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: 20260904T000122+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 722 mentions in open access literature.

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

Sakrepatna Nagaraj A, et al. (2026) Ex Vivo Immuno-Oncology Platform Reveals Spatial T-cell Infiltration Patterns Linked to ATR Inhibition Responses in High-Grade Serous Ovarian Cancer. Cancer immunology research, 14(4), 625.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. Cancer discovery, 16(4), 800.

Xu S, et al. (2026) Proteogenomic Characterization Reveals Subtype-Specific Therapeutic Potential for HER2-Low Breast Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(12), e13086.

Zhan Q, et al. (2026) Multi-Omics Analysis Reveals Sex-Specific Signatures for BCG Vaccine Efficacy. European journal of immunology, 56(2), e70144.

Khanum A, et al. (2026) Computational Phosphosite-Specific Network Analysis of YES1 Y426 Reveals Cancer-Associated Phosphorylation Patterns. Proteomes, 14(2).

Onat OE, et al. (2026) A homozygous missense variant, p.Ser166Leu in the PRPF40B gene, in a 7.7?Mb region of homozygosity in a consanguineous Turkish family with essential tremor. Frontiers in neurology, 17, 1796664.

Wang Y, et al. (2026) ALDH2 inhibits FASN stabilization via the E3 ligase CBL to suppress lipid accumulation and liver cancer development. Biology direct, 21(1).

Vijayan J, et al. (2026) Co-Phosphoregulatory Network Underlying Functional Coherence of TLK1 and TLK2 Kinase Paralogs. International journal of molecular sciences, 27(12).

Do AN, et al. (2026) CSF proteomic profiling with amyloid and tau pathology identifies distinctive sex-specific alteration of multiple proteins involved in Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(1), e71063.

Cho SP, et al. (2026) GRAFT: a graph-aware fusion transformer for cancer driver gene prediction. Briefings in bioinformatics, 27(1).

Barreto AD, et al. (2026) Discovery of kidney disease targets using multimodal human podocyte injury models. Stem cell reports, 21(4), 102868.

Kumar APKA, et al. (2026) Phosphoproteome landscape of ARID1A and its implications in DNA damage response and breast cancer pathogenesis. Discover oncology, 17(1), 312.

Llauradó-Pont J, et al. (2026) Maternal Chrono-Nutrition and Placental DNA Methylation: The BiSC Study. Molecular nutrition & food research, 70(9), e70465.

Ma F, et al. (2026) Proteome profiles of esophageal squamous cell carcinoma tie mitochondrial complex I to immunotherapy. EMBO molecular medicine, 18(5), 1884.

Yeh YC, et al. (2026) Natural Product 4-Acetylantroquinonol B Enhances NK Cell-Mediated Immunity Against Glioblastoma. Cancer medicine, 15(4), e71832.

Poojari TR, et al. (2026) Meta-cancer phosphoproteomic analysis unveils association of Tau phosphosites with DNA damage response. Frontiers in systems biology, 6, 1819794.

Dutta A, et al. (2026) LAG-3+ Regulatory T Cells Suppress Effector Function of T Cells and Allow Their Proliferation Into Regulatory T Cells. Immunology, 177(2), 317.

Clark SL, et al. (2026) A large-scale DNA methylation study of alcohol use identified robust associations and cell-type specific insights. Molecular psychiatry, 31(6), 3506.

Duan J, et al. (2026) Discovering proteo-transcriptomic networks via biologically informed heterogeneous graph learning. Nucleic acids research, 54(8).

Skoczek D, et al. (2026) Integrated transcriptome and proteome analyses unveil cytoskeletal alterations in an endothelial model of monogenic diabetes. Genome medicine, 18(1).