

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 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 application, software resource

**Keywords:** gene, genetic, genomic, c

**Resource Name:** MULTIMAPPER

**Resource ID:** SCR\_009305

**Alternate IDs:** nlx\_154495

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260905T133249+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.