Resource Summary Report

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MAPQTL

RRID:SCR_009284
Type: Tool

Proper Citation

MAPQTL (RRID:SCR_009284)

Resource Information

URL: http://www.mapqtl.nl

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Description: Software application for mapping of quantitative trait loci (QTLs) for several types of mapping populations: BC1, F2, RILs, (doubled) haploids, full-sib family of outbreeders. Analyses: interval mapping, composite interval mapping, nonparametric mapping, automatic cofactor selection, permutation test for interval mapping. QTL charts. Everything available in an intuitive MS-Windows user interface. (entry from Genetic Analysis Software)

Abbreviations: MAPQTL

Synonyms: Software for the calculation of QTL positions on genetic maps

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, ansi c, delphi, ms-windows, (95/98/me/nt4.0/2000)

Funding:

Resource Name: MAPQTL

Resource ID: SCR_009284

Alternate IDs: nlx_154468

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250420T015756+0000

Ratings and Alerts

No rating or validation information has been found for MAPQTL.

No alerts have been found for MAPQTL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 378 mentions in open access literature.

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

Chen X, et al. (2025) Unveiling the genetic architecture of barley embryo: QTL mapping, candidate genes identification and its relationship with kernel size and early vigour. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(1), 32.

Wu Y, et al. (2025) Construction of a High-Density Genetic Linkage Map and QTL Mapping for Stem Rot Resistance in Passion Fruit (Passiflora edulis Sims). Genes, 16(1).

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

Yang G, et al. (2024) Allelic variation of BBX24 is a dominant determinant controlling red coloration and dwarfism in pear. Plant biotechnology journal, 22(6), 1468.

Williams OR, et al. (2024) Physical seed dormancy in pea is genetically separable from seed coat thickness and roughness. Frontiers in plant science, 15, 1359226.

Ho WK, et al. (2024) A genomic toolkit for winged bean Psophocarpus tetragonolobus. Nature communications, 15(1), 1901.

Guo L, et al. (2024) Turnovers of Sex-Determining Mutation in the Golden Pompano and Related Species Provide Insights into Microevolution of Undifferentiated Sex Chromosome. Genome biology and evolution, 16(3).

Ismawanto S, et al. (2024) Genetic analysis of agronomic and physiological traits associated with latex yield revealed complex genetic bases in Hevea brasiliensis. Heliyon, 10(13), e33421.

Eckstein PE, et al. (2024) An island of receptor-like genes at the Rrs13 locus on barley chromosome 6HS co-locate with three novel sources of scald resistance. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(11), 249.

Emeriewen OF, et al. (2024) A putative gene-for-gene relationship between the Erwinia amylovora effector gene eop1 and the FB_Mar12 resistance locus of Malus ×arnoldiana accession MAL0004. Frontiers in plant science, 15, 1472536.

Mathiazhagan M, et al. (2024) A high-density linkage map construction in guava (Psidium guajava L.) using genotyping by sequencing and identification of QTLs for leaf, peel, and pulp color in an intervarietal mapping population. Frontiers in plant science, 15, 1335715.

Ji Y, et al. (2024) GWAS combined with QTL mapping reveals the genetic loci of leaf morphological characters in Nicotiana tabacum. BMC plant biology, 24(1), 583.

Guo J, et al. (2024) Genome-wide association mapping for seedling and adult resistance to powdery mildew in barley. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(3), 50.

Anankul N, et al. (2024) Genetic mapping and quantitative trait loci analysis for pistillate flowers per node and multi-pistillate flower traits in the F2 cucumber population. Breeding science, 74(3), 204.

Clevinger EM, et al. (2024) Comparison of Rps loci toward isolates, singly and combined inocula, of Phytophthora sojae in soybean PI 407985, PI 408029, PI 408097, and PI424477. Frontiers in plant science, 15, 1394676.

Hsiang TF, et al. (2024) The haplotype-phased genome assembly facilitated the deciphering of the bud dormancy-related QTLs in Prunus mume. DNA research : an international journal for rapid publication of reports on genes and genomes, 32(1).

Pérez de Los Cobos F, et al. (2024) QTL mapping of almond kernel quality traits in the F1 progeny of 'Marcona' × 'Marinada'. Frontiers in plant science, 15, 1504198.

Xie X, et al. (2024) Genetic dissection of Meloidogyne incognita resistance genes based on VIGS functional analysis in Cucumis metuliferus. BMC plant biology, 24(1), 964.

Gao S, et al. (2024) Identification of a novel and plant height-independent QTL for coleoptile length in barley and validation of its effect using near isogenic lines. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(3), 53.

Li Y, et al. (2024) A novel natural variation in the promoter of GmCHX1 regulates conditional gene expression to improve salt tolerance in soybean. Journal of experimental botany, 75(3), 1051.