

Resource Summary Report

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Weighted Gene Co-expression Network Analysis

RRID:SCR_003302

Type: Tool

Proper Citation

Weighted Gene Co-expression Network Analysis (RRID:SCR_003302)

Resource Information

URL: <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/>

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Description: Software R package for weighted correlation network analysis. WGCNA is also available as point-and-click application. Unfortunately this application is not maintained anymore. It is known to have compatibility problems with R-2.8.x and newer, and the methods it implements are not all state of the art., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: WGCNA

Synonyms: WGCNA: an R package for weighted correlation network analysis

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

Defining Citation: [PMID:19114008](#)

Keywords: gene, co-expression, analysis, network, bio.tools, bio.tools

Funding: NCI P50CA092131;
NIDA 1R01DA030913-01;
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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Weighted Gene Co-expression Network Analysis

Resource ID: SCR_003302

Alternate IDs: nif-0000-31889, biotools:crosslinkwgcn

Alternate URLs:

<http://labs.genetics.ucla.edu/horvath/htdocs/CoexpressionNetwork/Rpackages/WGCNA/#citation>,
<https://bio.tools/crosslinkwgcna>

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Ratings and Alerts

No rating or validation information has been found for Weighted Gene Co-expression Network Analysis.

No alerts have been found for Weighted Gene Co-expression Network Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1879 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Huang C, et al. (2026) Survival Genie 2: a next-generation web server for targeted and single-cell-based survival analyses. *Genome medicine*, 18(1).

Schulz A, et al. (2026) LAMA5 links extracellular matrix organization to a candidate WNT-associated endothelial signaling niche during human chondrogenesis. *iScience*, 29(8), 116687.

Hu Z, et al. (2026) Multi-omics integration and machine learning reveal gut-immune signatures in idiopathic pulmonary fibrosis: insights from bulk RNA-seq, single-cell profiles, spatial transcriptomics, and experimental validation. *Frontiers in immunology*, 17, 1730289.

Liu B, et al. (2026) Shared molecular features and candidate pathways underlying gastric cancer-depression comorbidity: a systems biology analysis. *Frontiers in bioinformatics*, 6, 1836419.

Bacong JRC, et al. (2026) NOVAGene: a nonlinear approach to improve biological resolution in weighted gene co-expression networks for low-variability datasets. *Frontiers in bioinformatics*, 6, 1813626.

Wehle DT, et al. (2026) Dissociation of the mTOR Protein Interaction Network Following Neuronal Activation Is Altered by Shank3 Mutation. *Journal of neurochemistry*, 170(1), e70353.

Leonardi L, et al. (2026) TLR7 induces autophagy in non-small cell lung cancer tumor cells and influences anti-tumors responses in patients. *Translational lung cancer research*, 15(4), 75.

Lei G, et al. (2026) Experimental evolution to thermal stress indicates climate resilience in a cosmopolitan arthropod. *eLife*, 15.

Alsina M, et al. (2026) Anti-B-cell Maturation Antigen Chimeric Antigen Receptor T-cell Therapy bb21217 for Relapsed and Refractory Multiple Myeloma: Results from the Phase I CRB-402 Study. *Cancer immunology research*, 14(4), 528.

Al Souz J, et al. (2026) Organ injury in systemic autoimmunity is mediated by stem-like CD8+ T cells arising from tissue-draining lymph nodes. *Immunity*, 59(6), 1667.

Huo RZ, et al. (2026) Immune hub genes and a proof-of-concept prognostic signature in EBV-associated gastric carcinoma. *iScience*, 29(4), 115243.

Wang Q, et al. (2026) Syncytin-a deficiency compromises murine sperm function by suppressing PRL/PGE2 and PI3K/AKT/mTOR pathway. *iScience*, 29(5), 115694.

Lu T, et al. (2026) PUMILIO proteins maintain lineage balance via post-transcriptional repression of germline fate and promotion of somatic differentiation. *Cell reports*, 45(7), 117682.

Roels J, et al. (2026) The Hippo Pathway Is Dysregulated in Cancer-Associated Fibroblasts in Anti-PD-L1-Resistant Cancer. *Cancer research*, 86(11), 2592.

Wu L, et al. (2026) Longitudinal Plasma Proteomics Reveals an Immuno-thrombotic Signature That Predicts Radiation Pneumonitis in Lung Cancer. *International journal of radiation oncology, biology, physics*.

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. *Cell host & microbe*, 34(5), 844.

Pasbala K, et al. (2026) Transcriptome profiling reveals the role of XIST/miR-335-5p regulatory axis as a crucial mediator of chemoresistance in esophageal cancer by influencing EMT and Ferroptosis. *Functional & integrative genomics*, 26(1).

Chen F, et al. (2026) q orA shapes organ-specific adaptation of ST59-MRSA via balancing immune evasion and metabolic trade-off. *iScience*, 29(7), 116272.

Gao X, et al. (2025) The integrated single-cell analysis interpret the lactate metabolism-driven immune suppression in triple-negative breast cancer. *Discover oncology*, 16(1), 784.

Ciconello FN, et al. (2025) Pig models reveal the interplay between fatty acids and cytokines in skeletal muscle. *Scientific reports*, 15(1), 19528.