Resource Summary Report

Generated by dkNET on Apr 24, 2025

GOstat

RRID:SCR_008535
Type: Tool

Proper Citation

GOstat (RRID:SCR_008535)

Resource Information

URL: http://gostat.wehi.edu.au

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Description: GOstat is a tool that allows you to find statistically overrepresented Gene Ontologies within a group of genes. The Gene-Ontology database (GO: http://www.geneontology.org) provides a useful tool to annotate and analyze the function of large numbers of genes. Modern experimental techniques, as e.g. DNA microarrays, often result in long lists of genes. To learn about the biology in this kind of data it is desirable to find functional annotation or Gene-Ontology groups which are highly represented in the data. This program (GOstat) should help in the analysis of such lists and will provide statistics about the GO terms contained in the data and sort the GO annotations giving the most representative GO terms first. Run GOstat: * Go to search form - Computes GO statistics of a list of genes selected from a microarray. * GOstat Display - You can store results from a previously run and view them here, either by uploading them as a file or putting them on a selected URL. * Upload Custom GO Annotations - This allows you to upload your own GO annotation database and use it with GOstat. Variants of GOstat: * Rank GOstat - Takes input from all genes on microarray instead of using a fixed cutoff and uses ranks using a Wilcoxon test or either ranks or pvalues to score GOs using Kolmogorov-Smirnov statistics. * Gene Abundance GOstats - Takes input from all genes on microarray and sums up the gene abundances for each GO to compute statistics. * Two list GOstat - Compares GO statistics in two independent lists of genes, not necessarily one of them being the complete list the other list is sampled from. Platform: Online tool

Abbreviations: GOstat

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

Defining Citation: PMID:14962934

Keywords: gene, gene ontology, annotation, statistical analysis, FASEB list

Funding: DFG

Availability: Free for academic use

Resource Name: GOstat

Resource ID: SCR_008535

Alternate IDs: nif-0000-30625

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250424T064957+0000

Ratings and Alerts

No rating or validation information has been found for GOstat.

No alerts have been found for GOstat.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 158 mentions in open access literature.

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

Tu CE, et al. (2025) D-ribose-5-phosphate inactivates YAP and functions as a metabolic checkpoint. Journal of hematology & oncology, 18(1), 2.

Yoshida Y, et al. (2024) Transcriptome analysis of the tardigrade Hypsibius exemplaris exposed to the DNA-damaging agent bleomycin. Proceedings of the Japan Academy. Series B, Physical and biological sciences, 100(7), 414.

Camera A, et al. (2024) Aging and putative frailty biomarkers are altered by spaceflight. Scientific reports, 14(1), 13098.

Kidere D, et al. (2023) Impact of the m.13513G>A Variant on the Functions of the OXPHOS System and Cell Retrograde Signaling. Current issues in molecular biology, 45(3), 1794.

Cai W, et al. (2023) The eQTL colocalization and transcriptome-wide association study identify potentially causal genes responsible for economic traits in Simmental beef cattle. Journal of animal science and biotechnology, 14(1), 78.

Zhao T, et al. (2023) Integration of eQTL and machine learning to dissect causal genes with pleiotropic effects in genetic regulation networks of seed cotton yield. Cell reports, 42(9), 113111.

Wang H, et al. (2022) Predicting the targets of IRF8 and NFATc1 during osteoclast differentiation using the machine learning method framework cTAP. BMC genomics, 23(1), 14.

Liu Z, et al. (2022) Whole genome sequencing of Luxi Black Head sheep for screening selection signatures associated with important traits. Animal bioscience, 35(9), 1340.

Alchahin AM, et al. (2022) A transcriptional metastatic signature predicts survival in clear cell renal cell carcinoma. Nature communications, 13(1), 5747.

Czapiewski R, et al. (2022) Genomic loci mispositioning in Tmem120a knockout mice yields latent lipodystrophy. Nature communications, 13(1), 321.

Gillnäs S, et al. (2022) Severe cerebellar malformations in mutant mice demonstrate a role for PDGF-C/PDGFR? signalling in cerebellar development. Biology open, 11(8).

Takashima Y, et al. (2021) Survival prediction based on the gene expression associated with cancer morphology and microenvironment in primary central nervous system lymphoma. PloS one, 16(6), e0251272.

Yu D, et al. (2021) Super-Enhancer Induced IL-20RA Promotes Proliferation/Metastasis and Immune Evasion in Colorectal Cancer. Frontiers in oncology, 11, 724655.

Schwabe M, et al. (2021) Next-Generation Sequencing Analysis of the Tineola bisselliella Larval Gut Transcriptome Reveals Candidate Enzymes for Keratin Digestion. Genes, 12(8).

Miyata Y, et al. (2021) Cas9-mediated genome editing reveals a significant contribution of calcium signaling pathways to anhydrobiosis in Pv11 cells. Scientific reports, 11(1), 19698.

Guo S, et al. (2021) Aging features of the migratory locust at physiological and transcriptional levels. BMC genomics, 22(1), 257.

Yoshida Y, et al. (2021) RNA sequencing data for gamma radiation response in the extremotolerant tardigrade Ramazzottius varieornatus. Data in brief, 36, 107111.

Fang DD, et al. (2021) MDM2 inhibitor APG-115 exerts potent antitumor activity and synergizes with standard-of-care agents in preclinical acute myeloid leukemia models. Cell death discovery, 7(1), 90.

Zhang Y, et al. (2021) The genome of the naturally evolved obesity-prone Ossabaw miniature pig. iScience, 24(9), 103081.

Dixon CR, et al. (2021) STING nuclear partners contribute to innate immune signaling responses. iScience, 24(9), 103055.