Resource Summary Report

Generated by RRID on Apr 11, 2025

GoMiner

RRID:SCR_002360
Type: Tool

Proper Citation

GoMiner (RRID:SCR_002360)

Resource Information

URL: http://discover.nci.nih.gov/gominer/

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Description: GoMiner is a tool for biological interpretation of "omic" data including data from gene expression microarrays. Omic experiments often generate lists of dozens or hundreds of genes that differ in expression between samples, raising the question, What does it all mean biologically? To answer this question, GoMiner leverages the Gene Ontology (GO) to identify the biological processes, functions and components represented in these lists. Instead of analyzing microarray results with a gene-by-gene approach, GoMiner classifies the genes into biologically coherent categories and assesses these categories. The insights gained through GoMiner can generate hypotheses to guide additional research. GoMiner displays the genes within the framework of the Gene Ontology hierarchy in two ways: * In the form of a tree, similar to that in AmiGO * In the form of a "Directed Acyclic Graph" (DAG) The program also provides: * Quantitative and statistical analysis * Seamless integration with important public databases GoMiner uses the databases provided by the GO Consortium. These databases combine information from a number of different consortium participants, include information from many different organisms and data sources, and are referenced using a variety of different gene product identification approaches.

Abbreviations: GoMiner

Resource Type: software resource, software application, data processing software

Defining Citation: PMID:12702209

Keywords: experiment, expression, function, gene, genomics, biological, genomic, microarray, omic, process, gene expression, gene ontology, biological process, biological function, biological component, proteomic, database, FASEB list

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Georgia Institute of Technology; Georgia; USA ;
Emory University; Georgia; USA

Resource Name: GoMiner

Resource ID: SCR_002360

Alternate IDs: nif-0000-21181

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250411T054729+0000

Ratings and Alerts

No rating or validation information has been found for GoMiner.

No alerts have been found for GoMiner.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 115 mentions in open access literature.

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

Hu ZY, et al. (2024) FOXF2 may inhibit esophageal squamous cell carcinoma growth and metastasis by regulating the EZR-ERBB2 axis. Translational cancer research, 13(12), 6970.

Yang C, et al. (2023) Mechanical Ventilation-Related High Stretch Mainly Induces Endoplasmic Reticulum Stress and Thus Mediates Inflammation Response in Cultured Human Primary Airway Smooth Muscle Cells. International journal of molecular sciences, 24(4).

Kustermann M, et al. (2023) Adoptively Transferred in vitro-Generated Myeloid-Derived Suppressor Cells Improve T-Cell Function and Antigen-Specific Immunity after Traumatic Lung Injury. Journal of innate immunity, 15(1), 78.

Stolwijk JM, et al. (2021) Red blood cells contain enzymatically active GPx4 whose abundance anticorrelates with hemolysis during blood bank storage. Redox biology, 46, 102073.

Jensen ARD, et al. (2021) Organ-Specific, Fibroblast-Derived Matrix as a Tool for Studying Breast Cancer Metastasis. Cancers, 13(13).

Gallet P, et al. (2021) Integrative genomics analysis of nasal intestinal-type adenocarcinomas demonstrates the major role of CACNA1C and paves the way for a simple diagnostic tool in male woodworkers. Clinical epigenetics, 13(1), 179.

Peng T, et al. (2021) Tissue-Resident-Memory CD8+ T Cells Bridge Innate Immune Responses in Neighboring Epithelial Cells to Control Human Genital Herpes. Frontiers in immunology, 12, 735643.

Chan YT, et al. (2020) GPER-induced signaling is essential for the survival of breast cancer stem cells. International journal of cancer, 146(6), 1674.

Huguet A, et al. (2020) Differences in Toxic Response Induced by Three Variants of the Diarrheic Shellfish Poisoning Phycotoxins in Human Intestinal Epithelial Caco-2 Cells. Toxins, 12(12).

Scheurer J, et al. (2020) Rapamycin-based graft-versus-host disease prophylaxis increases the immunosuppressivity of myeloid-derived suppressor cells without affecting T cells and anti-tumor cytotoxicity. Clinical and experimental immunology, 202(3), 407.

Banerjee P, et al. (2020) Rapastinel, an NMDAR positive modulator, produces distinct behavioral, sleep, and EEG profiles compared with ketamine. Behavioural brain research, 391, 112706.

Kim YK, et al. (2020) Recurrent Drought Conditions Enhance the Induction of Drought Stress Memory Genes in Glycine max L. Frontiers in genetics, 11, 576086.

Karasu E, et al. (2020) Complement C5a Induces Pro-inflammatory Microvesicle Shedding in Severely Injured Patients. Frontiers in immunology, 11, 1789.

Shereck E, et al. (2019) Immunophenotypic, cytotoxic, proteomic and genomic characterization of human cord blood vs. peripheral blood CD56Dim NK cells. Innate immunity, 25(5), 294.

Prokopec SD, et al. (2019) Transcriptomic Impact of IMA-08401, a Novel AHR Agonist Resembling Laquinimod, on Rat Liver. International journal of molecular sciences, 20(6).

Barghi N, et al. (2019) Genetic redundancy fuels polygenic adaptation in Drosophila. PLoS biology, 17(2), e3000128.

Cypris O, et al. (2019) Tracking of epigenetic changes during hematopoietic differentiation of induced pluripotent stem cells. Clinical epigenetics, 11(1), 19.

Lahtinen A, et al. (2019) A distinctive DNA methylation pattern in insufficient sleep. Scientific reports, 9(1), 1193.

Kumar M, et al. (2019) Strigolactone Signaling Genes Showing Differential Expression Patterns in Arabidopsis max Mutants. Plants (Basel, Switzerland), 8(9).

Espitia O, et al. (2018) Implication of molecular vascular smooth muscle cell heterogeneity among arterial beds in arterial calcification. PloS one, 13(1), e0191976.