

Resource Summary Report

Generated by [dkNET](#) on Sep 19, 2026

PathGuide: the pathway resource list

RRID:SCR_003248

Type: Tool

Proper Citation

PathGuide: the pathway resource list (RRID:SCR_003248)

Resource Information

URL: <http://www.pathguide.org/>

Proper Citation: PathGuide: the pathway resource list (RRID:SCR_003248)

Description: Catalog containing information about 547 biological pathway related resources and molecular interaction related resources. Databases that are free and those supporting BioPAX, CellML, PSI-MI or SBML standards are respectively indicated.

Abbreviations: Pathguide

Resource Type: catalog, data or information resource, database

Defining Citation: [PMID:16381921](#)

Keywords: gene interaction network, metabolic pathway, signaling pathway, pathway diagram, protein-compound interaction, protein-protein interaction, protein sequence focused, transcription factor, gene regulatory network, transcription factor target, genetic interaction, pathway, molecular interaction, FASEB list

Availability: Free, Freely available

Resource Name: PathGuide: the pathway resource list

Resource ID: SCR_003248

Alternate IDs: SciRes_000148, OMICS_01701, nif-0000-00640

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260912T195554+0000

Ratings and Alerts

No rating or validation information has been found for PathGuide: the pathway resource list.

No alerts have been found for PathGuide: the pathway resource list.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Friedrichs M, et al. (2023) A web-based platform for the annotation and analysis of NAR-published databases. PloS one, 18(10), e0293134.

Sadeghi M, et al. (2022) lncRNA-miRNA-mRNA ceRNA Network Involved in Sheep Prolificacy: An Integrated Approach. Genes, 13(8).

Doolan BJ, et al. (2022) A clinician's guide to omics resources in dermatology. Clinical and experimental dermatology, 47(5), 858.

Babur Ö, et al. (2021) Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. Patterns (New York, N.Y.), 2(6), 100257.

Westerlund AM, et al. (2021) Risk Prediction of Cardiovascular Events by Exploration of Molecular Data with Explainable Artificial Intelligence. International journal of molecular sciences, 22(19).

Guala D, et al. (2020) Genome-wide functional association networks: background, data & state-of-the-art resources. Briefings in bioinformatics, 21(4), 1224.

Rodchenkov I, et al. (2020) Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic acids research, 48(D1), D489.

Palombo V, et al. (2020) PANEV: an R package for a pathway-based network visualization. BMC bioinformatics, 21(1), 46.

Pawar G, et al. (2019) In Silico Toxicology Data Resources to Support Read-Across and (Q)SAR. Frontiers in pharmacology, 10, 561.

Jalili M, et al. (2018) Unveiling network-based functional features through integration of gene expression into protein networks. Biochimica et biophysica acta. Molecular basis of disease, 1864(6 Pt B), 2349.

Jeuken GS, et al. (2018) A simple null model for inferences from network enrichment analysis. PloS one, 13(11), e0206864.

Kramer F, et al. (2018) New perspectives: systems medicine in cardiovascular disease. BMC systems biology, 12(1), 57.

Crosara KTB, et al. (2018) Merging in-silico and in vitro salivary protein complex partners using the STRING database: A tutorial. Journal of proteomics, 171, 87.

Chen Z, et al. (2016) Urinary proteomics and metabolomics studies to monitor bladder health and urological diseases. BMC urology, 16, 11.

Haydarlou R, et al. (2016) BioASF: a framework for automatically generating executable pathway models specified in BioPAX. Bioinformatics (Oxford, England), 32(12), i60.

Ortea I, et al. (2016) Review on proteomics for food authentication. Journal of proteomics, 147, 212.

Alonso-López D, et al. (2016) APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. Nucleic acids research, 44(W1), W529.

Bhat A, et al. (2016) BcCluster: A Bladder Cancer Database at the Molecular Level. Bladder cancer (Amsterdam, Netherlands), 2(1), 65.

Ogilvie LA, et al. (2015) Predictive Modeling of Drug Treatment in the Area of Personalized Medicine. Cancer informatics, 14(Suppl 4), 95.

More T, et al. (2015) Metabolomics and its integration with systems biology: PSI 2014 conference panel discussion report. Journal of proteomics, 127(Pt A), 73.