Resource Summary Report

Generated by NIF on May 17, 2025

GOToolBox Functional Investigation of Gene Datasets

RRID:SCR_003192
Type: Tool

Proper Citation

GOToolBox Functional Investigation of Gene Datasets (RRID:SCR_003192)

Resource Information

URL: http://genome.crg.es/GOToolBox/

Proper Citation: GOToolBox Functional Investigation of Gene Datasets (RRID:SCR_003192)

Description: The GOToolBox web server provides a series of programs allowing the functional investigation of groups of genes, based on the Gene Ontology resource. The web version of the GOToolBox is free for non-commercial users only. Users from commercial companies are allowed to use the site during a reasonable testing period. For a regular use of the web version, a license fee should be paid. We have developed methods and tools based on the Gene Ontology (GO) resource allowing the identification of statistically over- or under-represented terms in a gene dataset; the clustering of functionally related genes within a set; and the retrieval of genes sharing annotations with a query gene. GO annotations can also be constrained to a slim hierarchy or a given level of the ontology. The source codes are available upon request, and distributed under the GPL license. Platform: Online tool

Abbreviations: GOToolBox

Synonyms: GOToolBox - Functional Investigation of Gene Datasets, GOToolBox : Functional Investigation of Gene Datasets

Resource Type: software resource, source code, service resource

Defining Citation: PMID:15575967

Keywords: gene, annotation, statistical analysis, slimmer-type tool, function, cluster, gene association, gene ontology

Funding: Action Bioinformatique inter-EPST ;
French Ministere de l'Education de la Recherche et de la Technologie ;

Fondation pour la Recherche Medicale

Availability: Free for academic use

Resource Name: GOToolBox Functional Investigation of Gene Datasets

Resource ID: SCR_003192

Alternate IDs: nif-0000-30623

Old URLs: http://burgundy.cmmt.ubc.ca/GOToolBox/

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250516T053700+0000

Ratings and Alerts

No rating or validation information has been found for GOToolBox Functional Investigation of Gene Datasets.

No alerts have been found for GOToolBox Functional Investigation of Gene Datasets.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Liu H, et al. (2021) The Sugar Transporter family in wheat (Triticum aestivum. L): genome-wide identification, classification, and expression profiling during stress in seedlings. PeerJ, 9, e11371.

Chavez-Dozal A, et al. (2021) Identification of a Transcriptomic Network Underlying the Wrinkly and Smooth Phenotypes of Vibrio fischeri. Journal of bacteriology, 203(3).

Castillo H, et al. (2018) Transcriptome analysis reveals a stress response of Shewanella oneidensis deprived of background levels of ionizing radiation. PloS one, 13(5), e0196472.

Johnson JA, et al. (2018) Fank1 and Jazf1 promote multiciliated cell differentiation in the mouse airway epithelium. Biology open, 7(4).

Glaab E, et al. (2018) Computational systems biology approaches for Parkinson's disease.

Cell and tissue research, 373(1), 91.

Kleinmanns JA, et al. (2017) BLISTER Regulates Polycomb-Target Genes, Represses Stress-Regulated Genes and Promotes Stress Responses in Arabidopsis thaliana. Frontiers in plant science, 8, 1530.

Becker E, et al. (2017) The protein expression landscape of mitosis and meiosis in diploid budding yeast. Journal of proteomics, 156, 5.

Laresgoiti U, et al. (2016) Lung epithelial tip progenitors integrate glucocorticoid- and STAT3-mediated signals to control progeny fate. Development (Cambridge, England), 143(20), 3686.

Bergeron KF, et al. (2016) Upregulation of the Nr2f1-A830082K12Rik gene pair in murine neural crest cells results in a complex phenotype reminiscent of Waardenburg syndrome type 4. Disease models & mechanisms, 9(11), 1283.

Xu C, et al. (2016) A de novo transcriptome analysis shows that modulation of the JAK-STAT signaling pathway by salmonid alphavirus subtype 3 favors virus replication in macrophage/dendritic-like TO-cells. BMC genomics, 17, 390.

Metzakopian E, et al. (2015) Genome-wide characterisation of Foxa1 binding sites reveals several mechanisms for regulating neuronal differentiation in midbrain dopamine cells. Development (Cambridge, England), 142(7), 1315.

Chatagnon A, et al. (2015) RAR/RXR binding dynamics distinguish pluripotency from differentiation associated cis-regulatory elements. Nucleic acids research, 43(10), 4833.

Costa C, et al. (2015) New Mechanisms of Flucytosine Resistance in C. glabrata Unveiled by a Chemogenomics Analysis in S. cerevisiae. PloS one, 10(8), e0135110.

Hussey SG, et al. (2015) Genome-wide mapping of histone H3 lysine 4 trimethylation in Eucalyptus grandis developing xylem. BMC plant biology, 15, 117.

Bergeron KF, et al. (2015) Male-biased aganglionic megacolon in the TashT mouse line due to perturbation of silencer elements in a large gene desert of chromosome 10. PLoS genetics, 11(3), e1005093.

Afsari B, et al. (2014) Learning dysregulated pathways in cancers from differential variability analysis. Cancer informatics, 13(Suppl 5), 61.

Deivasigamani S, et al. (2014) A genetic screen identifies Tor as an interactor of VAPB in a Drosophila model of amyotrophic lateral sclerosis. Biology open, 3(11), 1127.

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.

Butler T, et al. (2014) Transcriptome analysis of a petal anthocyanin polymorphism in the arctic mustard, Parrya nudicaulis. PloS one, 9(7), e101338.

Chalei V, et al. (2014) The long non-coding RNA Dali is an epigenetic regulator of neural differentiation. eLife, 3, e04530.