

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

Mouse Genome Informatics Transgenes

RRID:SCR_003468

Type: Tool

Proper Citation

Mouse Genome Informatics Transgenes (RRID:SCR_003468)

Resource Information

URL: http://ftp://ftp.informatics.jax.org/pub/reports/MGI_PhenotypicAllele.rpt

Proper Citation: Mouse Genome Informatics Transgenes (RRID:SCR_003468)

Description: Data set of collected and annotated expression and activity data for recombinase-containing transgenes and knock-in alleles. As the authoritative source of official names for mouse genes, alleles, and strains, MGI makes this list of transgenes available as a service and includes all known transgenes and synonyms. NIF provides a database interface so that researchers may have a better idea whether the transgene or transgenic animal that they are searching for is available. Nomenclature follows the rules and guidelines established by the International Committee on Standardized Genetic Nomenclature for Mice.

Abbreviations: MGI Transgene

Resource Type: data or information resource, data set

Keywords: transgene, allele, phenotype

Availability: Acknowledgement requested, Non-commercial, Commercial with permission, Copyrighted

Resource Name: Mouse Genome Informatics Transgenes

Resource ID: SCR_003468

Alternate IDs: nif-0000-34000

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260912T200313+0000

Ratings and Alerts

No rating or validation information has been found for Mouse Genome Informatics Transgenes.

No alerts have been found for Mouse Genome Informatics Transgenes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Dempsey KM, et al. (2014) Identifying aging-related genes in mouse hippocampus using gateway nodes. BMC systems biology, 8, 62.

White JK, et al. (2013) Genome-wide generation and systematic phenotyping of knockout mice reveals new roles for many genes. Cell, 154(2), 452.

Zhang Y, et al. (2010) Systematic analysis, comparison, and integration of disease based human genetic association data and mouse genetic phenotypic information. BMC medical genomics, 3, 1.