

Resource Summary Report

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QGene

RRID:SCR_003209

Type: Tool

Proper Citation

QGene (RRID:SCR_003209)

Resource Information

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

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

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: Free, Available for download, Freely available

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: 20260804T043214+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 126 mentions in open access literature.

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

Singh G, et al. (2026) Genetic analysis of a quantitative trait locus associated with resistance to the root-lesion nematode *Pratylenchus neglectus* in triticale. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(1), 24.

Breunig S, et al. (2025) Examining the genetic links between clusters of immune-mediated diseases and psychiatric disorders. Translational psychiatry, 15(1), 252.

Concepcion JCT, et al. (2025) Metabolite Quantitative Trait Loci Mapping for Fragrance and Fatty Acid Composition in Rice (*Oryza Sativa* L.). Rice (New York, N.Y.), 18(1), 96.

Manan F, et al. (2025) Genome-wide association and biparental mapping revealed a major quantitative trait locus associated with seedling resistance to bacterial leaf streak in durum. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(1), 10.

Simko I, et al. (2025) Integrative path modeling and QTL mapping identify maturity, stem strength, and cell wall composition driving lettuce resistance to *Sclerotinia minor*. Scientific reports, 15(1), 19824.

Dinh LT, et al. (2025) A novel allele of Days to Heading 8 promotes heading, potentially widening indica rice adaptation in Japan. The plant genome, 18(4), e70141.

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.

D??lfors 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.

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.

Jamison DR, et al. (2024) Identification of Quantitative Trait Loci (QTL) for Sucrose and Protein Content in Soybean Seed. *Plants (Basel, Switzerland)*, 13(5).

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

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.

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.

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.

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.

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.