



# The *Saccharomyces* Genome Database and the Gene Ontology: Best Buds



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The *Saccharomyces* Genome Database (SGD; [www.yeastgenome.org](http://www.yeastgenome.org)) is a comprehensive resource of curated molecular and genetic information on the genes and proteins of *Saccharomyces cerevisiae*. Since 2001, SGD has used the Gene Ontology (GO; [geneontology.org](http://geneontology.org)) to annotate the functions of gene products in budding yeast. Expert curators select GO terms to assign to gene products based on published scientific literature. While traditional experimental methods are the primary sources of GO annotations, results from comparative sequence and genomic studies, functional genomic analyses and proteomic data have provided valuable insights into the biological roles of gene products and these data are also incorporated into SGD. SGD has several web interfaces and analysis tools that display and use these data. These interfaces and tools are important parts of SGD's ongoing mission facilitate research, education, and discovery using the Gene Ontology. This work is funded by the US National Institutes of Health: National Human Genome Research Institute (NHGRI [U41HG001315]) and National Institute of General Medical Sciences (NHGRI NIGMS [U41HG002273]).

## What is GO?

- Controlled vocabulary of 43,000+ terms over three categories (aspects) with structured relationships: terms form a directed acyclic graph (DAG)
  - Molecular Function** ontology describes activities of entities
  - Biological Process** ontology places these MFs in a biological context
  - Cellular Component** ontology indicates subcellular localizations

### Gene Ontology Term: cell budding

GO ID: GO:0007114  
 Aspect: Biological Process  
 Description: A form of asexual reproduction, occurring in certain bacteria and fungi (e.g. yeasts) and some primitive animals in which an individual arises from a daughter cell formed by pinching off a part of the parent cell. The budlike outgrowths so formed may sometimes remain attached to the parent cell.  
 Synonyms: budding

A GO Term comprises computer-readable ID number + human-readable name + definition

Ancestor Chart from <https://www.ebi.ac.uk/QuickGO>

## Parts of a GO annotation

GO Term  
Links to SGD term page including term ID, definition, synonyms, and other entities annotated to this term (if any)

Qualifier	Gene Ontology Term	Annotation Extension	Evidence	Source	Assigned On	Reference
involved in	negative regulation of protein localization to nucleolus	happens during meiotic anaphase II, has input CDC14	IMP	SGD	2020-08-24	Paulissen SM, et al. (2020) PMID:32788308

**Evidence & Reference**

- Every GO annotation is directly supported by a **reference**
- Evidence** indicates type of support in reference
  - usually experimental, phylogenetic, or computational

### Qualifier

Relations Ontology (RO) term to indicate intended interpretation of the gene product ↔ GO term association

### Annotation Extension

Optional specification of GO term such as substrate, target protein, and/or biological phase

## Accessing GO at SGD

**Gene Ontology**

Summary: Protein involved in bud site selection; localizes to vacuole and bud neck

**Locus Summary Pages**

- GO Terms at-a-glance
- Lists manually curated, electronic, and high-throughput annotations

Manually Curated: • ena1

Biological Process

- involved in axial cellular bud site selection (IMP)
- involved in bipolar cellular bud site selection (IMP, IGI)
- involved in protein localization (IMP)

Component

- part of cellular bud neck (IDA)
- part of cellular bud scar (IDA)

Output: • part of fungal-type vacuole (HDA)

**YeastMine**

Search and retrieve *S. cerevisiae* data. Updated on: Aug-2-2020

Search: Search YeastMine. Enter name, identifier or keyword for genes, proteins, ontology terms, authors, abstract etc. (e.g. *rad54*, Act1p, DNA binding, Betel D).

SEARCH

GENOME PROTEINS **FUNCTION** PHENOTYPES

**Gene Ontology Enrichment**

GO terms enriched for items in this list. All items in your list have been analyzed.

Test Correction: Holm-Bonferroni | Max p-value: 0.05 | Ontology: biological\_process

Background population: Default Change

GO Term	p-Value	Matches
axial cellular bud site selection [GO:0007120]	2.873433e-41	15
cellular bud site selection [GO:0000282]	2.834726e-30	15
cell budding [GO:0007114]	9.158822e-29	15

Read more

Query for function:

- GO Term → All genes
- Gene → GO Terms
- GO Term name [and]
- GO ID → Genes
- Gene → Pathways
- Pathway → Genes
- GO Term name →
- GO Slim Term →

**YeastMine**

- Multifaceted search and retrieval environment
- Load & save custom lists of genes or GO Terms
  - Integrated **GO Term enrichment** widget
- Preloaded templates for straightforward searches

**Function Networks**

View shared GO annotations between proteins

**RAX1 / YOR301W Gene Ontology**

Summary: Protein involved in bud site selection; localizes to vacuole and bud neck

GO Slim Terms: molecular function, cell budding, cell division, reproduction, organelle, site of polarized growth, vacuole

Manually Curated

Biological Process 5 entries for 3 Gene Ontology terms

Qualifier	Gene Ontology Term	Annotation Extension	Evidence	Source	Assigned On	Reference
involved in	axial cellular bud site selection					
involved in	protein localization	has end location cellular bud scar, has input NBA1	IMP	SGD	2019-10-25	Meltinger F, et al. (2014) PMID:25416945
involved in	protein localization	has end location cellular bud scar, has input NIS1	IMP	SGD	2019-10-25	Meltinger F, et al. (2014) PMID:25416945
involved in	bipolar cellular bud site selection		IMP	SGD	2019-09-21	Fujita A, et al. (2004) PMID:14980713

**Gene Ontology Tab**

- Curator-written **Function Summaries**
- GO Slim terms from SGD's yeast-specific slim
- Full GO annotations

**Gene Ontology Term Finder**

Gene Ontology term	Cluster frequency	Genome frequency	Corrected P-value	FDR	False Positives	Genes annotated to the term
axial cellular bud site selection	15 of 15 genes, 100.0%	15 of 7166 genes, 0.2%	2.18e-44	0.00%	0.00	YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
cellular bud site selection	15 of 15 genes, 100.0%	89 of 7166 genes, 1.24%	8.33e-28	0.00%	0.00	YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
cell budding	15 of 15 genes, 100.0%	15 of 7166 genes, 0.2%	2.18e-44	0.00%	0.00	YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
axial cellular bud site selection	15 of 15 genes, 100.0%	15 of 7166 genes, 0.2%	2.18e-44	0.00%	0.00	YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
cellular bud site selection	15 of 15 genes, 100.0%	89 of 7166 genes, 1.24%	8.33e-28	0.00%	0.00	YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
cell budding	15 of 15 genes, 100.0%	15 of 7166 genes, 0.2%	2.18e-44	0.00%	0.00	YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
cytoskeleton organization	3 of 15 genes, 20.00%	253 of 6486 annotated genes, 3.90%				YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,
Golgi vesicle transport	2 of 15 genes, 13.33%	193 of 6486 annotated genes, 2.97%				YOL070C, YIL140W, YOR127W, YOR301W, YLR084C, YKL092C, YGR152C, YPR122W, YJR092W, YGL054C, YGR058W, YJR006C,

**GO Term Finder**

View & download significant shared GO Terms used to describe the genes from an input list

Results in Table and GO Tree formats

**Slim Mapper**

Bins your genes into broader categories of GO Terms

