Resource Summary Report

Generated by dkNET on May 21, 2025

QGene

RRID:SCR_003209
Type: Tool

Proper Citation

QGene (RRID:SCR_003209)

Resource Information

URL: http://www.qgene.org/

Proper Citation: QGene (RRID:SCR_003209)

Description: A free, open-source, computationally efficient Java program for comparative analyses of QTL mapping data and population simulation that runs on any computer operating system. (entry from Genetic Analysis Software) It is written with a plug-in architecture for ready extensibility. The software accommodates line-cross mating designs consisting of any arbitrary sequence of selfing, backcrossing, intercrossing and haploid-doubling steps that includes map, population, and trait simulators; and is scriptable. Source code is available on request.

Abbreviations: QGene

Synonyms: QGene - Software for QTL data exploration

Resource Type: simulation software, source code, software resource, data analysis software, software application, data processing software

Defining Citation: PMID:18940826

Keywords: gene, genetic, genomic, java, qtl mapping, trait analysis, trait, population, simulation, map, quantitative trait locus, comparison, bio.tools

Funding: NSF DBI 0109879;
USDA-NRI Applied Plant Genomics Program 2004-35317-14867

Availability: GNU General Public License, v3, Registration requested

Resource Name: QGene

Resource ID: SCR_003209

Alternate IDs: biotools:qgene, nif-0000-31383

Alternate URLs: https://bio.tools/qgene

Old URLs: http://coding.plantpath.ksu.edu/qgene

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250521T060912+0000

Ratings and Alerts

No rating or validation information has been found for QGene.

No alerts have been found for QGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 119 mentions in open access literature.

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

Schafleitner R, et al. (2024) Molecular markers associated with resistance to squash leaf curl China virus and tomato leaf curl New Delhi virus in tropical pumpkin (Cucurbita moschata Duchesne ex Poir.) breeding line AVPU1426. Scientific reports, 14(1), 6793.

Dodson BL, et al. (2024) Variable effects of transient Wolbachia infections on alphaviruses in Aedes aegypti. PLoS neglected tropical diseases, 18(11), e0012633.

Dölfors F, et al. (2024) Nitrate transporter protein NPF5.12 and major latex-like protein MLP6 are important defense factors against Verticillium longisporum. Journal of experimental botany, 75(13), 4148.

Wang SS, et al. (2024) PtrA, Piz-t, and a novel minor-effect QTL (qBR12_3.3-4.4) collectively contribute to the durable blast-resistance of rice cultivar Tainung 84. Botanical studies, 65(1), 37.

Jamison DR, et al. (2024) Identification of Quantitative Trait Loci (QTL) for Sucrose and

Protein Content in Soybean Seed. Plants (Basel, Switzerland), 13(5).

Sharma JS, et al. (2024) Identification of Sr67, a new gene for stem rust resistance in KU168-2 located close to the Sr13 locus in wheat. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(1), 30.

Stakheev AA, et al. (2024) Investigating the Structure of the Components of the PolyADP-Ribosylation System in Fusarium Fungi and Evaluating the Expression Dynamics of Its Key Genes. Acta naturae, 16(3), 83.

Clare SJ, et al. (2024) High resolution mapping of a novel non-transgressive hybrid susceptibility locus in barley exploited by P. teres f. maculata. BMC plant biology, 24(1), 622.

Huynh T, et al. (2024) Single- and multiple-trait quantitative trait locus analyses for seed oil and protein contents of soybean populations with advanced breeding line background. Molecular breeding : new strategies in plant improvement, 44(8), 51.

Artemova D, et al. (2024) M1 macrophages as promising agents for cell therapy of endometriosis. Heliyon, 10(16), e36340.

Dodson BL, et al. (2023) Variable effects of Wolbachia on alphavirus infection in Aedes aegypti. bioRxiv : the preprint server for biology.

Ghazimoradi MH, et al. (2023) Reprogramming of fibroblast cells to totipotent state by DNA demethylation. Scientific reports, 13(1), 1154.

Christen V, et al. (2023) Different effects of pesticides on transcripts of the endocrine regulation and energy metabolism in honeybee foragers from different colonies. Scientific reports, 13(1), 1985.

Sari H, et al. (2023) Mapping QTLs for Super-Earliness and Agro-Morphological Traits in RILs Population Derived from Interspecific Crosses between Pisum sativum × P. fulvum. Current issues in molecular biology, 45(1), 663.

Silva A, et al. (2023) Genetic bases of resistance to the rice hoja blanca disease deciphered by a quantitative trait locus approach. G3 (Bethesda, Md.), 13(12).

Thakro V, et al. (2023) A superior gene allele involved in abscisic acid signaling enhances drought tolerance and yield in chickpea. Plant physiology, 191(3), 1884.

Makhtoum S, et al. (2022) QTLs Controlling Physiological and Morphological Traits of Barley (Hordeum vulgare L.) Seedlings under Salinity, Drought, and Normal Conditions. Biotech (Basel (Switzerland)), 11(3).

Sharma JS, et al. (2022) Origin and genetic analysis of stem rust resistance in wheat line Tr129. Scientific reports, 12(1), 4585.

Sabouri H, et al. (2022) SSR Linkage Maps and Identification of QTL Controlling Morpho-Phenological Traits in Two Iranian Wheat RIL Populations. Biotech (Basel (Switzerland)), 11(3).

Damele L, et al. (2021) EZH1/2 Inhibitors Favor ILC3 Development from Human HSPC-CD34+ Cells. Cancers, 13(2).