

Resource Summary Report

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Biological Pathways Exchange

RRID:SCR_001681

Type: Tool

Proper Citation

Biological Pathways Exchange (RRID:SCR_001681)

Resource Information

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

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Description: Community standard for pathway data sharing. Standard language that aims to enable integration, exchange, visualization and analysis of biological pathway data. Supports data exchange between pathway data groups and thus reduces complexity of interchange between data formats by providing accepted standard format for pathway data. Open and collaborative effort by community of researchers, software developers, and institutions. BioPAX is defined in OWL DL and is represented in RDF/XML format. Uses W3C standard Web Ontology Language, OWL.

Synonyms: BioPAX, BioPAX: Biological Pathways Exchange

Resource Type: project portal, ontology, controlled vocabulary, portal, data or information resource

Defining Citation: [PMID:20829833](#)

Keywords: Standard language, community standard, pathway data sharing, biological pathway data, data exchange, W3C standard, Web Ontology Language, OWL,

Funding: U.S. Department of Energy Workshop ;
NHGRI P41HG004118

Availability: Free, Available for download, Freely available

Resource Name: Biological Pathways Exchange

Resource ID: SCR_001681

Alternate IDs: SCR_009881, nlx_157327, nif-0000-10171

Alternate URLs: <http://purl.bioontology.org/ontology/BP>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260731T042621+0000

Ratings and Alerts

No rating or validation information has been found for Biological Pathways Exchange.

No alerts have been found for Biological Pathways Exchange.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Kannan M, et al. (2025) Leveraging public AI tools to explore systems biology resources in mathematical modeling. NPJ systems biology and applications, 11(1), 15.

Wiedmer T, et al. (2025) Metabolic mapping of the human solute carrier superfamily. Molecular systems biology, 21(6), 560.

Mei H, et al. (2025) Network analysis of multivariate time series data in biological systems: methods and applications. Briefings in bioinformatics, 26(3).

Butt RN, et al. (2025) CanSeer: a translational methodology for developing personalized cancer models and therapeutics. Scientific reports, 15(1), 15080.

Wang Y, et al. (2025) Genome-wide terpene gene clusters analysis in Euphorbiaceae. Horticulture research, 12(7), uhaf097.

Stojanov R, et al. (2025) Applicability Assessment of Technologies for Predictive and Prescriptive Analytics of Nephrology Big Data. Proteomics, 25(11-12), e202400135.

Chang X, et al. (2024) GINv2.0: a comprehensive topological network integrating molecular interactions from multiple knowledge bases. NPJ systems biology and applications, 10(1), 4.

Yashar WM, et al. (2024) Predicting transcription factor activity using prior biological information. iScience, 27(3), 109124.

Beust C, et al. (2024) BioPAX in 2024: Where we are and where we are heading. Computational and structural biotechnology journal, 23, 3999.

Li F, et al. (2024) Identifying cell type-specific transcription factor-mediated activity immune modules reveal implications for immunotherapy and molecular classification of

pan-cancer. *Briefings in bioinformatics*, 25(5).

Bachman JA, et al. (2023) Automated assembly of molecular mechanisms at scale from text mining and curated databases. *Molecular systems biology*, 19(5), e11325.

Juign?? C, et al. (2023) Fixing molecular complexes in BioPAX standards to enrich interactions and detect redundancies using semantic web technologies. *Bioinformatics* (Oxford, England), 39(5).

Vignet P, et al. (2022) Discrete modeling for integration and analysis of large-scale signaling networks. *PLoS computational biology*, 18(6), e1010175.

Freeman TC, et al. (2022) Graphia: A platform for the graph-based visualisation and analysis of high dimensional data. *PLoS computational biology*, 18(7), e1010310.

Kolpakov F, et al. (2022) BioUML-towards a universal research platform. *Nucleic acids research*, 50(W1), W124.

Yan G, et al. (2022) BET inhibition induces vulnerability to MCL1 targeting through upregulation of fatty acid synthesis pathway in breast cancer. *Cell reports*, 40(11), 111304.

Kotlyar M, et al. (2022) IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. *Nucleic acids research*, 50(D1), D640.

Lee S, et al. (2021) RDFizing the biosynthetic pathway of E.coli O-antigen to enable semantic sharing of microbiology data. *BMC microbiology*, 21(1), 325.

Lefebvre M, et al. (2021) Large-scale regulatory and signaling network assembly through linked open data. *Database : the journal of biological databases and curation*, 2021.

Wong JV, et al. (2021) Author-sourced capture of pathway knowledge in computable form using Biofactoid. *eLife*, 10.