Resource Summary Report

Generated by dkNET on Apr 17, 2025

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: web service, data analysis service, data access protocol, database, data or information resource, analysis service resource, production service resource, software resource, service resource

Defining Citation: PMID:16246909

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

Funding: NIGMS GM080746

Availability: Free to the research and education community, Acknowledgement required

Resource Name: BioCyc

Resource ID: SCR_002298

Alternate IDs: nif-0000-00369

License: For academic and government users, complete licenses and data file licenses are available. A complete license includes access to software bundles and data files, is reviewed by SRI International, and is available for free. Data file licenses include access to data files, quick online licensing, and are free. For commercial users, the same benefits of each license type applies, with the exception that a fee is applied to the complete license.

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Record Last Update: 20250417T065108+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 896 mentions in open access literature.

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

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.

Zhang X, et al. (2025) Intestinal TM6SF2 protects against metabolic dysfunction-associated steatohepatitis through the gut-liver axis. Nature metabolism, 7(1), 102.

Pouyiourou I, et al. (2025) Ion permeability profiles of renal paracellular channel-forming claudins. Acta physiologica (Oxford, England), 241(2), e14264.

Qian Y, et al. (2025) A data-driven modeling framework for mapping genotypes to synthetic microbial community functions. bioRxiv : the preprint server for biology.

Baltsavia I, et al. (2025) MjCyc: Rediscovering the pathway-genome landscape of the first sequenced archaeon, Methanocaldococcus (Methanococcus) jannaschii. iScience, 28(1), 111546.

Alejo-Jacuinde G, et al. (2025) Gene family rearrangements and transcriptional priming drive the evolution of vegetative desiccation tolerance in Selaginella. The Plant journal : for cell and molecular biology, 121(1), e17169.

Tec-Campos D, et al. (2025) A genome-scale metabolic model for the denitrifying bacterium Thauera sp. MZ1T accurately predicts degradation of pollutants and production of polymers. PLoS computational biology, 21(1), e1012736.

Ramundi V, et al. (2025) Non-targeted metabolomics-based molecular networking enables the chemical characterization of Rumex sanguineus, a wild edible plant. Metabolomics : Official journal of the Metabolomic Society, 21(1), 19.

Onji M, et al. (2025) RANK drives structured intestinal epithelial expansion during pregnancy. Nature, 637(8044), 156.

Gupta SK, et al. (2025) Dietary Chia (Salvia hispanica L.) seeds oil supplementation augments growth performance and gut microbial composition in Labeo rohita fingerlings. Scientific reports, 15(1), 1866.

Guedes J, et al. (2025) Short-term effects of follicle-stimulating hormone on immune function, lipid, and vitamin metabolism in transiently castrated men. Endocrine connections, 14(2).

Castelli M, et al. (2025) Hepatincolaceae (Alphaproteobacteria) are Distinct From Holosporales and Independently Evolved to Associate With Ecdysozoa. Environmental microbiology, 27(1), e70028.

Ma Y, et al. (2025) Systematic dissection of pleiotropic loci and critical regulons in excitatory neurons and microglia relevant to neuropsychiatric and ocular diseases. Translational psychiatry, 15(1), 24.

Reynolds SR, et al. (2024) Tumor microenvironment deconvolution identifies cell-type-independent aberrant DNA methylation and gene expression in prostate cancer. Clinical epigenetics, 16(1), 5.

Baker M, et al. (2024) Convergence of resistance and evolutionary responses in Escherichia coli and Salmonella enterica co-inhabiting chicken farms in China. Nature communications, 15(1), 206.

Chen Y-C, et al. (2024) Uncovering the roles of Mycobacterium tuberculosis melH in redox and bioenergetic homeostasis: implications for antitubercular therapy. mSphere, 9(4), e0006124.

Castelli M, et al. (2024) Host association and intracellularity evolved multiple times independently in the Rickettsiales. Nature communications, 15(1), 1093.

Rijal R, et al. (2024) Gallein and isoniazid act synergistically to attenuate Mycobacterium tuberculosis growth in human macrophages. bioRxiv : the preprint server for biology.

Jeppe K, et al. (2024) Accurate detection of acute sleep deprivation using a metabolomic biomarker-A machine learning approach. Science advances, 10(10), eadj6834.