# Resource Summary Report

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## ConsensusPathDB

RRID:SCR_002231
Type: Tool

### Proper Citation

ConsensusPathDB (RRID:SCR_002231)

### Resource Information

**URL:** http://cpdb.molgen.mpg.de

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**Description:** An integrative interaction database that integrates different types of functional interactions from heterogeneous interaction data resources. Physical protein interactions, metabolic and signaling reactions and gene regulatory interactions are integrated in a seamless functional association network that simultaneously describes multiple functional aspects of genes, proteins, complexes, metabolites, etc. With human, yeast and mouse complex functional interactions, it currently constitutes the most comprehensive publicly available interaction repository for these species. Different ways of utilizing these integrated interaction data, in particular with tools for visualization, analysis and interpretation of high-throughput expression data in the light of functional interactions and biological pathways is offered.

**Abbreviations:** CPDB

**Synonyms:** ConsensusPathDB, ConsensusPathDB-human

**Resource Type:** data or information resource, database

**Defining Citation:** PMID:23143270, PMID:21071422, PMID:20847220, PMID:18940869

**Keywords:** gene regulatory network, pathway, gene regulatory network, molecular interaction, interaction, gene regulation, protein interaction, genetic interaction, biochemical reaction, drug-target interaction, molecule, visualization, gene, protein, complex, metabolite, FASEB list

**Funding:** European Union HEALTH-F4-2007-200767

**Availability:** Free, Freely available

**Resource Name:** ConsensusPathDB

**Resource ID:** SCR_002231

**Alternate IDs:** nif-0000-02684, OMICS_01903, r3d100012822

**Alternate URLs:** https://doi.org/10.17616/R3HF8Z

**Record Creation Time:** 20220129T080212+0000

**Record Last Update:** 20260729T044022+0000

## Ratings and Alerts

No rating or validation information has been found for ConsensusPathDB.

No alerts have been found for ConsensusPathDB.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 667 mentions in open access literature.

**Listed below are recent publications.** The full list is available at kravitz2 .

Ye S, et al. (2025) ACOX2 destabilizes the MRE11-RAD50-NBS1 complex and boosts anticancer immunity via the cGAS-STING pathway in clear cell renal cell carcinoma. Molecular cancer, 24(1), 263.

Gupta D, et al. (2025) A LisH-domain protein interaction map reveals a Lis1-ARIH2-dynein regulatory axis. iScience, 28(11), 113912.

Paul?? S, et al. (2025) Cellular composition and transcriptomics of subcutaneous adipose tissue linked to blood glycated haemoglobin. European journal of clinical investigation, 55(8), e70033.

Gatenby RA, et al. (2025) Parallel and convergent dynamics in the evolution of primary breast and lung adenocarcinomas. Communications biology, 8(1), 775.

Jia Z, et al. (2025) Integrative proteomic analysis reveals the potential diagnostic marker and drug target for the Type-2 diabetes mellitus. Journal of diabetes and metabolic disorders, 24(1), 55.

Temiz K, et al. (2025) 5-Repurposed Drug Candidates Identified in Motor Neurons and Muscle Tissues with Amyotrophic Lateral Sclerosis by Network Biology and Machine Learning Based on Gene Expression. Neuromolecular medicine, 27(1), 24.

Fern??ndez OL, et al. (2025) Interplay of human macrophage response and natural resistance of infection by L. (V.) panamensis to pentavalent antimony. PLoS neglected

tropical diseases, 19(10), e0013600.

Jung H, et al. (2025) Transcriptional responses of mouse proximal colon and colonoids during early whipworm infection. mBio, 16(10), e0217625.

Hyeon DY, et al. (2025) Proteogenomic characterization of molecular and cellular targets for treatment-resistant subtypes in locally advanced cervical cancers. Molecular cancer, 24(1), 77.

Chen J, et al. (2025) Identification of CSPG4 as a Biomarker and Therapeutic Target for Infantile Post-Hemorrhagic Hydrocephalus via Multi-Omics Analysis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(6), e2410056.

Lee JW, et al. (2025) BRCAGenie: A machine learning-driven 43-gene polygenic risk score model for precision prediction of breast cancer survival. Journal of translational medicine, 23(1), 1191.

Loh JY, et al. (2025) Multi-omics reveals FAT10 as an immunometabolic survival factor rewiring global metabolism in cancer. Cell communication and signaling : CCS, 23(1), 532.

Qi C, et al. (2025) Long-term DNA methylation changes mediate heterologous cytokine responses after BCG vaccination. Genome biology, 26(1), 180.

Zhang Y, et al. (2025) Jet lag-induced circadian disruption elevates glioma risk by altering molecular profiles in distinct brain regions. Discover oncology, 16(1), 1410.

Qian F, et al. (2025) Network analysis of master regulators associated with invasive phenotypes in multiple myeloma. Frontiers in cell and developmental biology, 13, 1586870.

Chen L, et al. (2025) Inflammation-induced loss of CFTR-expressing airway ionocytes in non-eosinophilic asthma. Respirology (Carlton, Vic.), 30(1), 25.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Albrecht E, et al. (2025) DIGGER 2.0: digging into the functional impact of differential splicing on human and mouse disorders. Nucleic acids research, 53(W1), W245.

He S, et al. (2025) Integrated plasma and vegetation proteomic characterization of infective endocarditis for early diagnosis and treatment. Nature communications, 16(1), 5052.

Dewangan B, et al. (2025) Target and biomarker exploration portal for drug discovery. Bioinformatics (Oxford, England), 41(12).