

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

BQTL

RRID:SCR_009137

Type: Tool

Proper Citation

BQTL (RRID:SCR_009137)

Resource Information

URL: <http://fmph.ucsd.edu/faculty/cberry/bqtl/>

Proper Citation: BQTL (RRID:SCR_009137)

Description: Software application for the mapping of genetic traits from line crosses and recombinant inbred lines. It performs (1) maximum likelihood estimation of multi-gene models; (2) Bayesian estimation of multi-gene models via Laplace Approximations; and (3) interval mapping and composite interval mapping of genetic loci (entry from Genetic Analysis Software)

Abbreviations: BQTL

Synonyms: Bayesian Quantitative Trait Locus mapping

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, s, c, fortran, the software is engineered to work in conjunction with r., unix, ms-windows, macos

Resource Name: BQTL

Resource ID: SCR_009137

Alternate IDs: nlx_154252

Old URLs: <http://hacuna.ucsd.edu/bqtl/>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260801T191054+0000

Ratings and Alerts

No rating or validation information has been found for BQTL.

No alerts have been found for BQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Roskams-Hieter B, et al. (2025) Epistatic contributions to human traits via transcription factor mechanisms. medRxiv : the preprint server for health sciences.