

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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: 20260905T132459+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 129 mentions in open access literature.

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

Menezes JM, et al. (2026) Dual Effect of EZH2 Gene Editing with CRISPR/Cas9 in Lung Cancer. *Biology*, 15(3).

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.

Llanos-Azcar K, et al. (2026) Thermal Stress Disrupts Gut Microbiota, Induces Oxidative DNA Damage, and Modulates Immune and Stress-Related Gene Expression in the Red Sea Urchin (*Loxechinus albus*). *Biology*, 15(12).

de Mello DC, et al. (2026) Targeting EZH2 reverses thyroid cell dedifferentiation and enhances iodide uptake in anaplastic thyroid cancer. *FEBS letters*, 600(2), 215.

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

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.

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.

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.

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

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.

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.

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

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.

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.

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.

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.

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.