Resource Summary Report

Generated by ASWG on Aug 3, 2026

BioCyc

RRID:SCR_002298
Type: Tool

Proper Citation

BioCyc (RRID:SCR_002298)

Resource Information

URL: http://biocyc.org/

Proper Citation: BioCyc (RRID:SCR_002298)

Description: A collection of Pathway/Genome Databases which describes the genome and metabolic pathways of a single organism. The BioCyc collection of Pathway/Genome Databases (PGDBs) provides an electronic reference source on the genomes and metabolic pathways of sequenced organisms. BioCyc PGDBs are generated by software that predicts the metabolic pathway complements of completely sequenced organisms from their genome sequences. They also include the results of a number of other computational inference procedures applied to these genomes, including predictions of which genes code for missing enzymes in metabolic pathways, and predicted operons. The BioCyc Web site provides a suite of software tools for database searching and visualization, for omics data analysis, and for comparative genomics and comparative pathway questions. The databases within the BioCyc collection are organized into tiers according to the amount of manual review and updating they have received. Tier 1 PGDBs have been created through intensive manual efforts, and receive continuous updating. Tier 2 PGDBs were computationally generated by the PathoLogic program, and have undergone moderate amounts of review and updating. Tier 3 PGDBs were computationally generated by the PathoLogic program, and have undergone no review and updating. There are 967 DBs in Tier 3. The downloadable version of BioCyc that includes the Pathway Tools software provides more speed and power than the BioCyc Web site.

Synonyms: BioCyc Database Collection

Resource Type: database, data or information resource

Defining Citation: PMID:16246909

Keywords: database, pathway/genome databases, PGDB, genome, metabolic pathway, microbiome, FASEB list

Funding: NIGMS GM080746

Availability: Restricted

Resource Name: BioCyc

Resource ID: SCR_002298

Alternate IDs: nif-0000-00369, r3d100011259

Alternate URLs: https://doi.org/10.17616/R36G8H

License URLs: http://www.sri.com/privacy

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260803T040317+0000

Ratings and Alerts

No rating or validation information has been found for BioCyc.

No alerts have been found for BioCyc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 970 mentions in open access literature.

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

Huang A, et al. (2026) Blood metabolites mediate causal inference studies on the effect of gut microbiota on the risk of vascular calcification. Journal of advanced research, 79, 619.

Sharma G, et al. (2025) IGF2BP3 redirects glycolytic flux to promote one-carbon metabolism and RNA methylation. Cell reports, 116330.

Naidoo TJ, et al. (2025) Mycobacterium tuberculosis curli pili (MTP) and heparin-binding hemagglutinin adhesin (HBHA) facilitate regulation of central carbon metabolism, enhancement of ATP synthesis and cell wall biosynthesis. Archives of microbiology, 207(7), 156.

Maluleke E, et al. (2025) Unravelling the transcriptomic dynamics of Hyphopichia pseudoburtonii in co-culture with Botrytis cinerea. PloS one, 20(1), e0316713.

Meyer AC, et al. (2025) Proteomic profiling of zinc homeostasis mechanisms in Pseudomonas aeruginosa through data-dependent and data-independent acquisition mass spectrometry. bioRxiv : the preprint server for biology.

Nocito MC, et al. (2025) A targetable antioxidant defense mechanism to EZH2 inhibitors enhances tumor cell vulnerability to ferroptosis. Cell death & disease, 16(1), 291.

Hernandez-Unzueta I, et al. (2025) Unravelling the antitumor mechanism of Ocoxin through cancer cell genomics. Frontiers in pharmacology, 16, 1540217.

Chen J, et al. (2025) Identification of CSPG4 as a Biomarker and Therapeutic Target for Infantile Post-Hemorrhagic Hydrocephalus via Multi-Omics Analysis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(6), e2410056.

Delgado-Nungaray JA, et al. (2025) Influence of Amino Acids on Quorum Sensing-Related Pathways in Pseudomonas aeruginosa PAO1: Insights from the GEM iJD1249. Metabolites, 15(4).

La Gioia D, et al. (2025) Leveraging the potential of 1.0-mm i.d. columns in UHPLC-HRMS-based untargeted metabolomics. Analytical and bioanalytical chemistry, 417(13), 2837.

Ismaeel A, et al. (2025) microRNA-1 regulates metabolic flexibility by programming adult skeletal muscle pyruvate metabolism. Molecular metabolism, 98, 102182.

Yang Q, et al. (2025) Programmable probiotic consortium employ an oleic acid-inducible system to sense and degrade cholesterol in high-fat diet mice. Gut microbes, 17(1), 2531198.

Bustad E, et al. (2025) Predicting fitness in Mycobacterium tuberculosis with transcriptional regulatory network-informed interpretable machine learning. Frontiers in tuberculosis, 3.

Morder KM, et al. (2025) Sucralose Consumption Ablates Cancer Immunotherapy Response through Microbiome Disruption. Cancer discovery, 15(11), 2278.

Xu Y, et al. (2025) Microbiota metabolite taurodeoxycholic acid maintains intestinal tissue residency of innate lymphoid cells via engagement with P2Y10 receptor. Science advances, 11(34), eadt9645.

Zhao X, et al. (2025) Integrated metabolomic and transcriptomic analysis highlight the flavonoid response to antioxidant activity and Aspergillus flavus resistance in peanut seed coats. BMC plant biology, 25(1), 1121.

Brenner LN, et al. (2025) Dysglycemia and the airway microbiome in cystic fibrosis. PloS one, 20(10), e0331847.

Zhu Q, et al. (2025) Proteomic screening of TMEM43 binding partners identifies VDAC leading to mitochondrial dysfunction. PloS one, 20(12), e0339129.

Braverman E, et al. (2025) AMPK agonism optimizes the in vivo activation and antileukemic efficacy of chimeric antigen receptor T cells. Journal for immunotherapy of cancer, 13(12).

Zhang J, et al. (2025) L-serine-O-sulfate alters cellular ultrastructure and mitigates the capacity of biofilm formation in Streptococcus mutans UA159 via interfering with glutamate racemase. Current research in microbial sciences, 9, 100427.