

Resource Summary Report

Generated by [NIF](#) on Aug 2, 2026

SPRET/EiJ

RRID:IMSR_JAX:001146

Type: Organism

Proper Citation

RRID:IMSR_JAX:001146

Organism Information

URL: <https://www.jax.org/strain/001146>

Proper Citation: RRID:IMSR_JAX:001146

Description: Mus musculus with name SPRET/EiJ from IMSR.

Species: Mus musculus

Notes: gene symbol note: cytochrome c oxidase subunit 7A2 like|aryl-hydrocarbon receptor; wild-derived inbred strain|inbred strain: Cox7a2l|Ahr

Affected Gene: cytochrome c oxidase subunit 7A2 like|aryl-hydrocarbon receptor

Genomic Alteration: long|b-3 variant

Catalog Number: JAX:001146

Database: JAX Mice and Services

Database Abbreviation: JAX

Availability: live

Organism Name: SPRET/EiJ

Record Creation Time: 20250513T053624+0000

Record Last Update: 20260801T050329+0000

Ratings and Alerts

No rating or validation information has been found for SPRET/EiJ.

No alerts have been found for SPRET/EiJ.

Data and Source Information

Source: [Integrated Animals](#)

Source Database: JAX Mice and Services

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

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

Halow JM, et al. (2021) Tissue context determines the penetrance of regulatory DNA variation. *Nature communications*, 12(1), 2850.

Li Y, et al. (2020) Pan-tissue analysis of allelic alternative polyadenylation suggests widespread functional regulation. *Molecular systems biology*, 16(4), e9367.

Liu J, et al. (2020) Robust inference of positive selection on regulatory sequences in the human brain. *Science advances*, 6(48).

Moeller AH, et al. (2019) Experimental Evidence for Adaptation to Species-Specific Gut Microbiota in House Mice. *mSphere*, 4(4).

Xia Z, et al. (2019) DeeReCT-PolyA: a robust and generic deep learning method for PAS identification. *Bioinformatics (Oxford, England)*, 35(14), 2371.

Yang C, et al. (2019) Genome-wide association study using diversity outcross mice identified candidate genes of pancreatic cancer. *Genomics*, 111(6), 1882.

Zhou Y, et al. (2019) Integrative system genetic analysis reveals mRNA-lncRNA network associated with mouse spontaneous lung cancer susceptibility. *Oncotarget*, 10(3), 339.

Link VM, et al. (2018) MMARGE: Motif Mutation Analysis for Regulatory Genomic Elements. *Nucleic acids research*, 46(14), 7006.

Filipescu D, et al. (2017) Essential role for centromeric factors following p53 loss and oncogenic transformation. *Genes & development*, 31(5), 463.

Canela A, et al. (2017) Genome Organization Drives Chromosome Fragility. *Cell*, 170(3), 507.

Xiao MS, et al. (2016) Global analysis of regulatory divergence in the evolution of mouse alternative polyadenylation. *Molecular systems biology*, 12(12), 890.

Gao Q, et al. (2015) Predominant contribution of cis-regulatory divergence in the evolution of mouse alternative splicing. *Molecular systems biology*, 11(7), 816.

Tang J, et al. (2015) Genetic Background Modulates lncRNA-Coordinated Tissue Response to Low Dose Ionizing Radiation. *International journal of genomics*, 2015, 461038.

Hou J, et al. (2015) Extensive allele-specific translational regulation in hybrid mice. *Molecular systems biology*, 11(8), 825.

Didion JP, et al. (2015) A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse chromosome 2. *PLoS genetics*, 11(2), e1004850.

Zhang P, et al. (2015) Identification of genetic loci that control mammary tumor susceptibility through the host microenvironment. *Scientific reports*, 5, 8919.

Lilue J, et al. (2013) Reciprocal virulence and resistance polymorphism in the relationship between *Toxoplasma gondii* and the house mouse. *eLife*, 2, e01298.

Takada T, et al. (2013) The ancestor of extant Japanese fancy mice contributed to the mosaic genomes of classical inbred strains. *Genome research*, 23(8), 1329.

Sastalla I, et al. (2013) Transcriptional analysis of the three Nlrp1 paralogs in mice. *BMC genomics*, 14, 188.