

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

UniPathway

RRID:SCR_010513

Type: Tool

Proper Citation

UniPathway (RRID:SCR_010513)

Resource Information

URL: <http://www.grenoble.prabi.fr/obiwarehouse/unipathway>

Proper Citation: UniPathway (RRID:SCR_010513)

Description: A manually curated database of enzyme-catalyzed and spontaneous chemical reactions. It provides a hierarchical representation of metabolic pathways and a controlled vocabulary for pathway annotation in UniProtKB. UniPathway data are cross-linked to existing metabolic resources such as ChEBI/Rhea, KEGG and MetaCyc. Users may do a quick search, browse pathway, browse compound, or browse organism.

Abbreviations: UniPathway

Synonyms: UniPathway: a metabolic door to UniProtKB/Swiss-Prot, UniPathway: a resource for the exploration of metabolic pathways

Resource Type: data or information resource, database

Defining Citation: [PMID:22102589](#)

Keywords: metabolic pathway, pathway annotation, pathway, annotation, chemical reaction, protein, compound

Funding: Swiss Federal Government ;
GIS-IBISA ;
European Union SISYPHE ;
European Union SLING 226073;
European Union Microme 222886-2;
French Government ANR MIRI BLAN08-1335497

Resource Name: UniPathway

Resource ID: SCR_010513

Alternate IDs: nlx_16723

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260905T133157+0000

Ratings and Alerts

No rating or validation information has been found for UniPathway.

No alerts have been found for UniPathway.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Versi A, et al. (2024) A severe asthma phenotype of excessive airway Haemophilus influenzae relative abundance associated with sputum neutrophilia. Clinical and translational medicine, 14(9), e70007.

Majzoub ME, et al. (2024) Refining microbial community metabolic models derived from metagenomics using reference-based taxonomic profiling. mSystems, 9(9), e0074624.

Wang Y, et al. (2023) Interaction between tissue-dwelling helminth and the gut microbiota drives mucosal immunoregulation. NPJ biofilms and microbiomes, 9(1), 43.

Goma-Tchimbakala EJCD, et al. (2023) Use of Shotgun Metagenomics to Assess the Microbial Diversity and Hydrocarbons Degrading Functions of Auto-Mechanic Workshops Soils Polluted with Gasoline and Diesel Fuel. Microorganisms, 11(3).

Kagaya Y, et al. (2022) ContactPFP: Protein function prediction using predicted contact information. Frontiers in bioinformatics, 2.

Wang S, et al. (2019) Diet-induced remission in chronic enteropathy is associated with altered microbial community structure and synthesis of secondary bile acids. Microbiome, 7(1), 126.

Mercier J, et al. (2018) GROOLS: reactive graph reasoning for genome annotation through biological processes. BMC bioinformatics, 19(1), 132.

Hicks AL, et al. (2018) Gut microbiomes of wild great apes fluctuate seasonally in response to diet. Nature communications, 9(1), 1786.

O'Hara NB, et al. (2017) Metagenomic characterization of ambulances across the USA. Microbiome, 5(1), 125.

Hsu T, et al. (2016) Urban Transit System Microbial Communities Differ by Surface Type and Interaction with Humans and the Environment. *mSystems*, 1(3).

Chen L, et al. (2016) iTRAQ-Based Quantitative Proteomics Analysis of Black Rice Grain Development Reveals Metabolic Pathways Associated with Anthocyanin Biosynthesis. *PloS one*, 11(7), e0159238.

Zou D, et al. (2015) Biological databases for human research. *Genomics, proteomics & bioinformatics*, 13(1), 55.

Saccenti E, et al. (2015) Assessing the Metabolic Diversity of *Streptococcus* from a Protein Domain Point of View. *PloS one*, 10(9), e0137908.

Petrella V, et al. (2015) De novo assembly and sex-specific transcriptome profiling in the sand fly *Phlebotomus perniciosus* (Diptera, Phlebotominae), a major Old World vector of *Leishmania infantum*. *BMC genomics*, 16, 847.

Wang S, et al. (2015) Differential Proteomic Analysis Using iTRAQ Reveals Alterations in Hull Development in Rice (*Oryza sativa* L.). *PloS one*, 10(7), e0133696.

Kang C, et al. (2013) Finding type 2 diabetes causal single nucleotide polymorphism combinations and functional modules from genome-wide association data. *BMC medical informatics and decision making*, 13 Suppl 1(Suppl 1), S3.

Durot M, et al. (2009) Genome-scale models of bacterial metabolism: reconstruction and applications. *FEMS microbiology reviews*, 33(1), 164.