

The Saccharomyces Genome Database and the Gene Ontology: Best Buds

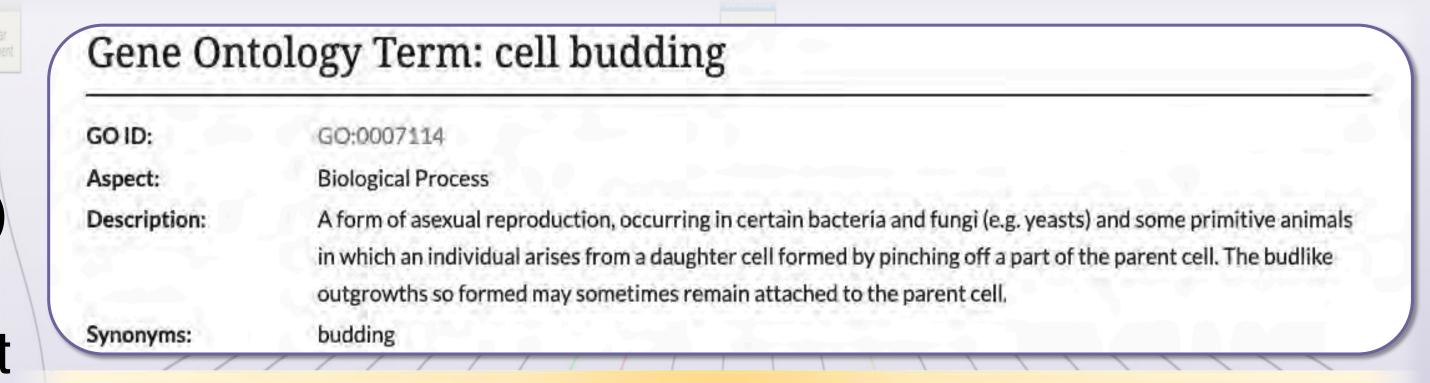


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The Saccharomyces Genome Database (SGD; www.yeastgenome.org) is a comprehensive resource of curated molecular and genetic information on the genes and proteins of Saccharomyces cerevisiae. Since 2001, SGD has used the Gene Ontology (GO; geneontology.org) 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)
 - Molecular Function ontology describes activities of entities
 - Biological Process ontology places these MFs in a biological context
 - Cellular Component ontology indicates subcellular localizations



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

