

Resource Summary Report

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Mouse Genome Informatics: The Gene Ontology Project

RRID:SCR_006447

Type: Tool

Proper Citation

Mouse Genome Informatics: The Gene Ontology Project (RRID:SCR_006447)

Resource Information

URL: <http://www.informatics.jax.org/mgihome/GO/project.shtml>

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Description: This resource is part of the Gene Ontology Consortium which seeks to provide controlled vocabularies for the description of the molecular function, biological process, and cellular component of gene products. These terms are to be used as attributes of gene products by collaborating databases, facilitating uniform queries across them. GO team members at MGI participate in ontology development, outreach, and functional curation of mouse gene products. The GO vocabularies have a hierarchical structure that permits a range of detail from high-level, broadly descriptive terms to very low level, highly specific terms. This broad range is useful both in annotating genes and in searching for gene information using these terms as search criteria. GO terms are defined, allowing all databases to use the terms consistently and properly. GO annotations in the databases additionally include the publication reference which allowed the association to be made and an evidence statement citing how the association was determined.

Synonyms: Gene Ontology (GO) Project, MGI: GO Project, Gene Ontology Project

Resource Type: controlled vocabulary, data or information resource, database

Keywords: function, gene, biological, cellular, component, molecular, process, product

Funding: NHGRI HG002273

Availability: Available to the research community

Resource Name: Mouse Genome Informatics: The Gene Ontology Project

Resource ID: SCR_006447

Alternate IDs: nif-0000-10304

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260905T132553+0000

Ratings and Alerts

No rating or validation information has been found for Mouse Genome Informatics: The Gene Ontology Project.

No alerts have been found for Mouse Genome Informatics: The Gene Ontology Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Hashikawa K, et al. (2026) Esr1-dependent signaling and transcriptional maturation in the medial preoptic area of the hypothalamus shape the development of mating behavior during adolescence. eLife, 14.

Huber A, et al. (2026) Phenotypic profiling of neutrophils in acute Clostridioides difficile infection identifies a TNF-induced activation signature associated with epithelial damage. Gut microbes, 18(1), 2659430.

Roy TA, et al. (2024) Discovery and validation of genes driving drug-intake and related behavioral traits in mice. Genes, brain, and behavior, 23(1), e12875.

Mihori S, et al. (2024) Microbiome-derived bacterial lipids regulate gene expression of proinflammatory pathway inhibitors in systemic monocytes. Frontiers in immunology, 15, 1415565.

Roy TA, et al. (2023) DISCOVERY AND VALIDATION OF GENES DRIVING DRUG-INTAKE AND RELATED BEHAVIORAL TRAITS IN MICE. bioRxiv : the preprint server for biology.

Feng W, et al. (2022) Single-cell transcriptomic analysis identifies murine heart molecular features at embryonic and neonatal stages. Nature communications, 13(1), 7960.

Bubier JA, et al. (2020) Discovery of a Role for Rab3b in Habituation and Cocaine Induced Locomotor Activation in Mice Using Heterogeneous Functional Genomic Analysis. Frontiers in neuroscience, 14, 721.

Hashikawa Y, et al. (2020) Transcriptional and Spatial Resolution of Cell Types in the Mammalian Habenula. *Neuron*, 106(5), 743.

Miao ZF, et al. (2020) A Metformin-Responsive Metabolic Pathway Controls Distinct Steps in Gastric Progenitor Fate Decisions and Maturation. *Cell stem cell*, 26(6), 910.

Hu Z, et al. (2019) Bayesian Detection of Convergent Rate Changes of Conserved Noncoding Elements on Phylogenetic Trees. *Molecular biology and evolution*, 36(5), 1086.

Khetchoumian K, et al. (2019) Pituitary cell translation and secretory capacities are enhanced cell autonomously by the transcription factor Creb3l2. *Nature communications*, 10(1), 3960.

Peng J, et al. (2019) TS-GOEA: a web tool for tissue-specific gene set enrichment analysis based on gene ontology. *BMC bioinformatics*, 20(Suppl 18), 572.

Mager LF, et al. (2017) The ESRP1-GPR137 axis contributes to intestinal pathogenesis. *eLife*, 6.

Subramaniam S, et al. (2013) Transcriptional profiling of mEq-dependent genes in Marek's disease resistant and susceptible inbred chicken lines. *PloS one*, 8(10), e78171.