

Resource Summary Report

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Cytoscape

RRID:SCR_003032

Type: Tool

Proper Citation

Cytoscape (RRID:SCR_003032)

Resource Information

URL: <http://cytoscape.org>

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Description: Software platform for complex network analysis and visualization. Used for visualization of molecular interaction networks and biological pathways and integrating these networks with annotations, gene expression profiles and other state data.

Synonyms: Complex Network Analysis Visualization, Cytoscape 2.6, Cytoscape 3.0

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

Defining Citation: [PMID:21149340](#), [PMID:14597658](#)

Keywords: biological, network, visualization, analysis, data, gene, pathway, molecular, interaction, FASEB list

Funding: National Resource for Network Biology ;
NCRR RR031228;
NIGMS GM070743

Availability: Free, Available for download, Freely available

Resource Name: Cytoscape

Resource ID: SCR_003032

Alternate IDs: nif-0000-30404

Alternate URLs: <https://sources.debian.org/src/cytoscape/>

License: GNU Lesser General Public License

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260729T044036+0000

Ratings and Alerts

No rating or validation information has been found for Cytoscape.

No alerts have been found for Cytoscape.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23431 mentions in open access literature.

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

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.

Pereira-Martins DA, et al. (2026) ?Np73 isoform defines a TP53-mutant-like poor-risk subgroup of acute myeloid leukemia. Cell reports. Medicine, 102540.

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the Drosophila brain. Cell genomics, 101125.

Ferreira JV, et al. (2026) LAMP2A regulates endosomal protein composition and membrane identity in exosome biogenesis. iScience, 29(1), 114305.

Li L, et al. (2026) Hyperoside prevents osteoporosis by activating the PI3K/AKT signaling pathway to inhibit oxidative stress and promote osteogenesis. Molecular medicine reports, 33(2).

He S, et al. (2026) CTSB mediates oxidative stress and intestinal epithelial barrier disruption in intestinal ischemia?reperfusion injury. Molecular medicine reports, 33(1).

Kang Q, et al. (2026) Identification of multimorbidity hub genes for knee osteoarthritis-atherosclerosis and potential clinical applications. Molecular medicine reports, 33(1).

Yang YF, et al. (2026) Integrative analysis identifies PIGK as an oncogenic glycosylphosphatidylinositol transamidase subunit with prognostic, immunological, and therapeutic relevance in head and neck cancer. International journal of medical sciences, 23(1), 161.

Cheng M, et al. (2026) Targeting p38 MAPK signaling pathway: Quercetin as a novel therapy for TMJ synovitis. International journal of molecular medicine, 57(1).

Sun B, et al. (2026) CDK1-induced regulation of p53 phosphorylation at Ser315 mediates cell cycle arrest and apoptosis of macrophages infected with clinical isolates of *Mycobacterium tuberculosis*. *Molecular medicine reports*, 33(1).

Chen C, et al. (2026) Identifying myosin heavy chain 11 as a predictive biomarker of prostate cancer progression and antiandrogen resistance. *Oncology letters*, 31(2), 77.

Huang L, et al. (2026) New insight into the epidemiological trends of respiratory syncytial virus infection and the underlying anti-respiratory syncytial virus mechanisms of andrographolide: integrating Global Burden of Disease database, network pharmacological analysis, and in vitro experiments. *Microbiology spectrum*, 14(1), e0234125.

Mok JH, et al. (2026) Gingival Crevicular Fluid Proteomic Shift: From Gingivitis to Periodontitis. *International dental journal*, 76(1), 109306.

Bell MB, et al. (2025) Brain Transcriptome Changes Associated With an Acute Increase of Protein O-GlcNAcylation and Implications for Neurodegenerative Disease. *Journal of neurochemistry*, 169(1), e16302.

Cao X, et al. (2025) Maturation and detoxification of synphilin-1 inclusion bodies regulated by sphingolipids. *eLife*, 12.

Ali M, et al. (2025) Multi-cohort cerebrospinal fluid proteomics identifies robust molecular signatures across the Alzheimer disease continuum. *Neuron*, 113(9), 1363.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. *Cancer discovery*, 15(8), 1630.

Zhang C, et al. (2025) Comprehensive characterization of respiratory genes based on a computational framework in pan-cancer to develop stratified treatment strategies. *PLoS computational biology*, 21(4), e1012963.

Gao Y, et al. (2025) Multiomics Insights into the Mechanism and Enhanced Efficacy of Tumor Treating Fields (TTFields) Therapy in Glioblastoma. *Journal of proteome research*.

Ebert SN, et al. (2025) Single-Cell Approaches Define the Murine Leptomeninges: Cortical Brain Interface as a Distinct Cellular Neighborhood Composed of Neural and Non-neural Cell Types. *eNeuro*, 12(8).