Resource Summary Report

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Generic GO Term Mapper

RRID:SCR_005806
Type: Tool

Proper Citation

Generic GO Term Mapper (RRID:SCR_005806)

Resource Information

URL: http://go.princeton.edu/cgi-bin/GOTermMapper

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Description: The Generic GO Term Mapper finds the GO terms shared among a list of genes from your organism of choice within a slim ontology, allowing them to be binned into broader categories. The user may optionally provide a custom gene association file or slim ontology, or a custom list of slim terms. The implementation of this Generic GO Term Mapper uses map2slim.pl script written by Chris Mungall at Berkeley Drosophila Genome Project, and some of the modules included in the GO-TermFinder distribution written by Gavin Sherlock and Shuai Weng at Stanford University, made publicly available through the GMOD project. GO Term Mapper serves a different function than the GO Term Finder. GO Term Mapper simply bins the submitted gene list to a static set of ancestor GO terms. In contrast, GO Term Finder finds the GO terms significantly enriched in a submitted list of genes. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: GOTermMapper, GO Term Mapper

Synonyms: Generic Gene Ontology Term Mapper, Generic Gene Ontology (GO) Term Mapper

Resource Type: analysis service resource, software resource, production service resource, data processing software, data analysis service, software application, service resource

Keywords: gene ontology, gene, gene association, slim ontology, slimmer-type tool, term enrichment, gene annotation, genomics, ontology, process, function, component, bio.tools

Funding:

Availability: Free for academic use

Resource Name: Generic GO Term Mapper

Resource ID: SCR_005806

Alternate IDs: nlx_149294, biotools:go_term_mapper

Alternate URLs: https://bio.tools/go_term_mapper

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250422T055254+0000

Ratings and Alerts

No rating or validation information has been found for Generic GO Term Mapper.

No alerts have been found for Generic GO Term Mapper.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Norris HL, et al. (2021) A Novel Role for Histatin 5 in Combination with Zinc to Promote Commensalism in C. albicans Survivor Cells. Pathogens (Basel, Switzerland), 10(12).

Kirchner P, et al. (2019) Proteome-wide analysis of chaperone-mediated autophagy targeting motifs. PLoS biology, 17(5), e3000301.

Samanta L, et al. (2019) Proteomic analysis reveals dysregulated cell signaling in ejaculated spermatozoa from infertile men. Asian journal of andrology, 21(2), 121.

Pena RN, et al. (2019) Five genomic regions have a major impact on fat composition in Iberian pigs. Scientific reports, 9(1), 2031.

Lie S, et al. (2018) The contribution of non-essential Schizosaccharomyces pombe genes to fitness in response to altered nutrient supply and target of rapamycin activity. Open biology,

8(5).

Blyth J, et al. (2018) Genes Important for Schizosaccharomyces pombe Meiosis Identified Through a Functional Genomics Screen. Genetics, 208(2), 589.

Acharya S, et al. (2017) Unsupervised gene selection using biological knowledge : application in sample clustering. BMC bioinformatics, 18(1), 513.

Onishi K, et al. (2017) Sonic Hedgehog switches on Wnt/planar cell polarity signaling in commissural axon growth cones by reducing levels of Shisa2. eLife, 6.

Davis GM, et al. (2017) Exploring Potential Germline-Associated Roles of the TRIM-NHL Protein NHL-2 Through RNAi Screening. G3 (Bethesda, Md.), 7(10), 3251.

Qu H, et al. (2016) Identification and validation of differentially expressed proteins in epithelial ovarian cancers using quantitative proteomics. Oncotarget, 7(50), 83187.

Gostner JM, et al. (2016) Cellular reactions to long-term volatile organic compound (VOC) exposures. Scientific reports, 6, 37842.

Kuang MC, et al. (2016) Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. eLife, 5.

Witzmann FA, et al. (2016) Label-free proteomic methodology for the analysis of human kidney stone matrix composition. Proteome science, 14, 4.

Vela-Corcía D, et al. (2016) De novo Analysis of the Epiphytic Transcriptome of the Cucurbit Powdery Mildew Fungus Podosphaera xanthii and Identification of Candidate Secreted Effector Proteins. PloS one, 11(10), e0163379.

Phan M, et al. (2016) Tooth agenesis and orofacial clefting: genetic brothers in arms? Human genetics, 135(12), 1299.

Brietzke A, et al. (2016) Transcriptome sequencing of maraena whitefish (Coregonus maraena). Marine genomics, 29, 27.

Patel S, et al. (2016) Gene Prioritization for Imaging Genetics Studies Using Gene Ontology and a Stratified False Discovery Rate Approach. Frontiers in neuroinformatics, 10, 14.

Chen Y, et al. (2016) Transcriptional profiling reveals molecular basis and novel genetic targets for improved resistance to multiple fermentation inhibitors in Saccharomyces cerevisiae. Biotechnology for biofuels, 9, 9.

Mangé A, et al. (2016) An integrated cell line-based discovery strategy identified follistatin and kallikrein 6 as serum biomarker candidates of breast carcinoma. Journal of proteomics, 142, 114.

Wilson JJ, et al. (2016) Analysis of Gene Expression in an Inbred Line of Soft-Shell Clams (Mya arenaria) Displaying Growth Heterosis: Regulation of Structural Genes and the NOD2 Pathway. International journal of genomics, 2016, 6720947.