

Resource Summary Report

Generated by T1D on Sep 19, 2026

Impress

RRID:SCR_006160

Type: Tool

Proper Citation

Impress (RRID:SCR_006160)

Resource Information

URL: <http://www.mousephenotype.org/impress>

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Description: Contains standardized phenotyping protocols essential for the characterization of mouse phenotypes. IMPReSS holds definitions of the phenotyping Pipelines and mandatory and optional Procedures and Parameters carried out and data collected by international mouse clinics following the protocols defined. This allows data to be comparable and shareable and ontological annotations permit interspecies comparison which may help in the identification of phenotypic mouse-models of human diseases. The IMPC (International Mouse Phenotyping Consortium) core pipeline describes the phenotype pipeline that has been agreed by the research institutions. IMPReSS has a SOAP web service machine interface. The WSDL can be accessed here: <http://www.mousephenotype.org/impress/soap/server?wsdl>

Abbreviations: IMPReSS

Synonyms: International Mouse Phenotyping Resource of Standardised Screens, IMPReSS - International Mouse Phenotyping Resource of Standardised Screens

Resource Type: data access protocol, data or information resource, experimental protocol, international standard specification, narrative resource, software resource, standard specification, web service

Keywords: phenotype, phenotyping, adult, embryonic, ontology, enu-induced gene knockout, gene, knockout mouse, ethylnitrosourea

Resource Name: Impress

Resource ID: SCR_006160

Alternate IDs: nlx_151661

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260919T195105+0000

Ratings and Alerts

No rating or validation information has been found for Impress.

No alerts have been found for Impress.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Oestereicher MA, et al. (2026) Rethinking ratio-based normalization towards model-based approaches in heart weight analysis. Scientific reports, 16(1).

Cox RM, et al. (2026) A protein interactome for the last eukaryotic common ancestor illuminates the biochemical basis of modern genetic diseases. Cell genomics, 6(6), 101254.

Bardet PMR, et al. (2026) Multiomics immune profiling of a patient-relevant orthotopic lung cancer model using SEPARATE-Seq. Nature communications, 17(1).

Chai RC, et al. (2026) Multiscale analysis and functional validation of the cellular and genetic determinants of skeletal disease. bioRxiv : the preprint server for biology.

Lindell E, et al. (2025) Identification of a small molecule targeting EPLIN as a novel strategy for the treatment of pediatric neuroblastoma and medulloblastoma. Cell death & disease, 16(1), 554.

Aigner B, et al. (2025) Variability of test parameters from mice of different age groups in published data sets. PloS one, 20(8), e0329357.

Corrà S, et al. (2025) Modelling POLG mutations in mice unravels a critical role of POL?? in regulating phenotypic severity. Nature communications, 16(1), 4782.

Adams DJ, et al. (2024) Genetic determinants of micronucleus formation in vivo. Nature, 627(8002), 130.

Garrett L, et al. (2024) Co-expression of prepulse inhibition and Schizophrenia genes in the mouse and human brain. Neuroscience applied, 3, 104075.

Prieto-Vila M, et al. (2024) Adult cardiomyocytes-derived EVs for the treatment of cardiac fibrosis. *Journal of extracellular vesicles*, 13(7), e12461.

Fang TZ, et al. (2023) Knockout or inhibition of USP30 protects dopaminergic neurons in a Parkinson's disease mouse model. *Nature communications*, 14(1), 7295.

Huang Z, et al. (2023) Artificial intelligence reveals features associated with breast cancer neoadjuvant chemotherapy responses from multi-stain histopathologic images. *NPJ precision oncology*, 7(1), 14.

Oestereich MA, et al. (2023) Comprehensive ECG reference intervals in C57BL/6N substrains provide a generalizable guide for cardiac electrophysiology studies in mice. *Mammalian genome : official journal of the International Mammalian Genome Society*, 34(2), 180.

Zhang Y, et al. (2023) Sexual Dimorphism of the Mouse Plasma Metabolome Is Associated with Phenotypes of 30 Gene Knockout Lines. *Metabolites*, 13(8).

Wilson LAB, et al. (2022) Sex differences in allometry for phenotypic traits in mice indicate that females are not scaled males. *Nature communications*, 13(1), 7502.

Guenin MJ, et al. (2022) A participatory approach for building ex ante impact pathways towards a prudent use of antimicrobials in pig and poultry sectors in France. *PloS one*, 17(11), e0277487.

Xie K, et al. (2022) Deep phenotyping and lifetime trajectories reveal limited effects of longevity regulators on the aging process in C57BL/6J mice. *Nature communications*, 13(1), 6830.

Wotton JM, et al. (2022) Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. *Pain*, 163(6), 1139.

Spielmann N, et al. (2022) Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. *Nature cardiovascular research*, 1(2), 157.

Prieto-Vila M, et al. (2022) High-grade bladder cancer cells secrete extracellular vesicles containing miRNA-146a-5p and promotes angiogenesis. *Journal of extracellular biology*, 1(8), e47.