in human ortholog ALG6 causes carbohydrate-deficient glycoprotein syndrome type-Ic; wild-type human ortholog ALG6 can partially complement yeast alg6 mutant
ALG8	Glucosyl transferase; involved in N-linked glycosylation; adds glucose to the dolichol-linked oligosaccharide precursor prior to transfer to protein during lipid-linked oligosaccharide biosynthesis; similar to Alg6p; human homolog ALG8 can complement yeast null mutant

Gene Ontology Term Finder

The GO Term Finder (Version 0.86) searches for significant shared GO terms, or parents of those GO terms, used to describe the genes in your list to help you discover what the genes may have in common. To map annotations of a group of genes to more general terms and/or to bin them in broad categories, use the GO Slim Mapper.

For this form, Steps 1 and 2 are required, and Steps 3 and 4 are optional. If using only Steps 1 and 2, the search will be done using these default settings: 1. All genes/features with GO annotations in the database, 2. All annotations in the database (manually curated, high-throughput, and computational), and 3. All hits with p-value < 0.01 will be displayed on results page..

Submit Form | Reset Form

Step 1. Query Set (Your Input)

Your gene list has been saved in the memory. Please pick the ontology and other options and Submit the form.

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

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.

Step 2. Choose Ontology

Pick an ontology aspect:

◉ Process ○ Function ○ Component

Search using default settings or use Step 3 and/or Step 4 below to customize your options.

Step 3. (Optional) Specify your background set of genes

Leave empty to use default background set (all features in the database that have GO annotations) **OR Enter Gene/ORF names** (separated by a return or a space):

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Browse... No file selected.

Step 4. Optional Input

Pick evidence codes to exclude for calculation:

☐ HDA ☐ HGI ☐ HMP ☐ IBA ☐ IC ☐ IEA ☐ IDA ☐ IEP
☐ IGI ☐ IKR ☐ IMP ☐ IMR ☐ IPI ☐ IRD ☐ ISA ☐ ISM
☐ ISO ☐ ISS ☐ NAS ☐ ND ☐ TAS

Pick a p-value below (default is 0.01):

0.01

Calculate false discovery rate (FDR)?

☑ FDR

Submit Form | Reset Form

GO Term Finder

Gene Ontology Term Finder

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Pick a p-value below (default is 0.01):

0.01

Calculate false discovery rate (FDR)?

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GO Term Finder

GO Term Finder

Gene Ontology Term Finder

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- (•) Process
- ( ) Function
- ( ) Component

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Pick a p-value below (default is 0.01):

0.01

Calculate false discovery rate (FDR)?

☑ FDR

Submit Form | Reset Form

GO Term Finder

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Browse... No file selected.

Step 2. Choose Ontology

Pick an ontology aspect:

- (●) Process
- ( ) Function
- ( ) Component

Search using default settings or use Step 3 and/or Step 4 below to customize your options.

Step 3. (Optional) Specify your background set of genes

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Note: If you have a big background 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.

Step 4. Optional Input

Pick evidence codes to exclude for calculation:

- [ ] HDA
- [ ] HGI
- [ ] HMP
- [x] IBA
- [ ] IC
- [x] IEA
- [ ] IDA
- [ ] IEP
- [ ] IGI
- [ ] IKR
- [ ] IMP
- [ ] IPI
- [ ] ISA
- [ ] ISM
- [ ] ISO
- [ ] ISS
- [ ] NAS
- [ ] ND
- [ ] TAS

Pick a p-value below (default is 0.01):

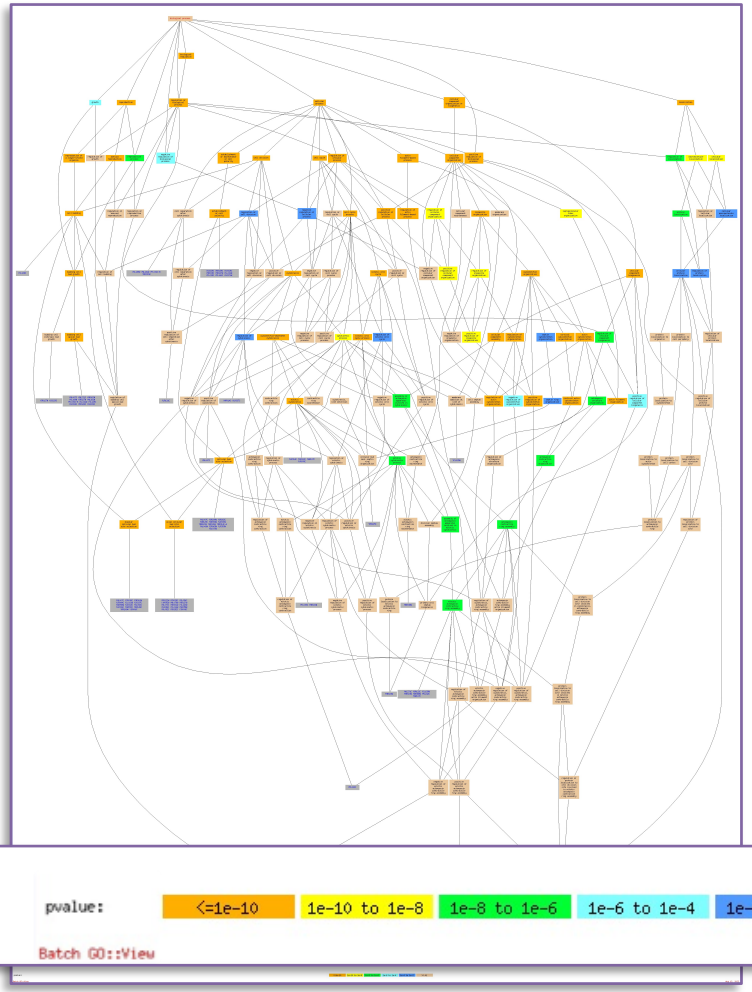
0.01

Calculate false discovery rate (FDR)?

- [x] FDR

Submit Form | Reset Form

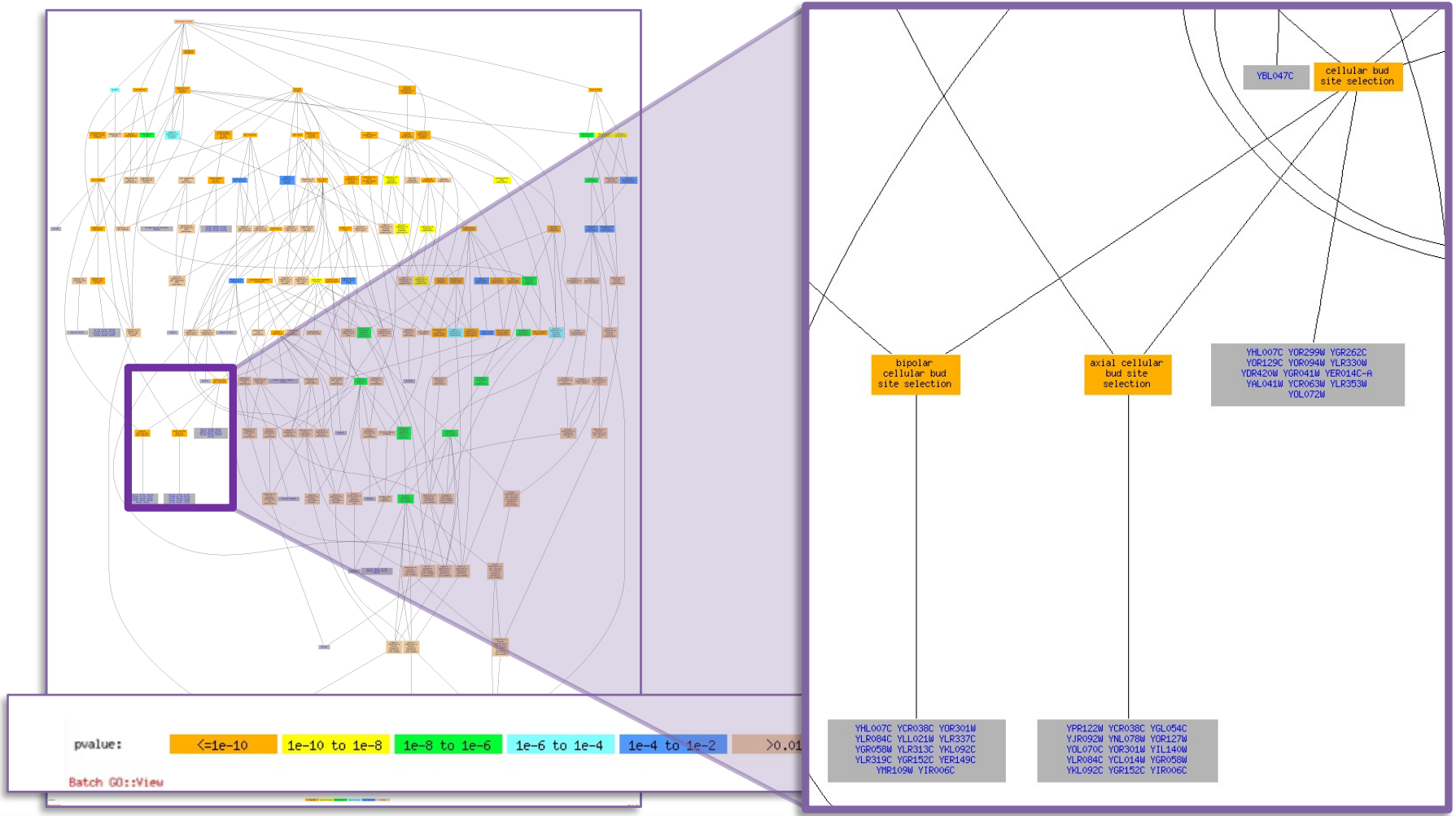
GO Term Finder



pvalue:	<=1e-10	1e-10 to 1e-8	1e-8 to 1e-6	1e-6 to 1e-4	1e-4 to 1e-2	>0.01

Batch GO::View

GO Term Finder



GO Term Finder

Of your input list, 200 gene name identifiers are known or unknown but not ambiguous. Identifiers unknown to the annotation provider are still included in the statistics. The total number of genes used to calculate the background distribution of GO terms is 7166. Displaying 155 terms out of a total of 1078 found.

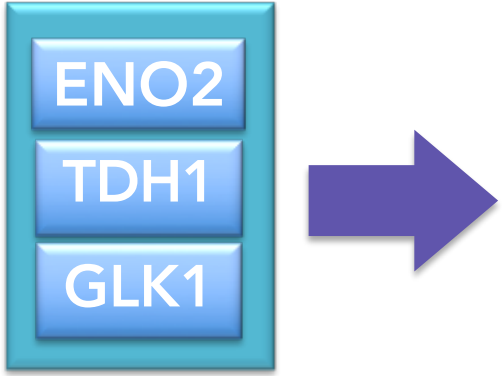
Result Table

Terms from the Process Ontology of gene_association.sgd with p-value <= 0.01

Evidence code filter included: HDA HGI HMP IC IDA IEP IGI IKR IMP IMR IPI IRD ISA ISM ISO ISS NAS ND TAS

Gene Ontology term	Cluster frequency	Genome frequency	Corrected P-value	FDR	False Positives	Genes annotated to the term
cell division	60 of 200 genes, 30.0%	127 of 7166 genes, 1.8%	1.03e-58	0.00%	0.00	YPR122W, YHL007C, YNL271C, YCR038C, YOR299W, YMR001C, YFL039C, YHR115C, YHR102W, YAR014C, YGR262C, YLR314C, YGL054C, YJR092W, YOR122C, YNL078W, YKL189W, YOR127W, YOL070C, YOR301W, YNL161W, YIL140W, YIL159W, YOR129C, YOR094W, YFL034C-B, YBR160W, YLR330W, YLR131C, YDR420W, YGR041W, YER014C-A, YHR023W, YLR084C, YDR388W, YLR371W, YLL021W, YAL041W, YCL014W, YBL047C, YCR002C, YPL242C, YLR337C, YGR058W, YLR313C, YBR038W, YIL129C, YKL092C, YCR063W, YLR319C, YGR152C, YER149C, YFL005W, YLR229C, YHR107C, YJR076C, YLR353W, YMR109W, YIR006C, YOL072W
cytokinesis	53 of 200 genes, 26.5%	92 of 7166 genes, 1.3%	1.78e-57	0.00%	0.00	YBR038W, YGR058W, YLR313C, YCR063W, YKL092C, YLR319C, YER149C, YGR152C, YFL005W, YHR107C, YLR353W, YJR076C, YOL072W, YMR109W, YIR006C, YLR371W, YLL021W, YCL014W, YAL041W, YBL047C, YCR002C, YPL242C, YLR337C, YOR122C, YNL078W, YOL070C, YOR127W, YIL140W, YIL159W, YOR301W, YOR094W, YOR129C, YBR160W, YLR330W, YDR420W, YGR041W, YHR023W, YER014C-A, YDR388W, YLR084C, YPR122W, YHL007C, YNL271C, YMR001C, YCR038C, YOR299W, YFL039C, YHR115C, YAR014C, YLR314C, YGL054C, YGR262C, YJR092W
mitotic cytokinesis	50 of 200 genes, 25.0%	81 of 7166 genes, 1.1%	3.68e-56	0.00%	0.00	YCR002C, YPL242C, YLR337C, YLR371W, YLL021W, YAL041W, YCL014W, YHR107C, YJR076C, YLR353W, YOL072W, YMR109W, YIR006C, YBR038W, YGR058W, YLR313C, YCR063W, YKL092C, YLR319C, YER149C, YGR152C, YHR115C, YLR314C, YGL054C, YGR262C, YJR092W, YPR122W, YHL007C, YNL271C, YMR001C, YCR038C, YOR299W, YFL039C, YBR160W, YLR330W, YDR420W, YGR041W, YHR023W, YER014C-A, YDR388W, YLR084C, YOR122C, YNL078W, YOL070C, YOR127W, YIL159W, YIL140W, YOR301W, YOR094W, YOR129C
cytoskeleton-dependent cytokinesis	50 of 200 genes, 25.0%	81 of 7166 genes, 1.1%	3.68e-56	0.00%	0.00	YCR063W, YKL092C, YBR038W, YGR058W, YLR313C, YER149C, YGR152C, YLR319C, YHR107C, YOL072W, YMR109W, YIR006C, YLR353W, YJR076C, YLR371W, YAL041W, YLL021W, YCL014W, YCR002C, YLR337C, YPL242C, YOR127W, YOL070C, YOR122C, YNL078W, YOR094W, YOR129C, YIL159W, YIL140W, YOR301W, YDR420W, YGR041W, YBR160W, YLR330W, YDR388W, YLR084C, YHR023W, YER014C-A, YHL007C, YNL271C, YPR122W, YFL039C, YMR001C, YCR038C, YOR299W, YHR115C, YJR092W, YLR314C, YGL054C, YGR262C
cellular bud site selection	34 of 200 genes, 17.0%	37 of 7166 genes, 0.5%	6.17e-48	0.00%	0.00	YOL072W, YIR006C, YLR084C, YMR109W, YLR353W, YER014C-A, YGR041W, YDR420W, YLR330W, YOR094W, YER149C, YOR129C, YGR152C, YIL140W, YLR319C, YOR301W, YCR063W, YOL070C, YOR127W, YKL092C, YLR313C, YNL078W, YGR058W, YLR337C, YJR092W, YGL054C, YGR262C, YLL021W, YAL041W, YCL014W, YOR299W, YCR038C, YHL007C, YPR122W
establishment of cell polarity	41 of 200 genes, 20.5%	67 of 7166 genes, 0.9%	4.23e-45	0.00%	0.00	YOL072W, YMR109W, YIR006C, YLR084C, YLR353W, YER014C-A, YDR420W, YGR041W, YLR229C, YLR330W, YOR094W, YER149C, YGR152C, YOR129C, YIL140W, YLR319C, YOR301W, YOR008C, YOL070C, YOR127W, YCR063W, YKL092C, YGR058W, YNL078W, YLR313C, YLR337C, YJR092W, YGL054C, YGR262C, YHR115C, YAL041W, YLL021W, YCL014W, YFL039C, YPL161C, YCR038C, YOR299W, YLR371W, YHL007C, YNL271C, YPR122W
establishment or maintenance of cell	47 of 200 genes,	105 of 7166	1.61e-43	0.00%	0.00	YFL039C, YCR038C, YOR299W, YHL007C, YNL271C, YPR122W, YJR092W, YLR314C, YGL054C, YGR262C, YHR115C, YFL034C-B, YOR094W, YOR129C, YIL140W, YOR301W, YNL161W, YOR127W, YOL070C, YNL078W, YLR084C, YER014C-A, YDR420W,

Gene Ontology Enrichment Analysis

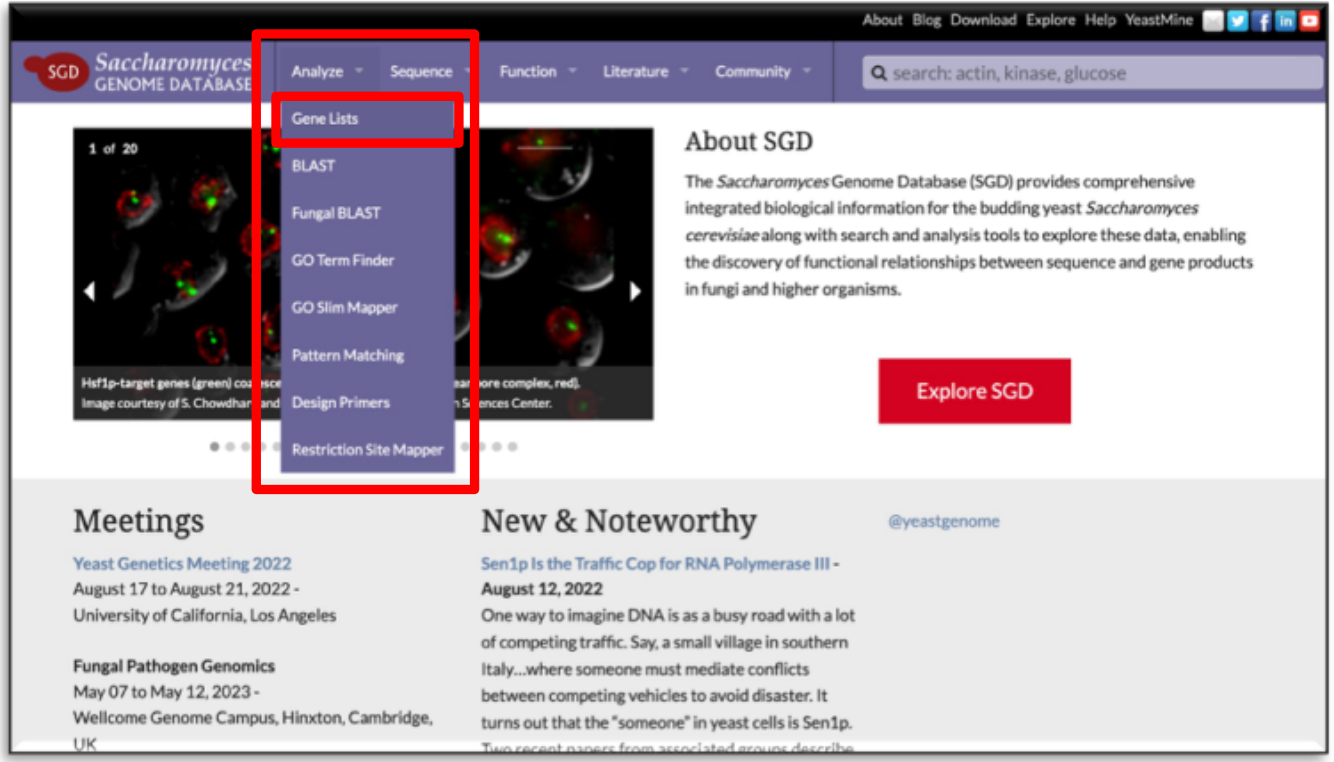


Differentially Expressed Genes

GO Terms

GO Terms

Gene Ontology Enrichment Analysis



Gene Ontology Enrichment Analysis

SGD YeastMine

Search and retrieve S. cerevisiae data with YeastMine, populated by SGD and powered by InterMine.

Data Updated on: Aug-9-2022

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Upload | View

Search: e.g. act1 GO

1 Upload list of identifiers | 2 Verify identifier matches | List analysis

Create a new list

Select the type of list to create and either enter in a list of identifiers or upload identifiers from a file. A search will be performed for all the identifiers in your list.

- Separate identifiers by a **comma**, **space**, **tab**, **new line** or **semi-colon**.
- Qualify any identifiers that contain whitespace with double quotes like so:"even skipped".

Select Type: Gene

for Organism: S. cerevisiae

Type/Paste in identifiers (click to see an example)

or Upload identifiers from a .txt file... Browse... No file selected.

☐ **Match on case**

Reset | Create List

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Upload | View

Search: e.g. act1 GO

Before we show you the results ...

Choose a name for the list

MyAwesomeGeneList (e.g. Smith 2013)

Add additional matches

You entered: 23 identifiers
We found: 22 Genes

Save a list of 22 Genes

Why are the numbers different? See below.

Duplicates found - which one(s) do you want?

Add all | Remove all

Page 1 of 2 1 2

5 rows per page

Identifier you provided	Matches							Action
	symbol	organism short name	name	length	secondary identifier	primary identifier	class	
acr1	SFC1	S. cerevisiae	Succinate-Fumarate Carrier	969	YJR095W	S000003856	ORF	Add
	SKO1	S. cerevisiae	Suppressor of Kinase Overexpression	1944	YNL167C	S000005111	ORF	Add

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Upload | View

Search: e.g. act1 GO

List Analysis for MyAwesomeGeneList (22 Genes)

Manage Columns | Manage Filters | Manage Relationships | Save as List | Generate Python code | Export

Showing 1 to 22 of 22 rows

Rows per page: 10

Gene Primary DBID	Gene Systematic Name	Gene Organism . Short Name	Gene Standard Name	Gene Name
S000000277	YBR073W	S. cerevisiae	RDH54	RAD54 Homolog
S000000897	YER095W	S. cerevisiae	RAD51	RADiation sensitive
S000000975	YER173W	S. cerevisiae	RAD24	RADiation sensitive
S000000981	YER179W	S. cerevisiae	DMC1	Disrupted Meiotic cDNA
S000001014	YHL022C	S. cerevisiae	SPO11	SPOrulation
S000001108	YHR066W	S. cerevisiae		Suppressor of ste4 (Four)
S000001162	YHR120W	S. cerevisiae		MutS Homolog
S000001166	YHR124W	S. cerevisiae		Non-DiTyrosine
S000002313	YDL154W	S. cerevisiae		[illegible] Homolog
S000002388	YDL229W	S. cerevisiae		[illegible]ress-Seventy subfamily B
S000002411	YDR004W	S. cerevisiae		RADiation sensitive
S000002483	YDR076W	S. cerevisiae		RADiation sensitive
S000002625	YDR217C	S. cerevisiae	RAD9	RADiation sensitive

Orthologues

A. fischeri NRRL 181 (20) A. flavus NRRL3357 (19) A. fumigatus Af293 (20)
A. nidulans FGSC A4 (19) A. niger ATCC 1015 (17) C. albicans SC5314 (19) C. albicans WO-1 (19)
C. dubliniensis CD36 (19) C. gattii VGII R265 (20) C. gattii WM276 (20) C. glabrata CBS 138 (22)
C. immitis H538.4 (24) C. immitis RS (20) C. neoformans var. grubii H99 (20)
C. neoformans var. neoformans JEC21 (20) C. parapsilosis CDC317 (19)
C. posadasii C735 delta SOWgp (21) H. capsulatum G186AR (22) N. crassa OR74A (18)
P. oryzae 70-15 (19) S. pombe (21) T. marneffei ATCC 18224 (20) U. maydis 521 (17)

View homologues in other Mines:

FlyMine
D. melanogaster x

HumanMine
H. sapiens x

MouseMine
Could not retrieve results

RatMine
Could not retrieve results

ZebrafishMine
Could not retrieve results

External Links

RatMine
D.rerio orthologues at ZFIN protomine
D.mel orthologues in FlyMine

SGD YeastMine

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Upload | View

Before we show you the results ...

Choose a name for the list

MyAwesomeGeneList

Add additional matches

You entered: 23 identifiers
We found: 22 Genes

Why are the numbers different? See below.

Duplicates found - which one(s) d

Page 1 of 2 1 2

Identifier you provided	Matches symbol	organism short name
acr1	SFC1	S. cerevisiae
	SKO1	S. cerevisiae

SGD YeastMi

Home | Templates | Li

Upload | View

1

Gene Ontology Enrichment Analysis

Gene Ontology Enrichment

GO terms enriched for items in this list.

Number of Genes in this list not analysed in this widget: 1

Test Correction	Max p-value	Ontology
Holm-Bonferroni	0.05	biological_process

Background population

Default Change

View Download

GO Term	p-Value	Matches
establishment of cell polarity [GO:0030010]	1.257571e-17	24
cellular bud site selection [GO:0000282]	1.271300e-16	19
establishment or maintenance of cell polarity [GO:0007163]	4.910459e-15	26
mitotic cytokinesis [GO:0000281]	6.895667e-15	23
cytokinesis [GO:0000910]	7.956850e-15	25

Gene Ontology Enrichment Analysis

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Number of Genes in this list not analysed in this widget: 1

Test Correction	Max p-value	Ontology
Holm-Bonferroni	0.05	biological_process

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Default Change

View Download

GO Term	p-Value	Matches
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establishment or maintenance of cell polarity [GO:0007163]	4.910459e-15	26
mitotic cytokinesis [GO:0000281]	6.895667e-15	23
cytokinesis [GO:0000910]	7.956850e-15	25

GO Citation Policy

Minimum citation:

Ashburner et al. **Gene ontology: tool for the unification of biology**. Nat Genet. May 2000. doi: 10.1038/75556

The Gene Ontology Consortium. **The Gene Ontology resource: enriching a GOld mine**. Nucleic Acids Res. Jan 2021. doi: 10.1093/nar/gkaa1113

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