

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>

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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: software resource, data processing software, software application, data analysis software, network analysis 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: 20260803T040752+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 356 mentions in open access literature.

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

Li X, et al. (2026) Dynamic transcriptomic landscape of myogenesis in Muscovy ducks (*Cairina moschata*): integrative analysis of hub genes post-hatching. *Animal bioscience*, 39(1), 250159.

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.

Hua S, et al. (2026) Spatiotemporal profiling of endocytic regulators in the immunosuppressive TAM microenvironment of glioma. *Brain research*, 1872, 150086.

Gogoi A, et al. (2026) Proteomics of In Vivo models of ischemic stroke: A systematic review with a systems biological perspective. *Ageing research reviews*, 113, 102937.

Burge KY, et al. (2025) Spatial transcriptomics delineates potential differences in intestinal phenotypes of cardiac and classical necrotizing enterocolitis. *iScience*, 28(4), 112166.

Hellbacher E, et al. (2025) The plasma proteome reveals distinct signaling pathways associated with PR3-ANCA positive and MPO-ANCA positive vasculitis. *Frontiers in immunology*, 16, 1600754.

Hu Q, et al. (2025) A bioinformatics analysis of the correlation between hepatic ischemia-reperfusion injury and postoperative cognitive dysfunction. *Frontiers in genetics*, 16, 1607446.

Maigoro AY, et al. (2025) In the battle of survival: transcriptome analysis of hypopharyngeal gland of the *Apis mellifera* under temperature-stress. *BMC genomics*, 26(1), 151.

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.

Liu Y, et al. (2025) Exploring the molecular mechanisms of subarachnoid hemorrhage and potential therapeutic targets: insights from bioinformatics and drug prediction. *Scientific*

reports, 15(1), 12861.

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.

Xie W, et al. (2025) IFI30 Knockdown Inhibits ESCC Progression by Promoting Apoptosis and Senescence via Activation of JNK and P21/P16 Pathways. *Thoracic cancer*, 16(7), e70063.

Charoensuksira S, et al. (2025) Progenitor Cell Dynamics in Androgenetic Alopecia: Insights from Spatially Resolved Transcriptomics. *International journal of molecular sciences*, 26(12).

He J, et al. (2025) Investigation of the relationship between chronic hepatitis B and tuberculosis using bioinformatics and systems biology approaches. *Frontiers in medicine*, 12, 1519216.

Guan T, et al. (2025) Identification of Potential Common Pathogenic Mechanisms Underlying Osteoarthritis and Major Depressive Disorder Using Bioinformatics Analysis. *Immunity, inflammation and disease*, 13(11), e70293.

Xu Z, et al. (2025) The ADCY1-mediated cAMP signaling pathway mediates functional effects of montelukast treatment in brain organoids. *Cellular and molecular life sciences : CMLS*, 82(1), 224.

Ahmed R, et al. (2025) Common molecular links and therapeutic insights between type 2 diabetes and kidney cancer. *PloS one*, 20(8), e0330619.

Jiang Q, et al. (2025) Differential changes in the microglial transcriptome between neonatal and adult mice after spinal cord injury. *Scientific reports*, 15(1), 13708.

Liu T, et al. (2025) Identification and functional characterization of hub genes CLTA, EDIL3, HAPLN1, and HIP1 as diagnostic biomarkers and therapeutic targets in thyroid cancer and Hashimoto's thyroiditis. *Clinical and experimental medicine*, 25(1), 162.

Alatawi FS, et al. (2025) Rutin attenuates bleomycin-induced acute lung injury via miR-9-5p mediated NF- κ B signaling inhibition: network pharmacology analysis and experimental evidence. *Frontiers in pharmacology*, 16, 1522690.