

Resource Summary Report

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BioPAX Ontology of Biological Pathways

RRID:SCR_009881

Type: Tool

Proper Citation

BioPAX Ontology of Biological Pathways (RRID:SCR_009881)

Resource Information

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

Proper Citation: BioPAX Ontology of Biological Pathways (RRID:SCR_009881)

Description: Ontology that is a standard language for formally representing biological pathways. BioPAX Level 3 supports the representation of metabolic pathways, signal transduction pathways, protein-protein interaction networks, gene regulatory networks and genetic interactions.

Abbreviations: BP

Synonyms: BioPAX, BioPAX: Biological Pathways Exchange

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

Keywords: owl

Resource Name: BioPAX Ontology of Biological Pathways

Resource ID: SCR_009881

Alternate IDs: nlx_157327

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

Record Creation Time: 20220129T080255+0000

Record Last Update: 20260903T235018+0000

Ratings and Alerts

No rating or validation information has been found for BioPAX Ontology of Biological Pathways.

No alerts have been found for BioPAX Ontology of Biological Pathways.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 64 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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).

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

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.

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.

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

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

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.

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

Munro LJ, et al. (2021) Intelligent host engineering for metabolic flux optimisation in biotechnology. The Biochemical journal, 478(20), 3685.

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

Li M, et al. (2021) The protein-protein interaction ontology: for better representing and capturing the biological context of protein interaction. BMC genomics, 22(Suppl 5), 544.

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

Hammoud Z, et al. (2020) Multipath: An R Package to Generate Integrated Reproducible Pathway Models. Biology, 9(12).

Psomopoulos FE, et al. (2020) Ancestral state reconstruction of metabolic pathways across pangenome ensembles. Microbial genomics, 6(11).