

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

[MouseCyc](#)

RRID:SCR_001791

Type: Tool

Proper Citation

MouseCyc (RRID:SCR_001791)

Resource Information

URL: <http://mousecyc.jax.org/>

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Description: A manually curated database of both known and predicted metabolic pathways for the laboratory mouse. It has been integrated with genetic and genomic data for the laboratory mouse available from the Mouse Genome Informatics database and with pathway data from other organisms, including human. The database records for 1,060 genes in Mouse Genome Informatics (MGI) are linked directly to 294 pathways with 1,790 compounds and 1,122 enzymatic reactions in MouseCyc. (Aug. 2013) BLAST and other tools are available. The initial focus for the development of MouseCyc is on metabolism and includes such cell level processes as biosynthesis, degradation, energy production, and detoxification. MouseCyc differs from existing pathway databases and software tools because of the extent to which the pathway information in MouseCyc is integrated with the wealth of biological knowledge for the laboratory mouse that is available from the Mouse Genome Informatics (MGI) database.

Abbreviations: MouseCyc

Synonyms: MouseCyc database, Mouse Genome Informatics: MouseCyc database

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:19682380](#)

Keywords: energy production, biosynthesis, cell, cellular, degradation, detoxification, metabolism, mouse, physiological, enzymatic reaction, gene, disease, genome, metabolic pathway, pathway, compound, enzymatic reaction, protein, rna, reaction, blast, human, mammal, genetic, genomic

Funding: NHGRI HG003622

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MouseCyc

Resource ID: SCR_001791

Alternate IDs: nif-0000-10303

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260905T132439+0000

Ratings and Alerts

No rating or validation information has been found for MouseCyc.

No alerts have been found for MouseCyc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Al-Azzam S, et al. (2026) Multi-omics profiling reveals microenvironmental remodeling as a key driver of house dust mite-induced lung cancer progression. *Neoplasia* (New York, N.Y.), 73, 101275.

Martín-Sánchez A, et al. (2021) Comorbidity between Alzheimer's disease and major depression: a behavioural and transcriptomic characterization study in mice. *Alzheimer's research & therapy*, 13(1), 73.

Kripnerová M, et al. (2021) Complex Interplay of Genes Underlies Invasiveness in Fibrosarcoma Progression Model. *Journal of clinical medicine*, 10(11).

Schilf P, et al. (2021) A Mitochondrial Polymorphism Alters Immune Cell Metabolism and Protects Mice from Skin Inflammation. *International journal of molecular sciences*, 22(3).

Rahmati S, et al. (2020) pathDIP 4: an extended pathway annotations and enrichment analysis resource for human, model organisms and domesticated species. *Nucleic acids research*, 48(D1), D479.

Kim Y, et al. (2018) Comparative genomic evidence for the involvement of schizophrenia risk genes in antipsychotic effects. *Molecular psychiatry*, 23(3), 708.

Kelly SA, et al. (2017) Prevention of tumorigenesis in mice by exercise is dependent on strain background and timing relative to carcinogen exposure. *Scientific reports*, 7, 43086.

Bryant WA, et al. (2017) In Silico Analysis of the Small Molecule Content of Outer Membrane Vesicles Produced by *Bacteroides thetaiotaomicron* Indicates an Extensive Metabolic Link between Microbe and Host. *Frontiers in microbiology*, 8, 2440.

Palfi A, et al. (2016) microRNA regulatory circuits in a mouse model of inherited retinal degeneration. *Scientific reports*, 6, 31431.

Richardson JE, et al. (2015) Visual annotation display (VLAD): a tool for finding functional themes in lists of genes. *Mammalian genome : official journal of the International Mammalian Genome Society*, 26(9-10), 567.