Resource Summary Report

Generated by dkNET on May 2, 2025

Phenotypes and Mutant Alleles

RRID:SCR_017523
Type: Tool

Proper Citation

Phenotypes and Mutant Alleles (RRID:SCR_017523)

Resource Information

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

Proper Citation: Phenotypes and Mutant Alleles (RRID:SCR_017523)

Description: Enables comparative phenotype analysis, searches for human disease models, and hypothesis generation by providing access to spontaneous, induced, and genetically engineered mutations and their strain-specific phenotypes.

Synonyms: Phenotypes, Alleles & Disease Models

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

Keywords: MGI, phenotype, human, disease, analysis, model, genetically, engineered, mutation, strain, specific, phenotype, data

Funding:

Availability: Free, Freely available

Resource Name: Phenotypes and Mutant Alleles

Resource ID: SCR_017523

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250502T060440+0000

Ratings and Alerts

No rating or validation information has been found for Phenotypes and Mutant Alleles.

No alerts have been found for Phenotypes and Mutant Alleles.

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 dkNET.

Jiang D, et al. (2024) Quantitative association between gene expression and blood cell production of individual hematopoietic stem cells in mice. Science advances, 10(4), eadk2132.

Hill DP, et al. (2023) Biochemical pathways represented by Gene Ontology-Causal Activity Models identify distinct phenotypes resulting from mutations in pathways. Genetics, 225(2).

Yang Q, et al. (2022) A proteomic atlas of ligand-receptor interactions at the ovine maternal-fetal interface reveals the role of histone lactylation in uterine remodeling. The Journal of biological chemistry, 298(1), 101456.

Wilhelmi I, et al. (2021) Enriched Alternative Splicing in Islets of Diabetes-Susceptible Mice. International journal of molecular sciences, 22(16).

Au KS, et al. (2021) Human myelomeningocele risk and ultra-rare deleterious variants in genes associated with cilium, WNT-signaling, ECM, cytoskeleton and cell migration. Scientific reports, 11(1), 3639.

Lee SH, et al. (2020) Bioinformatic analysis of membrane and associated proteins in murine cardiomyocytes and human myocardium. Scientific data, 7(1), 425.

Yang Q, et al. (2020) The proteome of IVF-induced aberrant embryo-maternal crosstalk by implantation stage in ewes. Journal of animal science and biotechnology, 11, 7.

Fu W, et al. (2020) Repression of FGF signaling is responsible for Dnmt3b inhibition and impaired de novo DNA methylation during early development of in vitro fertilized embryos. International journal of biological sciences, 16(15), 3085.

Laisk T, et al. (2020) The genetic architecture of sporadic and multiple consecutive miscarriage. Nature communications, 11(1), 5980.

Goding CR, et al. (2019) MITF-the first 25 years. Genes & development, 33(15-16), 983.