

Resource Summary Report

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R/qlt2

RRID:SCR_018181

Type: Tool

Proper Citation

R/qlt2 (RRID:SCR_018181)

Resource Information

URL: <https://www.rdocumentation.org/packages/qlt2/versions/0.24>

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Description: Software R package for mapping quantitative trait loci with high dimensional data and multiparent populations. Used for analysis of high dimensional data and complex crosses. Interactive software environment for mapping quantitative trait loci in experimental populations. R/qlt2 software expands scope of R/qlt software package to include multiparent populations derived from more than two founder strains, such as Collaborative Cross and Diversity Outbred mice, heterogeneous stocks, and MAGIC plant populations.

Synonyms: QTL, R/quantitative trait loci, QTL2, Quantitative Trait Locus 2, quantitative trait loci 2, R/qlt, qlt2

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:30591514](#)

Keywords: High density genotyping data, molecular phenotype, gene expression, proteomics, mapping trait loci, diversity outbred mice, bio.tools

Funding: NIGMS R01 GM070683;
NIGMS R01 GM074244;
NIGMS R01 GM123489

Availability: Free, Available for download, Freely available

Resource Name: R/qlt2

Resource ID: SCR_018181

Alternate IDs: biotools:R_qlt2, SCR_020965

Alternate URLs: https://bio.tools/R_qtl2, <https://kbroman.org/qtl2>,
<https://github.com/rqtl/qtl2>

License: GNU GPLv3

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260821T194142+0000

Ratings and Alerts

No rating or validation information has been found for R/qtl2.

No alerts have been found for R/qtl2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Atkins K, et al. (2025) Unlocking the power of AI for phenotyping fruit morphology in Arabidopsis. GigaScience, 14.

Keele GR, et al. (2025) Genetic architecture of the murine red blood cell proteome reveals central role of hemoglobin beta cysteine 93 in maintaining redox balance. Cell genomics, 101069.

Skelly DA, et al. (2024) Mapping the genetic landscape establishing a tumor immune microenvironment favorable for anti-PD-1 response in mice and humans. bioRxiv : the preprint server for biology.

Glenn RA, et al. (2024) A PLURIPOTENT STEM CELL PLATFORM FOR IN VITRO SYSTEMS GENETICS STUDIES OF MOUSE DEVELOPMENT. bioRxiv : the preprint server for biology.

Philip VM, et al. (2023) Gene expression genetics of the striatum of Diversity Outbred mice. bioRxiv : the preprint server for biology.

Philip VM, et al. (2023) Gene expression genetics of the striatum of Diversity Outbred mice. Scientific data, 10(1), 522.

Ashbrook DG, et al. (2021) A platform for experimental precision medicine: The extended BXD mouse family. Cell systems, 12(3), 235.

Dadu RHR, et al. (2021) Lens orientalis Contributes Quantitative Trait Loci and Candidate Genes Associated With Ascochyta Blight Resistance in Lentil. *Frontiers in plant science*, 12, 703283.

Lovell JT, et al. (2021) Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. *Nature communications*, 12(1), 4125.

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

McClatchy S, et al. (2020) Nine quick tips for efficient bioinformatics curriculum development and training. *PLoS computational biology*, 16(7), e1008007.

Katz DC, et al. (2020) Facial shape and allometry quantitative trait locus intervals in the Diversity Outbred mouse are enriched for known skeletal and facial development genes. *PloS one*, 15(6), e0233377.

Bubier JA, et al. (2020) Genetic variation regulates opioid-induced respiratory depression in mice. *Scientific reports*, 10(1), 14970.