

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



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The *Saccharomyces* Genome Database (SGD; 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) 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)

Gene Ont	ology Term: cell budding
GO ID:	GO:0007114
Aspect:	Biological Process

- Molecular Function ontology describes activities of entities
- Biological Process ontology places these MFs in a biological context
- Cellular Component ontology indicates subcellular localizations

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



	Cone Ontology ()		Cone Ontolom: Details			Gene Ontology Enrichment			
RAX1/YOR301W		Gene Ontology •		Gene Ontology Details O			GO terms enriched for items in this list.		
Locus Overview	Summany	Protoin involved in hud site colection: localizes to vacuale and hud neck	SGD	YeastMine	Search and retrieve S. cerevis	Test Correction	Max p-value	Ontology	
	Summary.	Froten involved in bud site selection, localizes to vacuole and bud neck		100000000000000000000000000000000000000	Data Updated on: Aug-2-202	Holm-Bonferroni v	0.05	v biological_process v	











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