Resource Summary Report

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Mouse Genome Informatics (MGI)

RRID:SCR_006460
Type: Tool

Proper Citation

Mouse Genome Informatics (MGI) (RRID:SCR_006460)

Resource Information

URL: http://www.informatics.jax.org

Proper Citation: Mouse Genome Informatics (MGI) (RRID:SCR_006460)

Description: International database for laboratory mouse. Data offered by The Jackson Laboratory includes information on integrated genetic, genomic, and biological data. MGI creates and maintains integrated representation of mouse genetic, genomic, expression, and phenotype data and develops reference data set and consensus data views, synthesizes comparative genomic data between mouse and other mammals, maintains set of links and collaborations with other bioinformatics resources, develops and supports analysis and data submission tools, and provides technical support for database users. Projects contributing to this resource are: Mouse Genome Database (MGD) Project, Gene Expression Database (GXD) Project, Mouse Tumor Biology (MTB) Database Project, Gene Ontology (GO) Project at MGI, and MouseCyc Project at MGI.

Abbreviations: MGI

Synonyms: , MGI, Mouse Genome Informatics

Resource Type: database, data or information resource

Defining Citation: PMID:19274630, PMID:18428715

Keywords: RIN, Resource Information Network, molecular neuroanatomy resource, human health, human disease, animal model, gene expression, phenotype, genotype, gene, pathway, orthology, tumor, strain, single nucleotide polymorphism, recombinase, function, blast, image, pathology, model, data analysis service, genome, genetics, gold standard

Funding: NHGRI HG000330;
NHGRI HG002273;

NICHD HD033745;
NCI CA089713

Availability: Free, Freely available

Resource Name: Mouse Genome Informatics (MGI)

Resource ID: SCR_006460

Alternate IDs: nif-0000-00096, OMICS_01656

Alternate URLs: http://www.informatics.jax.org/batch, http://www.informatics.jax.org/submit.shtml, http://www.informatics.jax.org/expression.shtml

License: CC BY 4.0

License URLs: https://www.informatics.jax.org/mgihome/other/copyright.shtml

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250412T055056+0000

Ratings and Alerts

No rating or validation information has been found for Mouse Genome Informatics (MGI).

No alerts have been found for Mouse Genome Informatics (MGI).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1079 mentions in open access literature.

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

Wang K, et al. (2025) Transcriptome analysis of muscle atrophy in Leizhou black goats: identification of key genes and insights into limb-girdle muscular dystrophy. BMC genomics, 26(1), 80.

Vo P, et al. (2025) Systematic ocular phenotyping of 8,707 knockout mouse lines identifies genes associated with abnormal corneal phenotypes. BMC genomics, 26(1), 48.

Lv J, et al. (2025) ASB1 engages with ELOB to facilitate SQOR ubiquitination and H2S homeostasis during spermiogenesis. Redox biology, 79, 103484.

Mitic N, et al. (2024) Dissecting the spatiotemporal diversity of adult neural stem cells. Molecular systems biology, 20(4), 321.

Funato N, et al. (2024) A regulatory variant impacting TBX1 expression contributes to basicranial morphology in Homo sapiens. American journal of human genetics, 111(5), 939.

Kannon T, et al. (2024) KANPHOS: Kinase-associated neural phospho-signaling database for data-driven research. Frontiers in molecular neuroscience, 17, 1379089.

Kim HJ, et al. (2024) Phosphorylated Tau in the Taste Buds of Alzheimer's Disease Mouse Models. Experimental neurobiology, 33(4), 202.

Arora UP, et al. (2024) Molecular evolution of the mammalian kinetochore complex. bioRxiv : the preprint server for biology.

Malekos E, et al. (2024) CRISPRware: an efficient method for contextual gRNA library design. bioRxiv : the preprint server for biology.

Besnard F, et al. (2024) Massive detection of cryptic recessive genetic defects in dairy cattle mining millions of life histories. Genome biology, 25(1), 248.

Song Y, et al. (2024) Single-Cell Transcriptome Analysis Reveals Development-Specific Networks at Distinct Synchronized Antral Follicle Sizes in Sheep Oocytes. International journal of molecular sciences, 25(2).

Qi L, et al. (2024) Transcriptome profile analysis in spinal cord injury rats with transplantation of menstrual blood-derived stem cells. Frontiers in molecular neuroscience, 17, 1335404.

Summers KM, et al. (2024) Genetic models of fibrillinopathies. Genetics, 226(1).

Nakagawa T, et al. (2024) The alteration of LBX1 expression is associated with changes in parameters related to energy metabolism in mice. PloS one, 19(8), e0308445.

Fisher SA, et al. (2024) The MexTAg collaborative cross: host genetics affects asbestos related disease latency, but has little influence once tumours develop. Frontiers in toxicology, 6, 1373003.

Van Sciver RE, et al. (2024) A prioritization tool for cilia-associated genes and their in vivo resources unveils new avenues for ciliopathy research. Disease models & mechanisms, 17(10).

Chen PB, et al. (2024) Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior. Cell genomics, 4(5), 100545.

Qiu C, et al. (2024) A single-cell time-lapse of mouse prenatal development from gastrula to birth. Nature, 626(8001), 1084.

Smith JJ, et al. (2024) A molecular atlas of adult C. elegans motor neurons reveals ancient diversity delineated by conserved transcription factor codes. Cell reports, 43(3), 113857.

Bouman BJ, et al. (2024) Single-cell time series analysis reveals the dynamics of HSPC response to inflammation. Life science alliance, 7(3).