## **Resource Summary Report**

Generated by NIF on May 21, 2025

# cytoHubba

RRID:SCR\_017677

Type: Tool

### **Proper Citation**

cytoHubba (RRID:SCR\_017677)

#### **Resource Information**

**URL:** <a href="http://apps.cytoscape.org/apps/cytohubba">http://apps.cytoscape.org/apps/cytohubba</a>

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

**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: 20250521T061716+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 NIF.

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.

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.

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.

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.

Elkhamary A, et al. (2024) Comparative proteomic profiling of the ovine and human PBMC inflammatory response. Scientific reports, 14(1), 14939.

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

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.

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.

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.