

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.

Abbreviations: WGCNA

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

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

Defining Citation: [PMID:19114008](https://pubmed.ncbi.nlm.nih.gov/19114008/)

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

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Availability: Acknowledgement requested

Resource Name: Weighted Gene Co-expression Network Analysis

Resource ID: SCR_003302

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

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 1549 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Huang T, et al. (2025) Dysregulation of REST and its target genes impacts the fate of neural progenitor cells in down syndrome. *Scientific reports*, 15(1), 2818.

Du L, et al. (2025) Integrating machine learning with mendelian randomization for unveiling causal gene networks in glioblastoma multiforme. *Discover oncology*, 16(1), 38.

Li X, et al. (2025) A comprehensive analysis to reveal the underlying molecular mechanisms of natural killer cell in thyroid carcinoma based on single-cell RNA sequencing data. *Discover oncology*, 16(1), 44.

Peng Y, et al. (2025) Temporal transcriptome profiling in the response to *Salmonella enterica* serovar enteritidis infection in chicken cecum. *Poultry science*, 104(2), 104773.

Huang L, et al. (2025) Elucidating the role of pyrimidine metabolism in prostate cancer and its therapeutic implications. *Scientific reports*, 15(1), 2003.

van Hijfte L, et al. (2025) Gemistocytic tumor cells programmed for glial scarring characterize

T cell confinement in IDH-mutant astrocytoma. *Nature communications*, 16(1), 1156.

Li G, et al. (2025) Identification of key genes associated with oxidative stress in ischemic stroke via bioinformatics integrated analysis. *BMC neuroscience*, 26(1), 3.

Ding H, et al. (2025) Integrating genetics and transcriptomics to characterize shared mechanisms in digestive diseases and psychiatric disorders. *Communications biology*, 8(1), 47.

Zhao N, et al. (2025) Identification of critical endoplasmic reticulum stress-related genes in advanced atherosclerotic plaque. *Scientific reports*, 15(1), 2107.

Testone G, et al. (2025) The molecular pathways leading to GABA and lactic acid accumulation in florets of organic broccoli rabe (*Brassica rapa* subsp. *sylvestris*) stored as fresh or as minimally processed product. *Horticulture research*, 12(1), uhae274.

Aggarwal B, et al. (2025) CellSP: Module discovery and visualization for subcellular spatial transcriptomics data. *bioRxiv : the preprint server for biology*.

Zhu Y, et al. (2025) NIPAL1 as a prognostic biomarker associated with pancreatic adenocarcinoma progression and immune infiltration. *BMC cancer*, 25(1), 165.

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Meshkinkhood N, et al. (2025) Unveiling Molecular Dynamics of MeCp2, CDKL5 and BDNF in the Hippocampus of Individuals With Intractable Mesial Temporal Lobe Epilepsy. *Journal of cellular and molecular medicine*, 29(3), e70373.

Burton J, et al. (2025) Networks of pre-diagnostic circulating RNA in testicular germ cell tumour. *Scientific reports*, 15(1), 1910.

Mao D, et al. (2025) Integrated bioinformatics analysis identified cuproptosis-related hub gene *Mpeg1* as potential biomarker in spinal cord injury. *Scientific reports*, 15(1), 1993.

Keady J, et al. (2025) Behavioral and genetic markers of susceptibility to escalate fentanyl intake. *bioRxiv : the preprint server for biology*.

Koyama T, et al. (2025) Differential Stress Responses to Rice Blast Fungal Infection Associated with the Vegetative Growth Phase in Rice. *Plants (Basel, Switzerland)*, 14(2).

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.

Liu S, et al. (2025) CEACAM5 exacerbates asthma by inducing ferroptosis and autophagy in airway epithelial cells through the JAK/STAT6-dependent pathway. *Redox report : communications in free radical research*, 30(1), 2444755.