

Resource Summary Report

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QTLNETWORK

RRID:SCR_009078

Type: Tool

Proper Citation

QTLNETWORK (RRID:SCR_009078)

Resource Information

URL: <http://ibi.zju.edu.cn/software/qtlnetwork>

Proper Citation: QTLNETWORK (RRID:SCR_009078)

Description: Software package for mapping and visualizing the genetic architecture underlying complex traits for experimental populations derived from a cross between two inbred lines. (entry from Genetic Analysis Software)

Abbreviations: QTLNETWORK

Resource Type: software resource, software application

Defining Citation: [PMID:18202029](#), [PMID:20593516](#)

Keywords: gene, genetic, genomic

Funding:

Resource Name: QTLNETWORK

Resource ID: SCR_009078

Alternate IDs: nlx_154076

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250416T063536+0000

Ratings and Alerts

No rating or validation information has been found for QTLNETWORK.

No alerts have been found for QTLNETWORK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Xu M, et al. (2024) Dissection of genetic architecture of nine hazardous component traits of mainstream smoke in tobacco (*Nicotiana tabacum* L.). *Frontiers in plant science*, 15, 1358953.

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.

Huang G, et al. (2023) Dynamic QTL mapping revealed primarily the genetic structure of photosynthetic traits in castor (*Ricinus communis* L.). *Scientific reports*, 13(1), 14071.

Yu ZP, et al. (2023) Genetic Dissection of Extreme Seed-Flooding Tolerance in a Wild Soybean PI342618B by Linkage Mapping and Candidate Gene Analysis. *Plants (Basel, Switzerland)*, 12(12).

Guo S, et al. (2023) Mapping of major QTL and candidate gene analysis for hull colour in foxtail millet (*Setaria italica* (L.) P. Beauv.). *BMC genomics*, 24(1), 458.

Bokore FE, et al. (2022) Main effect and epistatic QTL affecting spike shattering and association with plant height revealed in two spring wheat (*Triticum aestivum* L.) populations. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 135(4), 1143.

Sheng C, et al. (2021) QTL-Seq and Transcriptome Analysis Disclose Major QTL and Candidate Genes Controlling Leaf Size in Sesame (*Sesamum indicum* L.). *Frontiers in plant science*, 12, 580846.

Elattar MA, et al. (2021) Identification and Validation of Major QTLs, Epistatic Interactions, and Candidate Genes for Soybean Seed Shape and Weight Using Two Related RIL Populations. *Frontiers in genetics*, 12, 666440.

Xu F, et al. (2021) Fine Mapping of a Major Pleiotropic QTL Associated with Sesamin and

Sesamolin Variation in Sesame (*Sesamum indicum* L.). *Plants* (Basel, Switzerland), 10(7).

Thi KM, et al. (2020) Mapping of QTLs conferring high grain length-breadth relative expansion during cooking in rice cultivar Paw San Hmwe. *Breeding science*, 70(5), 551.

Hina A, et al. (2020) High-Resolution Mapping in Two RIL Populations Refines Major "QTL Hotspot" Regions for Seed Size and Shape in Soybean (*Glycine max* L.). *International journal of molecular sciences*, 21(3).

Prince SJ, et al. (2020) Mapping Quantitative Trait Loci for Soybean Seedling Shoot and Root Architecture Traits in an Inter-Specific Genetic Population. *Frontiers in plant science*, 11, 1284.

Cao J, et al. (2020) Identification and Validation of New Stable QTLs for Grain Weight and Size by Multiple Mapping Models in Common Wheat. *Frontiers in genetics*, 11, 584859.

Yang J, et al. (2020) Mapping of QTL for Grain Yield Components Based on a DH Population in Maize. *Scientific reports*, 10(1), 7086.

Wu X, et al. (2020) QTL mapping and transcriptome analysis identify candidate genes regulating pericarp thickness in sweet corn. *BMC plant biology*, 20(1), 117.

Dhariwal R, et al. (2020) Mapping of Major Fusarium Head Blight Resistance from Canadian Wheat cv. AAC Tenacious. *International journal of molecular sciences*, 21(12).

Li M, et al. (2020) Genetic dissection of stem WSC accumulation and remobilization in wheat (*Triticum aestivum* L.) under terminal drought stress. *BMC genetics*, 21(1), 50.

Wu X, et al. (2019) Construction of High-Density Genetic Map and Identification of QTLs Associated with Seed Vigor after Exposure to Artificial Aging Conditions in Sweet Corn Using SLAF-seq. *Genes*, 11(1).

Patil G, et al. (2018) Dissecting genomic hotspots underlying seed protein, oil, and sucrose content in an interspecific mapping population of soybean using high-density linkage mapping. *Plant biotechnology journal*, 16(11), 1939.

Bennewitz S, et al. (2018) QTL Mapping of the Shape of Type VI Glandular Trichomes in Tomato. *Frontiers in plant science*, 9, 1421.