Resource Summary Report

Generated by NIF on May 16, 2025

FuncAssociate: The Gene Set Functionator

RRID:SCR_005768
Type: Tool

Proper Citation

FuncAssociate: The Gene Set Functionator (RRID:SCR_005768)

Resource Information

URL: http://llama.mshri.on.ca/funcassociate/

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Description: A web-based tool that accepts as input a list of genes, and returns a list of GO attributes that are over- (or under-) represented among the genes in the input list. Only those over- (or under-) representations that are statistically significant, after correcting for multiple hypotheses testing, are reported. Currently 37 organisms are supported. In addition to the input list of genes, users may specify a) whether this list should be regarded as ordered or unordered; b) the universe of genes to be considered by FuncAssociate; c) whether to report over-, or under-represented attributes, or both; and d) the p-value cutoff. A new version of FuncAssociate supports a wider range of naming schemes for input genes, and uses more frequently updated GO associations. However, some features of the original version, such as sorting by LOD or the option to see the gene-attribute table, are not yet implemented. Platform: Online tool

Abbreviations: FuncAssociate

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

Defining Citation: PMID:19717575, PMID:14668247

Keywords: gene, gene ontology, statistical analysis, web service, bio.tools

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Availability: Free for academic use, Acknowledgement requested

Resource Name: FuncAssociate: The Gene Set Functionator

Resource ID: SCR_005768

Alternate IDs: biotools:funcassociate, OMICS_02264, nlx_149233

Alternate URLs: http://llama.mshri.on.ca/cgi/func/funcassociate,
https://bio.tools/funcassociate

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250516T053805+0000

Ratings and Alerts

No rating or validation information has been found for FuncAssociate: The Gene Set Functionator.

No alerts have been found for FuncAssociate: The Gene Set Functionator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Liu Y, et al. (2024) Translation efficiency covariation across cell types is a conserved organizing principle of mammalian transcriptomes. bioRxiv : the preprint server for biology.

Ozadam H, et al. (2023) Single-cell quantification of ribosome occupancy in early mouse development. Nature, 618(7967), 1057.

Dekens MPS, et al. (2022) Melanopsin elevates locomotor activity during the wake state of the diurnal zebrafish. EMBO reports, 23(5), e51528.

Dubois-Pot-Schneider H, et al. (2022) Transcriptional and Epigenetic Consequences of

DMSO Treatment on HepaRG Cells. Cells, 11(15).

Rao S, et al. (2021) Genes with 5' terminal oligopyrimidine tracts preferentially escape global suppression of translation by the SARS-CoV-2 Nsp1 protein. RNA (New York, N.Y.), 27(9), 1025.

Luo JH, et al. (2021) Transcriptome-wide analysis of epitranscriptome and translational efficiency associated with heterosis in maize. Journal of experimental botany, 72(8), 2933.

Rao S, et al. (2021) Genes with 5' terminal oligopyrimidine tracts preferentially escape global suppression of translation by the SARS-CoV-2 Nsp1 protein. bioRxiv : the preprint server for biology.

Sasaki Y, et al. (2020) Pemafibrate, a selective PPAR? modulator, prevents non-alcoholic steatohepatitis development without reducing the hepatic triglyceride content. Scientific reports, 10(1), 7818.

He P, et al. (2020) The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 583(7818), 760.

Kompella VPS, et al. (2019) Definition of the Minimal Contents for the Molecular Simulation of the Yeast Cytoplasm. Frontiers in molecular biosciences, 6, 97.

Xu S, et al. (2019) An Integrative Systems Biology and Experimental Approach Identifies Convergence of Epithelial Plasticity, Metabolism, and Autophagy to Promote Chemoresistance. Journal of clinical medicine, 8(2).

Cenik ES, et al. (2019) Maternal Ribosomes Are Sufficient for Tissue Diversification during Embryonic Development in C. elegans. Developmental cell, 48(6), 811.

Ingham NJ, et al. (2019) Mouse screen reveals multiple new genes underlying mouse and human hearing loss. PLoS biology, 17(4), e3000194.

Haque M, et al. (2018) A common neighbor based technique to detect protein complexes in PPI networks. Journal, genetic engineering & biotechnology, 16(1), 227.

Oeyen E, et al. (2018) Ultrafiltration and size exclusion chromatography combined with asymmetrical-flow field-flow fractionation for the isolation and characterisation of extracellular vesicles from urine. Journal of extracellular vesicles, 7(1), 1490143.

Caracausi M, et al. (2017) Systematic identification of human housekeeping genes possibly useful as references in gene expression studies. Molecular medicine reports, 16(3), 2397.

Lee YCG, et al. (2017) Genetic Architecture of Natural Variation Underlying Adult Foraging Behavior That Is Essential for Survival of Drosophila melanogaster. Genome biology and evolution, 9(5), 1357.

Motomura K, et al. (2016) Cellular Dynamics of Mouse Trophoblast Stem Cells: Identification of a Persistent Stem Cell Type. Biology of reproduction, 94(6), 122.

Styles EB, et al. (2016) Exploring Quantitative Yeast Phenomics with Single-Cell Analysis of DNA Damage Foci. Cell systems, 3(3), 264.

Canadell D, et al. (2015) Impact of high pH stress on yeast gene expression: A comprehensive analysis of mRNA turnover during stress responses. Biochimica et biophysica acta, 1849(6), 653.