Resource Summary Report

Generated by NIF on Apr 22, 2025

MULTIQTL

RRID:SCR_009043
Type: Tool

Proper Citation

MULTIQTL (RRID:SCR_009043)

Resource Information

URL: http://www.multiqtl.com/

Proper Citation: MULTIQTL (RRID:SCR_009043)

Description: Software application that integrates a broad spectrum of data mining, statistical analysis, interactive visualization and modeling tools that allow QTL analysis based on advanced and sophisticated methods for maximum extraction of the mapping information from data. (entry from Genetic Analysis Software)

Abbreviations: MULTIQTL

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: MULTIQTL

Resource ID: SCR_009043

Alternate IDs: nlx_154016

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250421T053711+0000

Ratings and Alerts

No rating or validation information has been found for MULTIQTL.

No alerts have been found for MULTIQTL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

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

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.

Errbii M, et al. (2024) Evolutionary genomics of socially polymorphic populations of Pogonomyrmex californicus. BMC biology, 22(1), 109.

Branchereau C, et al. (2022) New insights into flowering date in Prunus: fine mapping of a major QTL in sweet cherry. Horticulture research, 9.

John E, et al. (2022) Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat. PLoS pathogens, 18(1), e1010149.

Hübner S, et al. (2021) Tapping Diversity From the Wild: From Sampling to Implementation. Frontiers in plant science, 12, 626565.

Quero-García J, et al. (2021) Multi-year analyses on three populations reveal the first stable QTLs for tolerance to rain-induced fruit cracking in sweet cherry (Prunus avium L.). Horticulture research, 8(1), 136.

Fatiukha A, et al. (2021) Genomic Architecture of Phenotypic Plasticity in Response to Water Stress in Tetraploid Wheat. International journal of molecular sciences, 22(4).

Sekine D, et al. (2021) Improving Quantitative Traits in Self-Pollinated Crops Using Simulation-Based Selection With Minimal Crossing. Frontiers in plant science, 12, 729645.

Pshenichnikova TA, et al. (2021) Regions of Chromosome 2A of Bread Wheat (Triticum aestivum L.) Associated with Variation in Physiological and Agronomical Traits under Contrasting Water Regimes. Plants (Basel, Switzerland), 10(5).

Qiao J, et al. (2021) A novel miR167a-OsARF6-OsAUX3 module regulates grain length and weight in rice. Molecular plant, 14(10), 1683.

Bernard A, et al. (2020) Association and linkage mapping to unravel genetic architecture of phenological traits and lateral bearing in Persian walnut (Juglans regia L.). BMC genomics, 21(1), 203.

Zhang A, et al. (2020) Genetic Analysis for Cooking and Eating Quality of Super Rice and Fine Mapping of a Novel Locus qGC10 for Gel Consistency. Frontiers in plant science, 11, 342.

Klymiuk V, et al. (2020) Three previously characterized resistances to yellow rust are encoded by a single locus Wtk1. Journal of experimental botany, 71(9), 2561.

Petit J, et al. (2020) Elucidating the Genetic Architecture of Fiber Quality in Hemp (Cannabis sativa L.) Using a Genome-Wide Association Study. Frontiers in genetics, 11, 566314.

Cai L, et al. (2019) A fruit firmness QTL identified on linkage group 4 in sweet cherry (Prunus avium L.) is associated with domesticated and bred germplasm. Scientific reports, 9(1), 5008.

Emebiri L, et al. (2019) Unravelling the Complex Genetics of Karnal Bunt (Tilletia indica) Resistance in Common Wheat (Triticum aestivum) by Genetic Linkage and Genome-Wide Association Analyses. G3 (Bethesda, Md.), 9(5), 1437.

Gao Z, et al. (2019) The indica nitrate reductase gene OsNR2 allele enhances rice yield potential and nitrogen use efficiency. Nature communications, 10(1), 5207.

Avni R, et al. (2018) Genome Based Meta-QTL Analysis of Grain Weight in Tetraploid Wheat Identifies Rare Alleles of GRF4 Associated with Larger Grains. Genes, 9(12).

Tsvetkova NV, et al. (2018) Two Rye Genes Responsible for Abnormal Development of Wheat?Rye Hybrids Are Linked in the Vicinity of an Evolutionary Translocation on Chromosome 6R. Plants (Basel, Switzerland), 7(3).

Liu C, et al. (2017) Characterization of a major QTL for manganese accumulation in rice grain. Scientific reports, 7(1), 17704.