

Resource Summary Report

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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: data or information resource, database

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: 20260804T043151+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 [RRID](#).

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.

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-Wurtemberg, Germany), 12(6), e2410056.

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),

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*.

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

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

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).

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.

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.

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

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.

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.

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

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).

Keller MR, et al. (2025) Global response to antibiotic exposure uncovers a critical role for nucleotide metabolism in high-level β -lactam tolerance. *Research square*.