

Resource Summary Report

Generated by [RRID](#) on Jul 29, 2026

[NZO/HILtJ](#)

RRID:IMSR_JAX:002105

Type: Organism

Proper Citation

RRID:IMSR_JAX:002105

Organism Information

URL: <https://www.jax.org/strain/002105>

Proper Citation: RRID:IMSR_JAX:002105

Description: Mus musculus with name NZO/HILtJ from IMSR.

Species: Mus musculus

Synonyms: NZO/HIJ. New Zealand Obese. NZO/HILtJ

Notes: gene symbol note: phosphatidylcholine transfer protein|latent transforming growth factor beta binding protein 4|cytochrome c oxidase subunit 7A2 like; inbred strain: Pctp|Ltbp4|Cox7a2l

Affected Gene: phosphatidylcholine transfer protein|latent transforming growth factor beta binding protein 4|cytochrome c oxidase subunit 7A2 like

Genomic Alteration: R120H|Duchenne modifier 1 resistant|long

Catalog Number: JAX:002105

Database: JAX Mice and Services

Database Abbreviation: JAX

Availability: live

Organism Name: NZO/HILtJ

Record Creation Time: 20250513T053629+0000

Record Last Update: 20260725T044337+0000

Ratings and Alerts

No rating or validation information has been found for NZO/HILtJ.

No alerts have been found for NZO/HILtJ.

Data and Source Information

Source: [Integrated Animals](#)

Source Database: JAX Mice and Services

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Ren W, et al. (2025) A tandem repeat atlas for the genome of inbred mouse strains: A genetic variation resource. *iScience*, 28(11), 113703.

Murray KE, et al. (2025) Sex and Genotype Affect Mouse Hippocampal Gene Expression in Response to Blast-Induced Traumatic Brain Injury. *Molecular neurobiology*, 62(8), 9980.

Zhao Y, et al. (2024) Causal network perturbation analysis identifies known and novel type-2 diabetes driver genes. *bioRxiv : the preprint server for biology*.

Oliveira TY, et al. (2024) Quantitative trait loci mapping provides insights into the genetic regulation of dendritic cell numbers in mouse tissues. *Cell reports*, 43(6), 114296.

Zeineddine Y, et al. (2023) Genetic diversity modulates the physical and transcriptomic response of skeletal muscle to simulated microgravity in male mice. *NPJ microgravity*, 9(1), 86.

Emfinger CH, et al. (2023) Novel regulators of islet function identified from genetic variation in mouse islet Ca²⁺ oscillations. *eLife*, 12.

Sheppard K, et al. (2022) Stride-level analysis of mouse open field behavior using deep-learning-based pose estimation. *Cell reports*, 38(2), 110231.

Bachmann AM, et al. (2022) Genetic background and sex control the outcome of high-fat diet feeding in mice. *iScience*, 25(6), 104468.

Fonseca AH, et al. (2021) Analysis of ultrasonic vocalizations from mice using computer vision and machine learning. *eLife*, 10.

Keele GR, et al. (2021) Regulation of protein abundance in genetically diverse mouse populations. *Cell genomics*, 1(1).

Shi W, et al. (2021) Cardiac proteomics reveals sex chromosome-dependent differences between males and females that arise prior to gonad formation. *Developmental cell*, 56(21), 3019.

Forte E, et al. (2020) Dynamic Interstitial Cell Response during Myocardial Infarction Predicts Resilience to Rupture in Genetically Diverse Mice. *Cell reports*, 30(9), 3149.

Doolittle ML, et al. (2020) Genetic analysis of osteoblast activity identifies Zbtb40 as a regulator of osteoblast activity and bone mass. *PLoS genetics*, 16(6), e1008805.

Skelly DA, et al. (2020) Mapping the Effects of Genetic Variation on Chromatin State and Gene Expression Reveals Loci That Control Ground State Pluripotency. *Cell stem cell*, 27(3), 459.

Skorski M, et al. (2019) Distribution of endogenous gammaretroviruses and variants of the Fv1 restriction gene in individual mouse strains and strain subgroups. *PloS one*, 14(7), e0219576.

Maida A, et al. (2017) Repletion of branched chain amino acids reverses mTORC1 signaling but not improved metabolism during dietary protein dilution. *Molecular metabolism*, 6(8), 873.