

Resource Summary Report

Generated by SPARC SAWG on Sep 15, 2026

QTL Archive

RRID:SCR_006213

Type: Tool

Proper Citation

QTL Archive (RRID:SCR_006213)

Resource Information

URL: <https://phenome.jax.org/centers/QLTA>

Proper Citation: QTL Archive (RRID:SCR_006213)

Description: Raw data from various QTL (quantitative trait loci) studies using rodent inbred line crosses. Data are available in the .csv format used by R/qtl and pseudomarker programs. In some cases analysis scripts and/or results are posted to accompany the data. These data are provided as a courtesy to the genetic mapping community and may be used for purposes of developing or testing new analysis methods or software and for meta-analysis of quantitative traits. The authors of the datasets retain individual ownership of the data. As a courtesy to the authors, please alert them in advance of any publications that result from reanalysis of these data or obtain permission prior to redistribution of data or results. In all data sets and files, the marker locations have been translated to Cox build 37 coordinates unless otherwise stated. Please consider contributing your data to the QTL Archive.

Abbreviations: QTL Archive

Synonyms: Quantitative Trait Loci (QTL) Archive, Quantitative Trait Loci Archive

Resource Type: data or information resource, data repository, data set, service resource, storage service resource

Keywords: quantitative trait locus, inbred rat strain, phenotype, cross, genetics, inbreeding, genetic marker, quantitative genetics

Funding: NIGMS R01 GM070683

Availability: The community can contribute to this resource

Resource Name: QTL Archive

Resource ID: SCR_006213

Alternate IDs: r3d100010571, nlx_151757

Alternate URLs: <https://doi.org/10.17616/R3C02Z>

Old URLs: <http://qtlarchive.org/>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260912T195636+0000

Ratings and Alerts

No rating or validation information has been found for QTL Archive.

No alerts have been found for QTL Archive.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Arjas A, et al. (2020) Estimation of dynamic SNP-heritability with Bayesian Gaussian process models. *Bioinformatics* (Oxford, England), 36(12), 3795.

Bubier JA, et al. (2020) A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. *Genetics*, 214(3), 719.

Mader KS, et al. (2015) High-throughput phenotyping and genetic linkage of cortical bone microstructure in the mouse. *BMC genomics*, 16(1), 493.

Recla JM, et al. (2014) Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals Hydin as a novel pain gene. *Mammalian genome : official journal of the International Mammalian Genome Society*, 25(5-6), 211.

Grubb SC, et al. (2014) Mouse phenome database. *Nucleic acids research*, 42(Database issue), D825.

Broman KW, et al. (2012) Mapping quantitative trait loci onto a phylogenetic tree. *Genetics*, 192(1), 267.