Resource Summary Report

Generated by RRID on May 20, 2025

Pathway Interaction Database

RRID:SCR_006866
Type: Tool

Proper Citation

Pathway Interaction Database (RRID:SCR_006866)

Resource Information

URL: http://pid.nci.nih.gov

Proper Citation: Pathway Interaction Database (RRID:SCR_006866)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 27, 2016. Curated database of information about known biomolecular interactions and key cellular processes assembled into signaling pathways. All interactions are assembled into pathways, and can be accessed by performing searches for biomolecules, or processes, or by viewing predefined pathways. This was a collaborative project between the NCI and Nature Publishing Group (NPG) from 2006 until September 22nd, 2012, and is no longer being updated. PID is aimed at the cancer research community and others interested in cellular pathways, such as neuroscientists, developmental biologists, and immunologists. The database focuses on the biomolecular interactions that are known or believed to take place in human cells. It can be browsed as an online encyclopedia, used to run computational analyses, or employed in ways that combine these two approaches. In addition to PID""s predefined pathways, search results are displayed as dynamically constructed interaction networks. These features of PID render it a useful tool for both biologists and bioinformaticians. PID offers a range of search features to facilitate pathway exploration. Users can browse the predefined set of pathways or create interaction network maps centered on a single molecule or cellular process of interest. In addition, the batch query tool allows users to upload long list(s) of molecules, such as those derived from microarray experiments, and either overlay these molecules onto predefined pathways or visualize the complete molecular connectivity map. Users can also download molecule lists, citation lists and complete database content in extensible markup language (XML) and Biological Pathways Exchange (BioPAX) Level 2 format. The database is supplemented by a concise editorial section that includes specially written synopses of recent important research articles in areas related to cancer research, and specially commissioned Bioinformatics Primers that provide practical advice on how to make the most of other relevant online resources. The database and editorial content are updated monthly, and users can opt to

receive a monthly email alert to stay informed about new content. Note: as of September 23, 2012 the PID is no longer being actively curated. NCI will maintain the PID website and data for twelve months beyond September 2012 to allow interested parties to obtain the previously curated data before the site is retired in September 2013.

Abbreviations: PID, NCI Nature PID

Synonyms: Pathway Interaction Database

Resource Type: service resource, production service resource, data analysis service, database, analysis service resource, data or information resource

Defining Citation: PMID:18832364

Keywords: cellular process, interaction, neuroscience, pathway, molecule, cancer, molecular interaction, signaling pathway, visualization, connectivity, interaction network

Funding: NCI

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Pathway Interaction Database

Resource ID: SCR_006866

Alternate IDs: nif-0000-03286

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250519T203451+0000

Ratings and Alerts

No rating or validation information has been found for Pathway Interaction Database.

No alerts have been found for Pathway Interaction Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 95 mentions in open access literature.

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

Chen J, et al. (2025) Computational frameworks transform antagonism to synergy in optimizing combination therapies. NPJ digital medicine, 8(1), 44.

Wen W, et al. (2024) Rare variant association analyses reveal the significant contribution of carbohydrate metabolic disturbance in severe adolescent idiopathic scoliosis. Journal of medical genetics, 61(7), 666.

Wang H, et al. (2024) Deciphering the genomic insights into the coexistence of congenital scoliosis and congenital anomalies of the kidney and urinary tract. Frontiers in genetics, 15, 1399604.

Ng MTH, et al. (2024) A single cell atlas of frozen shoulder capsule identifies features associated with inflammatory fibrosis resolution. Nature communications, 15(1), 1394.

Pasquereau-Kotula E, et al. (2023) Global proteomic identifies multiple cancer-related signaling pathways altered by a gut pathobiont associated with colorectal cancer. Scientific reports, 13(1), 14960.

Guo Y, et al. (2021) MetaGSCA: A tool for meta-analysis of gene set differential coexpression. PLoS computational biology, 17(5), e1008976.

Vocale LG, et al. (2021) RNA-seq and GSEA identifies suppression of ligand-gated chloride efflux channels as the major gene pathway contributing to form deprivation myopia. Scientific reports, 11(1), 5280.

Wu YM, et al. (2021) RNA editing affects cis-regulatory elements and predicts adverse cancer survival. Cancer medicine, 10(17), 6114.

Elbialy A, et al. (2021) Ageing genetic signature of hypersomatotropism. Open biology, 11(4), 200265.

Manshaei R, et al. (2020) Genes and Pathways Implicated in Tetralogy of Fallot Revealed by Ultra-Rare Variant Burden Analysis in 231 Genome Sequences. Frontiers in genetics, 11, 957.

Wu Q, et al. (2020) DEFB4A is a potential prognostic biomarker for colorectal cancer. Oncology letters, 20(4), 114.

Zhang D, et al. (2020) Prognostic value and co-expression patterns of metabolic pathways in cancers. BMC genomics, 21(Suppl 11), 860.

Kato Y, et al. (2019) Lenvatinib plus anti-PD-1 antibody combination treatment activates CD8+ T cells through reduction of tumor-associated macrophage and activation of the interferon pathway. PloS one, 14(2), e0212513.

Alshabi AM, et al. (2019) Identification of Crucial Candidate Genes and Pathways in Glioblastoma Multiform by Bioinformatics Analysis. Biomolecules, 9(5).

Balashanmugam MV, et al. (2019) Analysis of Differentially Expressed Genes in Coronary Artery Disease by Integrated Microarray Analysis. Biomolecules, 10(1).

Kulpa DA, et al. (2019) Differentiation into an Effector Memory Phenotype Potentiates HIV-1 Latency Reversal in CD4+ T Cells. Journal of virology, 93(24).

Rosowski J, et al. (2019) Emulating the early phases of human tooth development in vitro. Scientific reports, 9(1), 7057.

Michalovicz LT, et al. (2019) Astrocyte-specific transcriptome analysis using the ALDH1L1 bacTRAP mouse reveals novel biomarkers of astrogliosis in response to neurotoxicity. Journal of neurochemistry, 150(4), 420.

Kumar R, et al. (2019) Exploring the new horizons of drug repurposing: A vital tool for turning hard work into smart work. European journal of medicinal chemistry, 182, 111602.

Alur VC, et al. (2019) Mining Featured Biomarkers Linked with Epithelial Ovarian CancerBased on Bioinformatics. Diagnostics (Basel, Switzerland), 9(2).