

Resource Summary Report

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MCODE

RRID:SCR_015828

Type: Tool

Proper Citation

MCODE (RRID:SCR_015828)

Resource Information

URL: <http://apps.cytoscape.org/apps/mcode>

Proper Citation: MCODE (RRID:SCR_015828)

Description: Software that clusters a given network based on topology to find densely connected regions. It can be used to find protein complexes and parts of pathways in protein-protein interaction networks or protein families in protein similarity networks.

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

Defining Citation: [PMID:12525261](#), [PMID:25570063](#)

Keywords: cluster, clustering, graph analysis, network, network topology, interconnectivity

Funding: Canadian Institutes of Health Research (CIHR) ;
Ontario Research and Development Challenge Fund ;
MDS-Sciex

Availability: Free, Available for download

Resource Name: MCODE

Resource ID: SCR_015828

Alternate URLs: <http://baderlab.org/Software/MCODE>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260731T042957+0000

Ratings and Alerts

No rating or validation information has been found for MCODE.

No alerts have been found for MCODE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1150 mentions in open access literature.

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

Baishya S, et al. (2026) Gene regulatory networks involved in activation of Notch signaling by AGEs in the pathogenesis of diabetic kidney disease. PloS one, 21(1), e0335768.

Cai S, et al. (2026) Identification and validation of novel inflammatory response-related diagnostic biomarkers in diabetic foot ulcers. Journal of diabetes investigation, 17(1), 103.

Yadav K, et al. (2025) Pancancer analysis of DNA damage repair gene mutations and their impact on immune regulatory gene expression. Scientific reports, 15(1), 15667.

Shi L, et al. (2025) FMRP-dependent translational control negatively regulates adapter protein complex 2-mediated endocytosis. iScience, 28(8), 113062.

Min XL, et al. (2025) Analysis and Identification of Therapeutic Targets for Neuronal Regeneration After Ischemic Stroke. Brain and behavior, 15(5), e70377.

Vafadar A, et al. (2025) Meta-analysis of microarray data to identify potential signature genes and MiRNAs associated with the pathogenesis of asthma. Journal of translational medicine, 23(1), 796.

Wang R, et al. (2025) Identification and validation of endoplasmic reticulum autophagy-related potential biomarkers in periodontitis. Scientific reports, 15(1), 24151.

Hernandez JB, et al. (2025) Microbiome and metabolome association network analysis identifies *Clostridium_sensu_stricto_1* as a stronger keystone genus candidate than *Bifidobacterium* in the gut of common marmosets. mSystems, 10(8), e0021425.

Noufal NR, et al. (2025) Evaluation of potential prognostic significance of JUNB in human prostate cancer: a bioinformatic and histopathological study. Journal of pathology and translational medicine, 59(5), 291.

Ren F, et al. (2025) A small-molecule TNIK inhibitor targets fibrosis in preclinical and clinical models. Nature biotechnology, 43(1), 63.

Li P, et al. (2025) Ability of SPP1 to Alleviate Post-Intracerebral Hemorrhage Ferroptosis via Nrf2/HO1 Pathway. Brain and behavior, 15(5), e70493.

Chaturvedi A, et al. (2025) Arsenic toxicity in the Drosophila brain at single cell resolution. *Frontiers in toxicology*, 7, 1636431.

Francis A, et al. (2025) Deconvolution-Based Transcriptomic Analysis in the Hippocampus Reveals Cell Type-Specific Risk Genes and Pathways Associated With Depression and Suicide. *Biological psychiatry global open science*, 5(5), 100530.

Tao F, et al. (2025) Insight into the composition and differentiation of endophytic microbial communities in kernels via 368 maize transcriptomes. *Journal of advanced research*, 71, 5.

Hong J, et al. (2025) Immune-related diagnostic indicators and targeted therapies for COPD combined with NASH were identified and verified via WGCNA and LASSO. *Frontiers in immunology*, 16, 1514422.

Liu Z, et al. (2025) Astaxanthin ameliorates benzalkonium chloride-induced dry eye disease through suppressing inflammation and oxidative stress via Keap1-Nrf2/HO-1 signaling pathways. *Animal models and experimental medicine*, 8(6), 1056.

Chen X, et al. (2025) CENPF as a prognostic marker of glioma: unraveling the molecular mechanisms. *Journal of cancer research and clinical oncology*, 151(2), 96.

Wang C, et al. (2025) Bioinformatics Analysis Screening and Identification of Key Biomarkers and Drug Targets in Human Glioblastoma. *Current medicinal chemistry*, 32(25), 5260.

Zhuang Y, et al. (2025) Core microbe *Bifidobacterium* in the hindgut of calves improves the growth phenotype of young hosts by regulating microbial functions and host metabolism. *Microbiome*, 13(1), 13.

Yuan HJ, et al. (2025) Exploration and verification of the therapeutic mechanism of shenfu injection in sepsis-induced myocardial injury. *PloS one*, 20(1), e0317738.