

Resource Summary Report

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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: data management software, software application, software resource

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: Free, Freely available

Resource Name: cPath

Resource ID: SCR_001749

Alternate IDs: nif-0000-10292

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

License: GNU Lesser General Public License

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260821T193629+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 187 mentions in open access literature.

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

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.

Alam A, et al. (2026) Targeting protein protein interactions and their modulators to enable new therapeutic strategies for human diseases. NPJ systems biology and applications, 12(1).

Neidlinger P, et al. (2026) A deep learning framework for efficient pathology image analysis. Nature communications, 17(1).

Butler MG, et al. (2026) Clinical Presentation, Genetics, and Laboratory Testing with Integrated Genetic Analysis of Molecular Mechanisms in Prader-Willi and Angelman Syndromes: A Review. International journal of molecular sciences, 27(3).

Zhao Z, et al. (2025) EIF3M as a pan-cancer biomarker: prognostic significance and immune infiltration association. Frontiers in molecular biosciences, 12, 1697083.

- Zhang W, et al. (2025) Targeted demethylation of the EphA7 promoter inhibits tumorigenesis via the SP1/DNMT1 and PI3K/AKT axes and improves the response to multiple therapies in cervical cancer. *Cell death & disease*, 16(1), 324.
- Hu Z, et al. (2025) OTUB1-SLC7A11 Axis Mediates 4-Octyl Itaconate Protection Against Acetaminophen-Induced Ferroptotic Liver Injury. *Antioxidants (Basel, Switzerland)*, 14(6).
- Li Z, et al. (2025) Role of NEL?like molecule?1 in osteogenesis/chondrogenesis (Review). *International journal of molecular medicine*, 55(1).
- Wang J, et al. (2025) Multi-Omics analysis and in vitro validation reveal diagnostic and therapeutic roles of novel hub genes in ovarian cancer. *Hereditas*, 162(1), 166.
- Wang C, et al. (2025) Elucidating the Neuroprotective Mechanisms of G-3702 in Ischemic Stroke via Integrated Metabolomics and Computational Approaches. *CNS neuroscience & therapeutics*, 31(4), e70352.
- Xiao Z, et al. (2025) Inflammatory Biomarkers in Coronary Artery Disease: Insights From Mendelian Randomization and Transcriptomics. *Journal of inflammation research*, 18, 3177.
- Zhang J, et al. (2025) Discovering biomarkers associated with infiltration of CD8+ T cells and tumor-associated fibrosis in colon adenocarcinoma using single-cell RNA sequencing and gene co-expression network. *Frontiers in immunology*, 16, 1496640.
- Butler MG, et al. (2025) Barriers, Limitations, and Experiences with Clinical Trials-Treatment in Rare Diseases with Prader-Willi Syndrome as an Example. *Genes*, 16(12).
- Zhu D, et al. (2025) Integrated transcriptomic and functional analysis reveals overlapping pathways in lung adenocarcinoma and chronic obstructive pulmonary disease. *Hereditas*, 163(1), 15.
- Alissa M, et al. (2025) Integrative analysis of *Helicobacter pylori*-driven stomach adenocarcinoma reveals epigenetic deregulation, immune evasion, and therapeutic resistance. *Hereditas*, 163(1), 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).
- Wang B, et al. (2025) A comprehensive in silico and invitro analysis revealed the diagnostic, prognostic and therapeutic potential of GNAI family genes in colon adenocarcinoma (COAD). *Hereditas*, 162(1), 162.
- Liao SN, et al. (2025) Association of TIMP-2 Expression with Postoperative Prognosis in Hepatocellular Carcinoma Patients and Development of a Predictive Model. *Journal of inflammation research*, 18, 11703.
- Mei H, et al. (2025) Network analysis of multivariate time series data in biological systems: methods and applications. *Briefings in bioinformatics*, 26(3).
- Miao R, et al. (2025) AWGE-ESPCA: An edge sparse PCA model based on adaptive noise elimination regularization and weighted gene network for *Hermetia illucens* genomic

data analysis. PLoS computational biology, 21(2), e1012773.