Resource Summary Report

Generated by T1D on Sep 5, 2026

QTL-ALL

RRID:SCR_009348
Type: Tool

Proper Citation

QTL-ALL (RRID:SCR_009348)

Resource Information

URL: http://watson.hgen.pitt.edu/register/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 16,2023. Software package designed to make as many as possible of the new statistics (e.g. score statistics) widely available. The software consists of a MEGA2-like interface for data analysis preparation and a library of R routines that computes linkage statistics. QTL-ALL reads in input data, creates re-formatted output data files, calls external IBD-generation software such as MERLIN or SIMWALK2, then computes statistics using our R library, and finally produces tables and plots of statistics and p-values. This entire sequence is highly automated, requiring minimal user-intervention. The initial release of the software computes a number of newer QTL-mapping statistics, including several score statistic variants, and can handle nuclear family data, including specialty designs such as discordant and concordant (affected) pairs. (entry from Genetic Analysis Software)

Abbreviations: QTL-ALL

Synonyms: QTL Analysis and Linkage Library

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: QTL-ALL

Resource ID: SCR_009348

Alternate IDs: nlx_154562

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260904T000435+0000

Ratings and Alerts

No rating or validation information has been found for QTL-ALL.

No alerts have been found for QTL-ALL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Casselbrant ML, et al. (2009) Otitis media: a genome-wide linkage scan with evidence of susceptibility loci within the 17q12 and 10q22.3 regions. BMC medical genetics, 10, 85.

Bhattacharjee S, et al. (2008) Robust score statistics for QTL linkage analysis. American journal of human genetics, 82(3), 567.

Gao X, et al. (2007) CHD7 gene polymorphisms are associated with susceptibility to idiopathic scoliosis. American journal of human genetics, 80(5), 957.

Liu F, et al. (2007) A genomewide screen for late-onset Alzheimer disease in a genetically isolated Dutch population. American journal of human genetics, 81(1), 17.

Wijsman EM, et al. (2006) Multipoint linkage analysis with many multiallelic or dense diallelic markers: Markov chain-Monte Carlo provides practical approaches for genome scans on general pedigrees. American journal of human genetics, 79(5), 846.

Lemire M, et al. (2006) SUP: an extension to SLINK to allow a larger number of marker loci to be simulated in pedigrees conditional on trait values. BMC genetics, 7, 40.

Sapp PC, et al. (2003) Identification of two novel loci for dominantly inherited familial amyotrophic lateral sclerosis. American journal of human genetics, 73(2), 397.

Seddon JM, et al. (2003) A genomewide scan for age-related macular degeneration provides evidence for linkage to several chromosomal regions. American journal of human genetics, 73(4), 780.

Ogdie MN, et al. (2003) A genomewide scan for attention-deficit/hyperactivity disorder in an extended sample: suggestive linkage on 17p11. American journal of human genetics, 72(5), 1268.