

Resource Summary Report

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qtltools

RRID:SCR_024200

Type: Tool

Proper Citation

qtltools (RRID:SCR_024200)

Resource Information

URL: <https://qtltools.github.io/qtltools/>

Proper Citation: qtltools (RRID:SCR_024200)

Description: Software tool set for molecular Quantitative Trait Loci discovery and analysis. Allows to go from raw sequence data to collection of molecular Quantitative Trait Loci in few easy-to-perform steps.

Resource Type: software resource, software toolkit, software library

Defining Citation: [PMID:28516912](#)

Keywords: molecular Quantitative Trait Loci, QTL discovery and analysis,

Availability: Free, Available for download, Freely available,

Resource Name: qtltools

Resource ID: SCR_024200

Alternate IDs: OMICS_18457

Alternate URLs: <https://sources.debian.org/src/qtltools/>

License: GPL-3.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260729T044602+0000

Ratings and Alerts

No rating or validation information has been found for qtltools.

No alerts have been found for qtltools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Wang W, et al. (2025) Impact of polymorphisms on gene expression and splicing in response to exercise and diet-induced weight loss in human skeletal muscle tissues. *Cell genomics*, 5(9), 100951.

Liang Q, et al. (2025) Impact of common variants on brain gene expression from RNA to protein to schizophrenia risk. *Nature communications*, 16(1), 10773.

Li J, et al. (2025) A multi-tissue atlas of allelic-specific expression reveals the characteristics, mechanisms, and relationship with dominant effects in cattle. *BMC biology*, 23(1), 148.

Ganapathy KR, et al. (2025) Improved Identification of Large-effect Rare Genetic Variants using Haplotype Aggregated Allele-specific Expression Data. *medRxiv : the preprint server for health sciences*.

Chen W, et al. (2025) Enhancer RNA Transcriptome-Wide Association Study Reveals a Distinctive Class of Pan-Cancer Susceptibility eRNAs. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(13), e2411974.

Cheng F, et al. (2025) Distinct methylomic signatures of high-altitude acclimatization and adaptation in the Tibetan Plateau. *Cell discovery*, 11(1), 45.

El Garwany O, et al. (2025) Splicing QTL mapping in stimulated macrophages associates low-usage splice junctions with immune-mediated disease risk. *Nature communications*, 16(1), 7205.

Zouache MA, et al. (2024) Levels of complement factor H-related 4 protein do not influence susceptibility to age-related macular degeneration or its course of progression. *Nature communications*, 15(1), 443.

Lykoskoufis NMR, et al. (2024) Transposable elements mediate genetic effects altering the expression of nearby genes in colorectal cancer. *Nature communications*, 15(1), 749.

Advani J, et al. (2024) QTL mapping of human retina DNA methylation identifies 87 gene-epigenome interactions in age-related macular degeneration. *Nature communications*, 15(1), 1972.

Chen Y, et al. (2024) Cross-ancestry analysis of brain QTLs enhances interpretation of schizophrenia genome-wide association studies. *American journal of human genetics*,

111(11), 2444.

Ueda MT, et al. (2024) Functional and dynamic profiling of transcript isoforms reveals essential roles of alternative splicing in interferon response. *Cell genomics*, 4(10), 100654.

Tian C, et al. (2024) Single-cell RNA sequencing of peripheral blood links cell-type-specific regulation of splicing to autoimmune and inflammatory diseases. *Nature genetics*, 56(12), 2739.

Mapel XM, et al. (2024) Molecular quantitative trait loci in reproductive tissues impact male fertility in cattle. *Nature communications*, 15(1), 674.

Hodonsky CJ, et al. (2024) Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. *Cell genomics*, 4(1), 100465.

Luo J, et al. (2024) Genetic regulation of human brain proteome reveals proteins implicated in psychiatric disorders. *Molecular psychiatry*, 29(11), 3330.

Leonard AS, et al. (2024) RNA-DNA differences in variant calls from cattle tissues result in erroneous eQTLs. *BMC genomics*, 25(1), 750.

Nishiyama NC, et al. (2024) eQTL in diseased colon tissue identifies novel target genes associated with IBD. *bioRxiv : the preprint server for biology*.

Jo Y, et al. (2024) Interpretation of SNP combination effects on schizophrenia etiology based on stepwise deep learning with multi-precision data. *Briefings in functional genomics*, 23(5), 663.

Thériault S, et al. (2024) Integrative genomic analyses identify candidate causal genes for calcific aortic valve stenosis involving tissue-specific regulation. *Nature communications*, 15(1), 2407.