Resource Summary Report

Generated by NIF on Apr 16, 2025

WebGestalt: WEB-based GEne SeT AnaLysis Toolkit

RRID:SCR_006786
Type: Tool

Proper Citation

WebGestalt: WEB-based GEne SeT AnaLysis Toolkit (RRID:SCR_006786)

Resource Information

URL: http://www.webgestalt.org/

Proper Citation: WebGestalt: WEB-based GEne SeT AnaLysis Toolkit (RRID:SCR_006786)

Description: Web based gene set analysis toolkit designed for functional genomic, proteomic, and large-scale genetic studies from which large number of gene lists (e.g. differentially expressed gene sets, co-expressed gene sets etc) are continuously generated. WebGestalt incorporates information from different public resources and provides a way for biologists to make sense out of gene lists. This version of WebGestalt supports eight organisms, including human, mouse, rat, worm, fly, yeast, dog, and zebrafish.

Abbreviations: WebGestalt

Synonyms: GOTM, Gene Ontology Tree Machine, WebGestalt2, WEB-based GEne SeT AnaLysis Toolkit, WebGestalt

Resource Type: web application, web service, software resource, data access protocol

Defining Citation: PMID:24233776, PMID:15980575, PMID:14975175

Keywords: proteomic, gene expression, genome wide association study, statistical analysis, functional genomics, protein protein interaction, pathway, regulatory module, analysis toolkit, web application

Funding: NIAAA U01 AA016662;
NIAAA U01 AA013512;
NIDA P01 DA015027;
NIMH P50 MH078028;
NIMH P50 MH096972;
NCI U24 CA159988;

NIGMS R01 GM088822

Availability: Free, Freely available

Resource Name: WebGestalt: WEB-based GEne SeT AnaLysis Toolkit

Resource ID: SCR_006786

Alternate IDs: OMICS_02222, nif-0000-30622

Old URLs: http://bioinfo.vanderbilt.edu/webgestalt/

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250416T063445+0000

Ratings and Alerts

No rating or validation information has been found for WebGestalt: WEB-based GEne SeT AnaLysis Toolkit.

No alerts have been found for WebGestalt: WEB-based GEne SeT AnaLysis Toolkit.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2507 mentions in open access literature.

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

Alkhatabi HA, et al. (2025) Untangling the complex mechanisms associated with Alzheimer's disease in elderly patients using high-throughput RNA sequencing data and next-generation knowledge discovery methods: Focus on potential gene signatures and drugs for dementia. Heliyon, 11(1), e41266.

Hao F, et al. (2025) Reverse-engineering the FLT3-PI3K/AKT axis to enhance TILs function and improve prognosis in ovarian and cervical cancers. Journal of ovarian research, 18(1), 14.

Scuderi G, et al. (2025) Comprehensive Analysis of TSPAN32 Regulatory Networks and Their Role in Immune Cell Biology. Biomolecules, 15(1).

Oguz AK, et al. (2025) The Platelet-Specific Gene Signature in the Immunoglobulin G4-Related Disease Transcriptome. Medicina (Kaunas, Lithuania), 61(1).

Liang J, et al. (2025) Transcriptomic Insights into Post-Spawning Death and Muscle Atrophy in Ayu (Plecoglossus altivelis). International journal of molecular sciences, 26(2).

Colakoglu Bergel C, et al. (2025) Second-generation BRAF inhibitor Encorafenib resistance is regulated by NCOA4-mediated iron trafficking in the drug-resistant malignant melanoma cells. Scientific reports, 15(1), 2422.

Shekhar S, et al. (2025) Sensory quiescence induces a cell-non-autonomous integrated stress response curbed by condensate formation of the ATF4 and XRP1 effectors. Nature communications, 16(1), 252.

Richter A, et al. (2025) The master male sex determinant Gdf6Y of the turquoise killifish arose through allelic neofunctionalization. Nature communications, 16(1), 540.

Arseni L, et al. (2025) Longitudinal omics data and preclinical treatment suggest the proteasome inhibitor carfilzomib as therapy for ibrutinib-resistant CLL. Nature communications, 16(1), 1041.

Hashemi Karoii D, et al. (2025) Identification of novel cytoskeleton protein involved in spermatogenic cells and sertoli cells of non-obstructive azoospermia based on microarray and bioinformatics analysis. BMC medical genomics, 18(1), 19.

An W, et al. (2025) Exploration of the shared diagnostic genes and molecular mechanism between obesity and atherosclerosis via bioinformatic analysis. Scientific reports, 15(1), 2301.

Nascimento Da Conceicao V, et al. (2025) Naltriben promotes tumor growth by activating the TRPM7-mediated development of the anti-inflammatory M2 phenotype. NPJ precision oncology, 9(1), 29.

Yu GT, et al. (2025) Mapping epidermal and dermal cellular senescence in human skin aging. Aging cell, 24(1), e14358.

Weber M, et al. (2025) Transcriptomic and proteomic profiling identifies feline fibrosarcoma as clinically amenable model for aggressive sarcoma subtypes. Neoplasia (New York, N.Y.), 60, 101104.

Mercado-Evans V, et al. (2025) Tamm-Horsfall protein augments neutrophil NETosis during urinary tract infection. JCI insight, 10(1).

Jaygude U, et al. (2025) Exploring the role of the Rab network in epithelial-to-mesenchymal transition. Bioinformatics advances, 5(1), vbae200.

Wang F, et al. (2025) Novel Integration of Spatial and Single-Cell Omics Data Sets Enables Deeper Insights into IPF Pathogenesis. Proteomes, 13(1).

Khan J, et al. (2025) Identification and validation of a metabolic-related gene risk model predicting the prognosis of lung, colon, and breast cancers. Scientific reports, 15(1), 1374.

Long H, et al. (2025) Proteomic Characterization of Liver Cancer Cells Treated with Clinical Targeted Drugs for Hepatocellular Carcinoma. Biomedicines, 13(1).

Britto GSG, et al. (2025) Genome-Wide Insights into Internalizing Symptoms in Admixed Latin American Children. Genes, 16(1).