Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 30, 2025

Generic GO Term Finder

RRID:SCR_008870
Type: Tool

Proper Citation

Generic GO Term Finder (RRID:SCR_008870)

Resource Information

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

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Description: The Generic GO Term Finder finds the significant GO terms shared among a list of genes from an organism, displaying the results in a table and as a graph (showing the terms and their ancestry). The user may optionally provide background information or a custom gene association file or filter evidence codes. This tool is capable of batch processing multiple queries at once. GO::TermFinder comprises a set of object-oriented Perl modules GO::TermFinder can be used on any system on which Perl can be run, either as a command line application, in single or batch mode, or as a web-based CGI script. This implementation, developed at the Lewis-Sigler Institute at Princeton, depends on the GO-TermFinder software written by Gavin Sherlock and Shuai Weng at Stanford University and the GO:View module written by Shuai Weng. It is made publicly available through the GMOD project. The full source code and documentation for GO:TermFinder are freely available from http://search.cpan.org/dist/GO-TermFinder/. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: GOTermFinder, GO-TermFinder, GO Term Finder, GO::TermFinder

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

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

Defining Citation: PMID:15297299

Keywords: gene ontology, gene, graph, visualization, genomics, gene association, ontology or annotation visualization, term enrichment, ontology, process, function, component, enrichment, bio.tools

Funding: NHGRI 1R01HG002732

Availability: Free for academic use

Resource Name: Generic GO Term Finder

Resource ID: SCR_008870

Alternate IDs: nlx_149293, biotools_go_term_finder

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

Record Creation Time: 20220129T080249+0000

Record Last Update: 20250330T060856+0000

Ratings and Alerts

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

No alerts have been found for Generic GO Term Finder.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 107 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Di Rienzo M, et al. (2022) AMBRA1 regulates mitophagy by interacting with ATAD3A and promoting PINK1 stability. Autophagy, 18(8), 1752.

He L, et al. (2021) Electrical stimulation at nanoscale topography boosts neural stem cell neurogenesis through the enhancement of autophagy signaling. Biomaterials, 268, 120585.

Nguyen Hoang AT, et al. (2021) CSNK1G2 differently sensitizes tamoxifen-induced decrease in PI3K/AKT/mTOR/S6K and ERK signaling according to the estrogen receptor existence in breast cancer cells. PloS one, 16(4), e0246264.

Mukherjee K, et al. (2021) EKLF/KLF1 expression defines a unique macrophage subset during mouse erythropoiesis. eLife, 10.

Zhu Z, et al. (2020) Comparative Proteomics and Secretomics Revealed Virulence and Antibiotic Resistance-Associated Factors in Vibrio parahaemolyticus Recovered From Commonly Consumed Aquatic Products. Frontiers in microbiology, 11, 1453.

Li P, et al. (2020) Legionella pneumophila Infection Rewires the Acanthamoeba castellanii Transcriptome, Highlighting a Class of Sirtuin Genes. Frontiers in cellular and infection microbiology, 10, 428.

Juergens H, et al. (2020) Contribution of Complex I NADH Dehydrogenase to Respiratory Energy Coupling in Glucose-Grown Cultures of Ogataea parapolymorpha. Applied and environmental microbiology, 86(15).

Xiang H, et al. (2020) Characterization of blood-derived exosomal proteins after exercise. The Journal of international medical research, 48(9), 300060520957541.

Wang C, et al. (2020) Rrp6 Moonlights in an RNA Exosome-Independent Manner to Promote Cell Survival and Gene Expression during Stress. Cell reports, 31(10), 107754.

Chen Y, et al. (2019) sRNA OsiA Stabilizes Catalase mRNA during Oxidative Stress Response of Deincoccus radiodurans R1. Microorganisms, 7(10).

Tay YD, et al. (2019) Fission Yeast NDR/LATS Kinase Orb6 Regulates Exocytosis via Phosphorylation of the Exocyst Complex. Cell reports, 26(6), 1654.

Sellam A, et al. (2019) The p38/HOG stress-activated protein kinase network couples growth to division in Candida albicans. PLoS genetics, 15(3), e1008052.

Temoche-Diaz MM, et al. (2019) Distinct mechanisms of microRNA sorting into cancer cell-derived extracellular vesicle subtypes. eLife, 8.

Chang EY, et al. (2019) MRE11-RAD50-NBS1 promotes Fanconi Anemia R-loop suppression at transcription-replication conflicts. Nature communications, 10(1), 4265.

Milbury KL, et al. (2019) Exonuclease domain mutants of yeast DIS3 display genome instability. Nucleus (Austin, Tex.), 10(1), 21.

Esnault C, et al. (2019) Transposable element insertions in fission yeast drive adaptation to environmental stress. Genome research, 29(1), 85.

Fiorucci AS, et al. (2019) Arabidopsis S2Lb links AtCOMPASS-like and SDG2 activity in H3K4me3 independently from histone H2B monoubiquitination. Genome biology, 20(1), 100.

Alhoch B, et al. (2019) Comparative Genomic Screen in Two Yeasts Reveals Conserved Pathways in the Response Network to Phenol Stress. G3 (Bethesda, Md.), 9(3), 639.

Dogra V, et al. (2019) Impaired PSII proteostasis triggers a UPR-like response in the var2 mutant of Arabidopsis. Journal of experimental botany, 70(12), 3075.

Brauer E, et al. (2019) Collagen Fibrils Mechanically Contribute to Tissue Contraction in an In Vitro Wound Healing Scenario. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 6(9), 1801780.