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: database, data or information resource

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 for academic use, And under the license terms of each of the contributing databases

Resource Name: ConsensusPathDB

Resource ID: SCR_002231

Alternate IDs: nif-0000-02684, OMICS_01903

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250412T054657+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 621 mentions in open access literature.

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

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.

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.

Melero I, et al. (2025) Neutralizing GDF-15 can overcome anti-PD-1 and anti-PD-L1 resistance in solid tumours. Nature, 637(8048), 1218.

Ding Y, et al. (2025) The expression landscape and clinical significance of methyltransferase-like 17 in human cancer and hepatocellular carcinoma: a pan-cancer analysis using multiple databases. Cancer cell international, 25(1), 15.

Li L, et al. (2024) Comprehensive Proteogenomic Profiling Reveals the Molecular Characteristics of Colorectal Cancer at Distinct Stages of Progression. Cancer research, 84(17), 2888.

Perampalam P, et al. (2024) Netrin signaling mediates survival of dormant epithelial ovarian cancer cells. eLife, 12.

Li Z, et al. (2024) An atlas of cell-type-specific interactome networks across 44 human tumor types. Genome medicine, 16(1), 30.

Noriega Landa E, et al. (2024) Urinary fatty acid biomarkers for prostate cancer detection. PloS one, 19(2), e0297615.

Jiang Y, et al. (2024) Central regulation of feeding and body weight by ciliary GPR75. The Journal of clinical investigation, 134(19).

Liu Z, et al. (2024) Sex-specific epigenetic signatures of circulating urate and its increase after BCG vaccination. Research square.

Kim H, et al. (2024) Development of a Fit-For-Purpose Multi-Marker Panel for Early Diagnosis of Pancreatic Ductal Adenocarcinoma. Molecular & cellular proteomics : MCP, 23(9), 100824.

Kwon HJ, et al. (2024) Genomic Landscape of Pulmonary Sarcomatoid Carcinoma. Cancer research and treatment, 56(2), 442.

Holbrook KL, et al. (2024) Detection and Validation of Organic Metabolites in Urine for Clear Cell Renal Cell Carcinoma Diagnosis. Metabolites, 14(10).

Akawi N, et al. (2024) Profiling genetic variants in cardiovascular disease genes among a Heterogeneous cohort of Mendelian conditions patients and electronic health records. Frontiers in molecular biosciences, 11, 1451457.

Lin M, et al. (2024) Atherosclerosis-related biomarker PABPC1 predicts pan-cancer events. Stroke and vascular neurology, 9(2), 108.

Marchi G, et al. (2024) Extensive mutational ctDNA profiles reflect High-grade serous cancer tumors and reveal emerging mutations at recurrence. Translational oncology, 39, 101814.

Lee S, et al. (2024) Angiogenesis-on-a-chip coupled with single-cell RNA sequencing reveals spatially differential activations of autophagy along angiogenic sprouts. Nature communications, 15(1), 230.

Moutin EB, et al. (2024) Extracellular Matrix Orchestration of Tissue Remodeling in the Chronically Inflamed Mouse Colon. Cellular and molecular gastroenterology and hepatology, 17(4), 639.

Lentilhas-Graça J, et al. (2024) The secretome of macrophages has a differential impact on spinal cord injury recovery according to the polarization protocol. Frontiers in immunology, 15, 1354479.