

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>

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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 analysis software, data processing software, software application, algorithm resource, image analysis software, software resource

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: 20260814T042931+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 1254 mentions in open access literature.

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

Shi L, et al. (2026) Protocol for identifying surface membrane proteins and their associated proteome from mouse cortical neuron cultures by in situ biotinylation. STAR protocols, 7(1), 104418.

Ratnawati H, et al. (2026) The ubiquitin-proteasome system is an important driver of EBV-associated nasopharyngeal carcinoma progression: a meta-analysis of transcriptomic data. Scientific reports, 16(1).

Wang A, et al. (2026) Proteomic Landscape of Sweat Glands in Neuronal Intranuclear Inclusion Disease Reveals a Pathogenic Triad of Abnormal Autophagy, Mitochondrial Dysfunction, and a Failed Oxidative Stress Response. Journal of neurochemistry, 170(1), e70352.

Wei S, et al. (2026) Risk assessment for hydrophobic disinfectants and antiseptics as contaminants in freshwater using risk quotient and network pharmacology approaches. iScience, 29(7), 116339.

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.

Zhao Y, et al. (2026) Inflammation-induced impairment of synaptic plasticity accelerates atherosclerosis co-depression disease: insights from bioinformatics analysis and transcriptomics. Cell & bioscience, 16(1).

Zhuang C, et al. (2026) Mechanisms of deoxynivalenol-induced multi-organ toxicity in broiler chickens: The central role of the Rap1/MAPK pathway revealed by network pharmacology and molecular docking. Poultry science, 105(4), 106494.

Yang Y, et al. (2026) Integrative network pharmacology and experimental study of Qingda granule in hypertension-induced endothelial dysfunction. Experimental animals, 75(2), 131.

Qin Z, et al. (2026) Cockroach-Derived Leucokinin VIII Peptide Accelerates Diabetic Skin Wound Healing by Enhancing Keratinocyte Filopodia Formation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(24), e22333.

Zhao H, et al. (2026) Comprehensive analysis of mitophagy-related genes reveals prognostic signatures in breast cancer: based on immune landscapes and treatment target predict. *Frontiers in immunology*, 17, 1740830.

Gao Y, et al. (2026) Radiomics predicts poorly differentiated hepatocellular carcinoma and uncovers ribosomal-immune dysregulation mechanism. *iScience*, 29(2), 114699.

Can VG, et al. (2026) Molecular Characterization of Muscle-Invasive Bladder Cancer: Key MicroRNAs, Transcription Factors, and Differentially Expressed Genes. *Genes*, 17(2).

Li H, et al. (2026) Study on the Potential Mechanism of Astragaloside IV on Renoprotection in Db/Db Mice via Network Pharmacology and Experimental Validation. *Journal of diabetes research*, 2026(1), e5345971.

Yang C, et al. (2026) AMBP gene activation promotes cholangiocarcinoma progression through the WNT/ β -catenin signaling pathway: Regulatory effect of polysaccharides from *Auricularia auricula-judae*. *Medicine*, 105(11), e47710.

Song L, et al. (2026) Triptonide Suppresses AML via PI3K/AKT Signaling: A Network Pharmacology Approach Validated by Molecular Docking and Experimental Studies. *Current issues in molecular biology*, 48(3).

Hong Y, et al. (2026) Protocol for analyzing potential targets of environmental pollutants in human diseases using network toxicology and molecular docking. *STAR protocols*, 7(2), 104555.

Chen Y, et al. (2026) Wubie Fanchun Formula-inducible metabolites in primary ovarian insufficiency model mice that facilitate ovarian renovation. *Pharmaceutical biology*, 64(1), 725.

Chen Z, et al. (2026) Literature-derived serum miRNA signatures associated with cognitive decline in Alzheimer's disease: integrated analysis and machine learning-based diagnostic modeling. *Alzheimer's research & therapy*, 18(1).

Banerjee S, et al. (2026) Tumor-infiltrating lymphocytes display prognostic signatures associated with chemotherapy response in TNBC patients. *iScience*, 29(6), 116295.

Zhang ZQ, et al. (2026) Bone marrow CCR3 dictates eosinophil lineage commitment of CD34⁺ progenitors to orchestrate allergic rhinitis: A composite study. *PloS one*, 21(6), e0351726.