

Resource Summary Report

Generated by T1D on Aug 9, 2026

Cytoscape

RRID:SCR_003032

Type: Tool

Proper Citation

Cytoscape (RRID:SCR_003032)

Resource Information

URL: <http://cytoscape.org>

Proper Citation: Cytoscape (RRID:SCR_003032)

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 resource, software application, data analysis software, data visualization software, data processing 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: 20260808T185751+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 25317 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Shaheen MT, et al. (2026) The Lysine Demethylase KDM4C Is an Oncogenic Driver and Regulates ERK Activity in KRAS-Mutant Pancreatic Ductal Adenocarcinoma. Cancer research communications, 6(1), 245.

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

Katko A, et al. (2026) Gene regulatory network determinants of rapid recall in human memory CD4+ T cells. Cell reports, 45(4), 117103.

Kim JK, et al. (2026) Loss of ABCA3 disrupts lipid balance and leads to AMPK-dependent suppression of SREBP1 in glioblastoma stem cells. Oncogene, 45(15), 1357.

Ismail J, et al. (2026) Single-cell transcriptomics reveal altered B cell responses and T cell senescence in geriatric non-responders to COVID-19 mRNA vaccination. iScience, 29(5), 115730.

Zhao Y, et al. (2026) IDH1 Reprograms Nucleotide Metabolism by Inducing Chromatin Remodeling and DHODH Transcription to Drive Chemoresistance in Nasopharyngeal Carcinoma. Cancer research, 86(8), 2004.

Podsiwa??ow-Bartnicka P, et al. (2026) Transcriptional readthrough precedes alternative splicing programs triggered in CML cells by imatinib. Science advances, 12(12), eaea2475.

Huo RZ, et al. (2026) Immune hub genes and a proof-of-concept prognostic signature in EBV-associated gastric carcinoma. iScience, 29(4), 115243.

Goodin DA, et al. (2026) Glioblastoma region-specific metabolic signatures reflect patient survival duration. Journal of neuro-oncology, 177(3).

Su Q, et al. (2026) Integrated bulk RNA-seq and scRNA-seq identification of a novel "PET-SPI1-MYL9" transcriptional axis in lung adenocarcinoma driven by polyethylene terephthalate exposure. *Translational cancer research*, 15(3), 173.

Lefranc C, et al. (2026) Transient remodeling of gut metabolism supports juvenile growth and adult fitness in *Drosophila*. *Nature communications*, 17(1).

Dalilah Y, et al. (2026) Site-specific evaluation of mutation-based mimics of histone glycation in the nucleosome. *Frontiers in molecular biosciences*, 13, 1838713.

Preston R, et al. (2026) Accelerated basement membrane remodeling and serum matrix fragments as biomarkers of fibrosis in Alport syndrome. *Cell reports*, 45(5), 117356.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Franciosa G, et al. (2026) The proteomics and phosphoproteomics landscape of melanoma under T cell attack. *Cell reports. Medicine*, 7(6), 102829.

Nassar A, et al. (2026) Ex-vivo culture of human hypertrophic cardiomyopathy hearts: Functional and metabolic changes during long-term culture. *iScience*, 29(4), 115308.

Rathore U, et al. (2026) Systematic discovery of pro- and anti-HIV host factors in primary human CD4⁺ T cells. *Cell*, 189(12), 3651.

Jiang M, et al. (2026) Analysis of the molecular mechanism underlying di(2-ethylhexyl) phthalate-induced bladder carcinogenesis via network toxicology and molecular docking approaches: An observational study. *Medicine*, 105(6), e47378.

Zhou Z, et al. (2026) Using an Unbiased Coexpression Network to Reveal Cross-Talking Pathways of Phosphoinositide-3-Kinase Regulatory Subunit 1 in Skin Aging and Rejuvenation. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(2), e71466.

Yogo A, et al. (2026) Spatial Transcriptomics Reveals Location-Specific Tumor Cell Subtypes and Signaling within Multifocal Small Intestinal Neuroendocrine Tumors. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(10), 2098.