Resource Summary Report

Generated by NIF on May 21, 2025

cPath

RRID:SCR_001749
Type: Tool

Proper Citation

cPath (RRID:SCR_001749)

Resource Information

URL: http://www.pathwaycommons.org/

Proper Citation: cPath (RRID:SCR_001749)

Description: Data management software that runs the Pathway Commons web service. It makes it easy to aggregate custom pathway data sets available in standard exchange formats from multiple databases, present pathway data to biologists via a customizable web interface, and export pathway data via a web service to third-party software, such as Cytoscape, for visualization and analysis. cPath is software only, and does not include new pathway information. Main features: * Import pipeline capable of aggregating pathway and interaction data sets from multiple sources, including: MINT, IntAct, HPRD, DIP, BioCyc, KEGG, PUMA2 and Reactome. * Import/Export support for the Proteomics Standards Initiative Molecular Interaction (PSI-MI) and the Biological Pathways Exchange (BioPAX) XML formats. * Data visualization and analysis via Cytoscape. * Simple HTTP URL based XML web service. * Complete software is freely available for local install. Easy to install and administer. * Partly funded by the U.S. National Cancer Institute, via the Cancer Biomedical Informatics Grid (caBIG) and aims to meet silver-level requirements for software interoperability and data exchange.

Abbreviations: cPath

Synonyms: cPath2

Resource Type: software resource, software application, data management software

Defining Citation: PMID:17101041

Keywords: exchange, molecular, pathway, proteomics, storing, visualization, visualizing, biological pathway, metabolic pathway, protein interaction network, signal transduction

pathway, gene regulatory network, biological process, exchange format, FASEB list

Funding: NCI ;
Alfred W. Bressler Scholars Endowment Fund

Availability: GNU Lesser General Public License

Resource Name: cPath

Resource ID: SCR_001749

Alternate IDs: nif-0000-10292

Old URLs: http://cbio.mskcc.org/cpath/home.do

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250519T203147+0000

Ratings and Alerts

No rating or validation information has been found for cPath.

No alerts have been found for cPath.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 153 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Li Z, et al. (2025) Role of NEL?like molecule?1 in osteogenesis/chondrogenesis (Review). International journal of molecular medicine, 55(1).

Yang L, et al. (2025) S100A16 stabilizes the ITGA3?mediated ECM?receptor interaction pathway to drive the malignant properties of lung adenocarcinoma cells via binding MOV10. Molecular medicine reports, 31(1).

Shi H, et al. (2024) Nur77-IRF1 axis inhibits esophageal squamous cell carcinoma growth and improves anti-PD-1 treatment efficacy. Cell death discovery, 10(1), 254.

Zhu J, et al. (2024) RNF115 aggravates tumor progression through regulation of CDK10 degradation in thyroid carcinoma. Cell biology and toxicology, 40(1), 14.

Liu XT, et al. (2024) Targeting the SphK1/S1P/PFKFB3 axis suppresses hepatocellular carcinoma progression by disrupting glycolytic energy supply that drives tumor angiogenesis. Journal of translational medicine, 22(1), 43.

Gupta K, et al. (2024) Secretome from iPSC-derived MSCs exerts proangiogenic and immunosuppressive effects to alleviate radiation-induced vascular endothelial cell damage. Stem cell research & therapy, 15(1), 230.

Buxbaum Grice AS, et al. (2024) Transient peripheral blood transcriptomic response to ketamine treatment in children with ADNP syndrome. Translational psychiatry, 14(1), 307.

Chen Y, et al. (2024) Effect of human heart valve-derived ECM and NP/PCL electrospun nanofibrous sheet on mice bone marrow mononuclear cells and cardiac repair. Heliyon, 10(11), e31821.

Grice ASB, et al. (2024) Transient peripheral blood transcriptomic response to ketamine treatment in children with ADNP syndrome. medRxiv : the preprint server for health sciences.

Yashar WM, et al. (2024) Predicting transcription factor activity using prior biological information. iScience, 27(3), 109124.

Chen J, et al. (2024) Exploring DNA Damage and Repair Mechanisms: A Review with Computational Insights. Biotech (Basel (Switzerland)), 13(1).

Lin MH, et al. (2024) PTGES is involved in myofibroblast differentiation via HIF-1?-dependent glycolysis pathway. Journal of cellular and molecular medicine, 28(20), e70157.

Zhou H, et al. (2023) Transcriptional expression, prognostic value and immune infiltration of SFRP family in colorectal cancer: a study based on comprehensive bioinformatics and in vitro analyses. Translational cancer research, 12(8), 1912.

Xu X, et al. (2023) Comprehensive bioinformatic analysis of the expression and prognostic significance of TSC22D domain family genes in adult acute myeloid leukemia. BMC medical genomics, 16(1), 117.

El-Gazzar A, et al. (2023) Bi-allelic mutation in SEC16B alters collagen trafficking and increases ER stress. EMBO molecular medicine, 15(4), e16834.

Sun H, et al. (2023) DUSP1 Signaling Pathway Regulates Cytarabine Sensitivity in Acute Myeloid Leukemia. Technology in cancer research & treatment, 22, 15330338231207765.

Tsai CY, et al. (2023) HOXC8 mediates osteopontin expression in gastric cancer cells. Journal of Cancer, 14(13), 2552.

Lee S, et al. (2023) IndepthPathway: an integrated tool for in-depth pathway enrichment

analysis based on single-cell sequencing data. Bioinformatics (Oxford, England), 39(6).

Piroeva KV, et al. (2023) Nucleosome repositioning in chronic lymphocytic leukemia. Genome research, 33(10), 1649.

Carbonetto P, et al. (2023) GoM DE: interpreting structure in sequence count data with differential expression analysis allowing for grades of membership. Genome biology, 24(1), 236.