

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

MULTIMAPPER

RRID:SCR_009305

Type: Tool

Proper Citation

MULTIMAPPER (RRID:SCR_009305)

Resource Information

URL: <http://www.rni.helsinki.fi/~mjs/>

Proper Citation: MULTIMAPPER (RRID:SCR_009305)

Description: Bayesian QTL mapping software for analysing backcross, double haploid, and F2 data from designed crossing experiments of inbred lines (entry from Genetic Analysis Software)

Abbreviations: MULTIMAPPER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c

Resource Name: MULTIMAPPER

Resource ID: SCR_009305

Alternate IDs: nlx_154495

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260731T042814+0000

Ratings and Alerts

No rating or validation information has been found for MULTIMAPPER.

No alerts have been found for MULTIMAPPER.

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 [PRECISE-TBI](#) .

Bhattacharjee M, et al. (2015) Prediction of complex human diseases from pathway-focused candidate markers by joint estimation of marker effects: case of chronic fatigue syndrome. Human genomics, 9(1), 8.