

Resource Summary Report

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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/>

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

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

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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: 20260729T044137+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 2760 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Yan C, et al. (2026) RAS/MEK/PI3K pathway inhibition augments response to CD40 agonism by targeting CD11b+ Bregs thereby overcoming melanoma PD1-resistance. Nature communications, 17(1), 162.

Dovey Z, et al. (2026) Network and Gene Set Enrichment Analysis of Adipokine Drivers of Prostate Cancer; Unravelling the Mechanistic Link Between Excess Adiposity and Prostate Cancer Risk. Cancer medicine, 15(1), e71468.

Gou X, et al. (2026) Identification of a Two-Gene Biomarker Correlated with Sensitivity to Combined PARP7 Inhibition and AHR Activation in Cancer Cells. Cancer research communications, 6(1), 5.

Al-Ahmadi W, et al. (2026) Spaceflight alters molecular networks linked to diverse human diseases in a single cellular model. Science advances, 12(1), eadw7832.

Chen H, et al. (2025) PARP7 Inhibitors and AHR Agonists Act Synergistically across a Wide Range of Cancer Models. Molecular cancer therapeutics, 24(1), 56.

Dumesic PA, et al. (2025) RBM43 controls PGC1?? translation and a PGC1??-STING signaling axis. Cell metabolism, 37(3), 742.

Laplante P, et al. (2025) Effect of MisMatch repair deficiency on metastasis occurrence in a syngeneic mouse model. *Neoplasia* (New York, N.Y.), 62, 101145.

Gonsales Spindola D, et al. (2025) Endothelial cells retain inflammatory memory through chromatin remodeling in a two-hit model of infection-induced inflammation. *American journal of physiology. Cell physiology*, 329(6), C1994.

Hsieh LT, et al. (2025) The Mycobacterium ulcerans toxin mycolactone causes destructive Sec61-dependent loss of the endothelial glycocalyx and vessel basement membrane to drive skin necrosis. *eLife*, 12.

Hu F, et al. (2025) The systemic wrinkled skin phenotype involves aberrant expression and variation of genes related to the oxidative stress and extracellular matrix in Xiang pigs. *BMC genomics*, 26(1), 1034.

Biggs KE, et al. (2025) Coronin1A Regulates the Trafficking of Alpha Synuclein in Microglia. *The Journal of neuroscience : the official journal of the Society for Neuroscience*, 45(11).

Alessandrini F, et al. (2025) TDP-43 dysfunction compromises UPF1-dependent mRNA metabolism in ALS. *Neuron*.

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.

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).

Picone JA, et al. (2025) The function of the ZFP189 transcription factor in the nucleus accumbens facilitates cocaine-specific transcriptional and behavioral adaptations. *Molecular psychiatry*, 30(6), 2490.

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.

Binks SNM, et al. (2025) Novel risk loci in LGI1-antibody encephalitis: genome-wide association study discovery and validation cohorts. *Brain : a journal of neurology*, 148(3), 737.

Kroon S, et al. (2025) Sublethal systemic LPS in mice enables gut-luminal pathogens to bloom through oxygen species-mediated microbiota inhibition. *Nature communications*, 16(1), 2760.