Resource Summary Report

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SGD Gene Ontology Slim Mapper

RRID:SCR_005784
Type: Tool

Proper Citation

SGD Gene Ontology Slim Mapper (RRID:SCR_005784)

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: production service resource, analysis service resource, data analysis service, 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

Funding:

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

Record Last Update: 20250516T053806+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.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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 Deadenylase 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.

Imamura Y, et al. (2015) RSC Chromatin-Remodeling Complex Is Important for Mitochondrial Function in Saccharomyces cerevisiae. PloS one, 10(6), e0130397.

Carvalho-Netto OV, et al. (2015) Saccharomyces cerevisiae transcriptional reprograming due to bacterial contamination during industrial scale bioethanol production. Microbial cell factories, 14, 13.

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.

Costanzo MC, et al. (2014) Saccharomyces genome database provides new regulation data. Nucleic acids research, 42(Database issue), D717.

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.