Resource Summary Report

Generated by RRID on Apr 19, 2025

Biological Pathways Exchange

RRID:SCR_001681
Type: Tool

Proper Citation

Biological Pathways Exchange (RRID:SCR_001681)

Resource Information

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

Proper Citation: Biological Pathways Exchange (RRID:SCR_001681)

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: portal, controlled vocabulary, project portal, ontology, 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

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: 20250419T054824+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 84 mentions in open access literature.

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

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.

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

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

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.

Juigné 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).

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.

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.

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.

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.

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.

Good BM, et al. (2021) Reactome and the Gene Ontology: digital convergence of data resources. Bioinformatics (Oxford, England), 37(19), 3343.

Joshi T, et al. (2021) Antimicrobial activity of methanolic extracts of Vernonia cinerea against Xanthomonas oryzae and identification of their compounds using in silico techniques. PloS one, 16(6), e0252759.

Agapito G, et al. (2021) Using BioPAX-Parser (BiP) to enrich lists of genes or proteins with pathway data. BMC bioinformatics, 22(Suppl 13), 376.

Rougny A, et al. (2021) A detailed map of coupled circadian clock and cell cycle with qualitative dynamics validation. BMC bioinformatics, 22(1), 240.

Wang J, et al. (2021) Dissecting immune cell stat regulation network reveals biomarkers to predict ICB therapy responders in melanoma. Journal of translational medicine, 19(1), 296.

Glavaški M, et al. (2021) Humans and machines in biomedical knowledge curation: hypertrophic cardiomyopathy molecular mechanisms' representation. BioData mining, 14(1), 45.