

# Resource Summary Report

Generated by [NIF](#) on Sep 18, 2026

## SGD Gene Ontology Slim Mapper

RRID:SCR\_005784

Type: Tool

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### Proper Citation

SGD Gene Ontology Slim Mapper (RRID:SCR\_005784)

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### Resource Information

**URL:** <http://www.yeastgenome.org/cgi-bin/GO/goSlimMapper.pl>

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**Description:** The GO Slim Mapper (aka GO Term Mapper) maps the specific, granular GO terms used to annotate a list of budding yeast gene products to corresponding more general parent GO slim terms. Uses the SGD GO Slim sets. Three GO Slim sets are available at SGD: \* Macromolecular complex terms: protein complex terms from the Cellular Component ontology \* Yeast GO-Slim: GO terms that represent the major Biological Processes, Molecular Functions, and Cellular Components in *S. cerevisiae* \* Generic GO-Slim: broad, high level GO terms from the Biological Process and Cellular Component ontologies selected and maintained by the Gene Ontology Consortium (GOC)  
Platform: Online tool

**Abbreviations:** GO Slim Mapper

**Synonyms:** GO Term Mapper, Gene Ontology Slim Mapper

**Resource Type:** analysis service resource, data analysis service, production service resource, service resource

**Keywords:** gene, annotation, gene ontology, protein complex, biological process, molecular function, cellular component, gene ontology, orf, yeast, statistical analysis, slimmer-type tool, function

**Availability:** Free for academic use

**Resource Name:** SGD Gene Ontology Slim Mapper

**Resource ID:** SCR\_005784

**Alternate IDs:** nlx\_149258

**Record Creation Time:** 20220129T080232+0000

## Ratings and Alerts

No rating or validation information has been found for SGD Gene Ontology Slim Mapper.

No alerts have been found for SGD Gene Ontology Slim Mapper.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 31 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#) .

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. *Molecular cell*, 85(19), 3661.

Qiu C, et al. (2022) Biosensor-Coupled In Vivo Mutagenesis and Omics Analysis Reveals Reduced Lysine and Arginine Synthesis To Improve Malonyl-Coenzyme A Flux in *Saccharomyces cerevisiae*. *mSystems*, 7(2), e0136621.

Burgard J, et al. (2020) The secretome of *Pichia pastoris* in fed-batch cultivations is largely independent of the carbon source but changes quantitatively over cultivation time. *Microbial biotechnology*, 13(2), 479.

Gibney PA, et al. (2020) A tps1?? persister-like state in *Saccharomyces cerevisiae* is regulated by MKT1. *PloS one*, 15(5), e0233779.

Cohen-Zontag O, et al. (2019) A secretion-enhancing cis regulatory targeting element (SECRETE) involved in mRNA localization and protein synthesis. *PLoS genetics*, 15(7), e1008248.

Knighton LE, et al. (2019) Dataset of *Nematostella vectensis* Hsp70 isoform interactomes upon heat shock. *Data in brief*, 27, 104580.

Dai Z, et al. (2018) Global rewiring of cellular metabolism renders *Saccharomyces cerevisiae* Crabtree negative. *Nature communications*, 9(1), 3059.

Miller JE, et al. (2018) Genome-Wide Mapping of Decay Factor-mRNA Interactions in Yeast Identifies Nutrient-Responsive Transcripts as Targets of the Deadenylation Ccr4. *G3 (Bethesda, Md.)*, 8(1), 315.

Huang M, et al. (2017) Efficient protein production by yeast requires global tuning of metabolism. *Nature communications*, 8(1), 1131.

- Kyriakou D, et al. (2016) Functional characterisation of long intergenic non-coding RNAs through genetic interaction profiling in *Saccharomyces cerevisiae*. *BMC biology*, 14(1), 106.
- Kuang MC, et al. (2016) Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. *eLife*, 5.
- Williams TC, et al. (2016) The *Saccharomyces cerevisiae* pheromone-response is a metabolically active stationary phase for bio-production. *Metabolic engineering communications*, 3, 142.
- Bilanchone V, et al. (2015) Ty3 Retrotransposon Hijacks Mating Yeast RNA Processing Bodies to Infect New Genomes. *PLoS genetics*, 11(9), e1005528.
- Carvalho-Netto OV, et al. (2015) *Saccharomyces cerevisiae* transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. *Microbial cell factories*, 14, 13.
- Imamura Y, et al. (2015) RSC Chromatin-Remodeling Complex Is Important for Mitochondrial Function in *Saccharomyces cerevisiae*. *PloS one*, 10(6), e0130397.
- Truman AW, et al. (2015) Quantitative proteomics of the yeast Hsp70/Hsp90 interactomes during DNA damage reveal chaperone-dependent regulation of ribonucleotide reductase. *Journal of proteomics*, 112, 285.
- Edri S, et al. (2014) Quantifying the effect of ribosomal density on mRNA stability. *PloS one*, 9(7), e102308.
- Salas-Santiago B, et al. (2014) *Saccharomyces cerevisiae* essential genes with an Opi-phenotype. *G3 (Bethesda, Md.)*, 4(4), 761.
- Zhao S, et al. (2014) Comparative proteomic analysis of *Saccharomyces cerevisiae* under different nitrogen sources. *Journal of proteomics*, 101, 102.
- Walker ME, et al. (2014) Genome-wide identification of the Fermentome; genes required for successful and timely completion of wine-like fermentation by *Saccharomyces cerevisiae*. *BMC genomics*, 15(1), 552.