Resource Summary Report

Generated by NIF on Apr 22, 2025

High-Throughput GoMiner

RRID:SCR_000173
Type: Tool

Proper Citation

High-Throughput GoMiner (RRID:SCR_000173)

Resource Information

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

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Description: A web program that organizes lists of genes of interest (for example, under- and overexpressed genes from a microarray experiment) for biological interpretation in the context of the Gene Ontology and automates the analysis of multiple microarrays then integrates the results across all of them in exportable output files and visualizations. High-Throughput GoMiner is an enhancement of GoMiner and is implemented with both a command line interface and a web interface. The program can also: efficiently perform automated batch processing of an arbitrary number of microarrays; produce a human- or computer-readable report that rank-orders the multiple microarray results according to the number of significant GO categories; integrate the multiple microarray results by providing organized, global clustered image map visualizations of the relationships of significant GO categories; provide a fast form of false discovery rate multiple comparisons calculation; and provide annotations and visualizations for relating transcription factor binding sites to genes and GO categories.

Resource Type: software resource, web application

Defining Citation: PMID:15998470

Keywords: term enrichment, gene ontology, gene, microarray, common variable immune deficiency, high-throughput, visualization, database

Funding: NCI 1Z01BC010842-01

Availability: Free for academic use, Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Resource Name: High-Throughput GoMiner

Resource ID: SCR_000173

Alternate IDs: nlx_149300

Record Creation Time: 20220129T080200+0000

Record Last Update: 20250422T054900+0000

Ratings and Alerts

No rating or validation information has been found for High-Throughput GoMiner.

No alerts have been found for High-Throughput GoMiner.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Potok ME, et al. (2013) Reprogramming the maternal zebrafish genome after fertilization to match the paternal methylation pattern. Cell, 153(4), 759.

Radulovich N, et al. (2010) Differential roles of cyclin D1 and D3 in pancreatic ductal adenocarcinoma. Molecular cancer, 9, 24.