

Resource Summary Report

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cytoHubba

RRID:SCR_017677

Type: Tool

Proper Citation

cytoHubba (RRID:SCR_017677)

Resource Information

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

Proper Citation: cytoHubba (RRID:SCR_017677)

Description: Software tool for identifying hub objects and sub-networks from complex interactome. Predicts and explore nodes and subnetworks in given network by several topological algorithms. Provides interface to analyze topology of protein-protein interaction networks, such as human, yeast, rat, mouse, fly etc. Plugin works with Cytoscape 2.6 or above, which requires Java 1.5 or above.

Synonyms: cytoHubba 1.6

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

Defining Citation: [PMID:25521941](#)

Keywords: Identify, network, subnetwork, topological, algorithm, analyze, protein, interaction, hub, object, intercome

Funding: Ministry of Science and Technology (MOST) ; Taiwan

Availability: Free, Available for download, Freely available

Resource Name: cytoHubba

Resource ID: SCR_017677

Alternate URLs: <http://hub.iis.sinica.edu.tw/cytoHubba/>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250426T060636+0000

Ratings and Alerts

No rating or validation information has been found for cytoHubba.

No alerts have been found for cytoHubba.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 283 mentions in open access literature.

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

Li J, et al. (2025) Knockdown of CENPF induces cell cycle arrest and inhibits epithelial?mesenchymal transition progression in glioma. *Oncology letters*, 29(1), 61.

Yang H, et al. (2025) Exploring the Cardioprotective Mechanisms of Ligusticum wallichii in Myocardial Infarction Through Network Pharmacology and Experimental Validation. *Drug design, development and therapy*, 19, 281.

Lu C, et al. (2025) Identification of biomarkers associated with coronary artery disease and non-alcoholic fatty liver disease by bioinformatics analysis and machine learning. *Scientific reports*, 15(1), 3557.

Li Z, et al. (2025) Transcriptomic profiling and machine learning reveal novel RNA signatures for enhanced molecular characterization of Hashimoto's thyroiditis. *Scientific reports*, 15(1), 677.

Yu R, et al. (2025) ATRX mutation modifies the DNA damage response in glioblastoma multiforme tumor cells and enhances patient prognosis. *Medicine*, 104(2), e41180.

Jiang F, et al. (2025) Key wound healing genes as diagnostic biomarkers and therapeutic targets in uterine corpus endometrial carcinoma: an integrated in silico and in vitro study. *Hereditas*, 162(1), 5.

Heidari R, et al. (2025) The miRNA-mRNA Regulatory Network in Human Hepatocellular Carcinoma by Transcriptomic Analysis From GEO. *Cancer reports (Hoboken, N.J.)*, 8(1),

e70098.

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.

Luo H, et al. (2025) Pathogenic variants of TUBB8 cause oocyte spindle defects by disrupting with EB1/CAKP5 interactions and potential treatment targeting microtubule acetylation through HDAC6 inhibition. *Clinical and translational medicine*, 15(1), e70193.

Dong Z, et al. (2025) A KSHV-targeted small molecule efficiently blocks SARS-CoV-2 infection via inhibiting expression of EGFR and Cyclin A2. *Emerging microbes & infections*, 14(1), 2440490.

Yang Y, et al. (2025) Complement classical and alternative pathway activation contributes to diabetic kidney disease progression: a glomerular proteomics on kidney biopsies. *Scientific reports*, 15(1), 495.

Yang A, et al. (2025) Regional brain iron correlates with transcriptional and cellular signatures in Alzheimer's disease. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(1), e14459.

Jiang C, et al. (2024) Exploring the relationship between immune heterogeneity characteristic genes of rheumatoid arthritis and acute myeloid leukemia. *Discover. Oncology*, 15(1), 1.

Alqahtani SM, et al. (2024) System biology approach to identify the novel biomarkers in glioblastoma multiforme tumors by using computational analysis. *Frontiers in pharmacology*, 15, 1364138.

Yu X, et al. (2024) NDC80 Kinetochore Complex Serves as a Potential Prognostic Predictor and Correlates with Immune Infiltrates in Epithelial Ovarian Cancer Patients. *International journal of general medicine*, 17, 1789.

Wang Y, et al. (2024) A comparative study on the dose-effect of low-dose radiation based on microdosimetric analysis and single-cell sequencing technology. *Scientific reports*, 14(1), 11524.

Tang H, et al. (2024) Analyses of lncRNA and mRNA profiles in recurrent atrial fibrillation after catheter ablation. *European journal of medical research*, 29(1), 244.

Dai Q, et al. (2024) Identification of Lupus-Associated Genes in the Pathogenesis of Pre-eclampsia Via Bioinformatic Analysis. *Bioinformatics and biology insights*, 18, 11779322241271558.

Zhao S, et al. (2024) Comparative analysis of gene expression between mice and humans in acetaminophen-induced liver injury by integrating bioinformatics analysis. *BMC medical genomics*, 17(1), 80.

Ray AK, et al. (2024) A bioinformatics approach to elucidate conserved genes and pathways

in *C. elegans* as an animal model for cardiovascular research. Scientific reports, 14(1), 7471.