

Resource Summary Report

Generated by [dkNET](#) on Sep 8, 2026

[hdWGCNA](#)

RRID:SCR_027496

Type: Tool

Proper Citation

hdWGCNA (RRID:SCR_027496)

Resource Information

URL: <https://github.com/smorabit/hdWGCNA>

Proper Citation: hdWGCNA (RRID:SCR_027496)

Description: Software R package for performing weighted gene co-expression network analysis in high dimensional transcriptomics data such as single-cell RNA-seq or spatial transcriptomics.

Synonyms: hd Weighted Gene Co-expression Network Analysis

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:37426759](#)

Keywords: weighted gene co-expression network, high dimensional transcriptomics data, single-cell RNA-seq, transcriptomics

Funding: NIA 1RF1AG071683;
NIA 3U19AG068054;
NIA U54 AG054349;
NIDA 1U01DA053826;
NINDS P01NS084974

Availability: Free, Available for download, Freely available

Resource Name: hdWGCNA

Resource ID: SCR_027496

License: GNU GPL v3

Record Creation Time: 20251002T061356+0000

Record Last Update: 20260905T133549+0000

Ratings and Alerts

No rating or validation information has been found for hdWGCNA.

No alerts have been found for hdWGCNA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Han Z, et al. (2026) Single-Nucleus Transcriptome Reveals Cellular Heterogeneity and Transcriptional Response to Heat Stress in Skeletal Muscle. *Journal of cachexia, sarcopenia and muscle*, 17(1), e70217.

Wu M, et al. (2026) Dynamic changes of the immune microenvironment in ovarian cancer following neoadjuvant chemotherapy. *Cell death discovery*, 12(1).

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Wang Y, et al. (2024) Pathomics and single-cell analysis of papillary thyroid carcinoma reveal the pro-metastatic influence of cancer-associated fibroblasts. *BMC cancer*, 24(1), 710.

Huang Y, et al. (2024) Deciphering the impact of aging on splenic endothelial cell heterogeneity and immunosenescence through single-cell RNA sequencing analysis. *Immunity & ageing : I & A*, 21(1), 48.

Ross JL, et al. (2024) Microglia and monocyte-derived macrophages drive progression of pediatric high-grade gliomas and are transcriptionally shaped by histone mutations. *Immunity*, 57(11), 2669.

Kan JY, et al. (2024) Metabolic shifts in lipid utilization and reciprocal interactions within the lung metastatic niche of triple-negative breast cancer revealed by spatial multi-omics. *Cell death & disease*, 15(12), 899.

Kypraios A, et al. (2024) Identifying Candidate Gene Drivers Associated with Relapse in Pediatric T-Cell Acute Lymphoblastic Leukemia Using a Gene Co-Expression Network Approach. *Cancers*, 16(9).

Tsai YC, et al. (2023) Single-cell transcriptomic profiles in the pathophysiology within the microenvironment of early diabetic kidney disease. *Cell death & disease*, 14(7), 442.

Huang YC, et al. (2022) Single-Cell Transcriptomic Profiles of Lung Pre-Metastatic Niche Reveal Neutrophil and Lymphatic Endothelial Cell Roles in Breast Cancer. *Cancers*, 15(1).