

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on May 13, 2025

## 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

**Funding:**

**Resource Name:** MULTIMAPPER

**Resource ID:** SCR\_009305

**Alternate IDs:** nlx\_154495

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

**Record Last Update:** 20250513T061102+0000

### Ratings and Alerts

No rating or validation information has been found for MULTIMAPPER.

No alerts have been found for MULTIMAPPER.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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.