# **Resource Summary Report**

Generated by dkNET on May 11, 2025

# **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/

**Proper Citation:** Weighted Gene Co-expression Network Analysis (RRID:SCR\_003302)

**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: software resource, data analysis software, software application, data

processing software

**Defining Citation:** PMID:19114008

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

Funding: NCI P50CA092131; NIDA 1R01DA030913-01; NIDCR R01DE019255; NIAID U19 AI063603-01

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

**Record Creation Time:** 20220129T080218+0000

Record Last Update: 20250509T055606+0000

## 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 dkNET.

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.

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.

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.

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.

van Gelderen TA, et al. (2025) Gonadal miRNomes and transcriptomes in infected fish reveal sexually dimorphic patterns of the immune response. Functional & integrative genomics, 25(1), 29.

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.