Resource Summary Report

Generated by NIF on Apr 21, 2025

R/QTL

RRID:SCR_009085
Type: Tool

Proper Citation

R/QTL (RRID:SCR_009085)

Resource Information

URL: http://www.rqtl.org

Proper Citation: R/QTL (RRID:SCR_009085)

Description: Software program for mapping quantitative trait loci in experimental crosses. (entry from Genetic Analysis Software)

Abbreviations: R/QTL

Resource Type: software resource, software application

Defining Citation: DOI:10.1093/bioinformatics/btg112

Keywords: gene, genetic, genomic, c and r, unix, ms-windows, macos

Funding:

Resource Name: R/QTL

Resource ID: SCR_009085

Alternate IDs: OMICS_07093, nlx_154097

Alternate URLs: https://sources.debian.org/src/r-cran-qtl/

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053715+0000

Ratings and Alerts

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

No alerts have been found for R/QTL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 953 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Amado D, et al. (2025) The genetic architecture of resistance to flubendiamide insecticide in Helicoverpa armigera (Hübner). PloS one, 20(1), e0318154.

Soler-Garzón A, et al. (2025) Mapping resistance to Sclerotinia white mold in two pinto bean recombinant inbred line populations. The plant genome, 18(1), e20538.

Goldberg LR, et al. (2025) Atp1a2 and Kcnj9 Are Candidate Genes Underlying Sensitivity to Oxycodone-Induced Locomotor Activation and Withdrawal-Induced Anxiety-Like Behaviors in C57BL/6 Substrains. Genes, brain, and behavior, 24(1), e70009.

Liu JN, et al. (2025) Pan-genome analyses of 11 Fraxinus species provide insights into salt adaptation in ash trees. Plant communications, 6(1), 101137.

Zhang Y, et al. (2025) Identification of superior haplotypes and candidate gene for seed size-related traits in soybean (Glycine max L.). Molecular breeding : new strategies in plant improvement, 45(1), 3.

Yamazaki H, et al. (2025) QTL-Based Evidence of Population Genetic Divergence in Male Territorial Aggressiveness of the Japanese Freshwater Threespine Stickleback. Ecology and evolution, 15(1), e70795.

Liu L, et al. (2025) Natural variation in MdNAC5 contributes to fruit firmness and ripening divergence in apple. Horticulture research, 12(1), uhae284.

Bergmann T, et al. (2025) Identification of Quantitative Trait Loci (QTLs) and candidate genes for trichome development in Brassica villosa using genetic, genomic, and transcriptomic approaches. Molecular genetics and genomics : MGG, 300(1), 13.

Ouellet-Fagg CL, et al. (2025) Complex and Dynamic Gene-by-Age and Gene-by-Environment Interactions Underlie Functional Morphological Variation in Adaptive Divergence in Arctic Charr (Salvelinus alpinus). Evolution & development, 27(1), e70000.

Pallotta M, et al. (2024) Diversity in bread and durum wheat stigma morphology and linkage

of increased stigma length to dwarfing gene Rht14. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(7), 160.

Al-Yazeedi T, et al. (2024) The contribution of an X chromosome QTL to non-Mendelian inheritance and unequal chromosomal segregation in Auanema freiburgense. Genetics, 227(1).

Mirzaei M, et al. (2024) Aphid resistance segregates independently of cardiac glycoside and glucosinolate content in an Erysimum cheiranthoides (wormseed wallflower) F2 population. bioRxiv : the preprint server for biology.

Wen T, et al. (2024) A SLAF-based high-density genetic map construction and genetic architecture of thermotolerant traits in maize (Zea mays L.). Frontiers in plant science, 15, 1338086.

Kanai M, et al. (2024) Identification of the drug/metabolite transporter 1 as a marker of quinine resistance in a NF54×Cam3.II P. falciparum genetic cross. bioRxiv : the preprint server for biology.

Xu G, et al. (2024) High-density genetic map construction and QTL mapping to identify genes for blight defense- and yield-related traits in sesame (Sesamum indicum L.). Frontiers in plant science, 15, 1446062.

Konuma J, et al. (2024) Odd-Paired is Involved in Morphological Divergence of Snail-Feeding Beetles. Molecular biology and evolution, 41(6).

Wang Z, et al. (2024) QTL mapping and BSR-seq revealed loci and candidate genes associated with the sporadic multifoliolate phenotype in soybean (Glycine max). TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(12), 262.

Sturm A, et al. (2024) QTL mapping provides new insights into emamectin benzoate resistance in salmon lice, Lepeophtheirus salmonis. BMC genomics, 25(1), 1212.

Brindisi LJ, et al. (2024) Genetic linkage mapping and quantitative trait locus (QTL) analysis of sweet basil (Ocimum basilicum L.) to identify genomic regions associated with cold tolerance and major volatiles. PloS one, 19(4), e0299825.

Njau SN, et al. (2024) QTL mapping for pod quality and yield traits in snap bean (Phaseolus vulgaris L.). Frontiers in plant science, 15, 1422957.