

Resource Summary Report

Generated by [NIF](#) on Sep 4, 2026

MADMAPPER

RRID:SCR_009267

Type: Tool

Proper Citation

MADMAPPER (RRID:SCR_009267)

Resource Information

URL: <http://www.atgc.org/XLinkage/MadMapper/>

Proper Citation: MADMAPPER (RRID:SCR_009267)

Description: Suite of Python scripts for quality control of genetic markers, group analysis and inference of linear order of markers on linkage groups. MadMapper_RECBIT analyses raw marker scores for recombinant inbred lines. MadMapper_RECBIT generates pairwise distance scores for all markers, clusters based on pairwise distances, identifies genetic bins, assigns new markers to known linkage groups, validates allele calls, and assigns quality classes to each marker based on several criteria and cutoff values.

MadMapper_XDELTA utilizes new algorithm, Minimum Entropy Approach and Best-Fit Extension, to infer linear order of markers. MadMapper_XDELTA analyzes two-dimensional matrices of all pairwise scores and finds best map that has minimal total sum of differences between adjacent cells (map with lowest entropy). MadMapper is freely available at <http://www.atgc.org/XLinkage/MadMapper/> (entry from Genetic Analysis Software)

Abbreviations: MADMAPPER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, python

Resource Name: MADMAPPER

Resource ID: SCR_009267

Alternate IDs: nlx_154447

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260904T000428+0000

Ratings and Alerts

No rating or validation information has been found for MADMAPPER.

No alerts have been found for MADMAPPER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Wang C, et al. (2024) Mapping quantitative trait loci associated with self-(in)compatibility in goji berries (*Lycium barbarum*). *BMC plant biology*, 24(1), 441.

Lee HN, et al. (2021) Virtual reality environment using a dome screen for procedural pain in young children during intravenous placement: A pilot randomized controlled trial. *PloS one*, 16(8), e0256489.

Zhan S, et al. (2021) Zea mays RNA-seq estimated transcript abundances are strongly affected by read mapping bias. *BMC genomics*, 22(1), 285.

Tong Z, et al. (2020) Construction of a high-density genetic map with whole genome sequencing in *Nicotiana tabacum* L. *Genomics*, 112(2), 2028.

Jin Y, et al. (2019) Genome-Wide Variant Identification and High-Density Genetic Map Construction Using RADseq for *Platycladus orientalis* (Cupressaceae). *G3 (Bethesda, Md.)*, 9(11), 3663.

Ulloa M, et al. (2017) Insights Into Upland Cotton (*Gossypium hirsutum* L.) Genetic Recombination Based on 3 High-Density Single-Nucleotide Polymorphism and a Consensus Map Developed Independently With Common Parents. *Genomics insights*, 10, 1178631017735104.

Ko YJ, et al. (2017) misMM: An Integrated Pipeline for Misassembly Detection Using Genotyping-by-Sequencing and Its Validation with BAC End Library Sequences and Gene Synteny. *Genomics & informatics*, 15(4), 128.

Reyes-Chin-Wo S, et al. (2017) Genome assembly with in vitro proximity ligation data and whole-genome triplication in lettuce. *Nature communications*, 8, 14953.

Bhadauria V, et al. (2017) QTL mapping reveals genetic determinants of fungal disease resistance in the wild lentil species *Lens ervoides*. *Scientific reports*, 7(1), 3231.

Gujaria-Verma N, et al. (2016) Gene-based SNP discovery in tepary bean (*Phaseolus acutifolius*) and common bean (*P. vulgaris*) for diversity analysis and comparative mapping. *BMC genomics*, 17, 239.

Bhakta MS, et al. (2015) Punctuated distribution of recombination hotspots and demarcation of pericentromeric regions in *Phaseolus vulgaris* L. PloS one, 10(1), e0116822.

Hill T, et al. (2015) Ultra-High Density, Transcript-Based Genetic Maps of Pepper Define Recombination in the Genome and Synteny Among Related Species. G3 (Bethesda, Md.), 5(11), 2341.

Truco MJ, et al. (2013) An Ultra-High-Density, Transcript-Based, Genetic Map of Lettuce. G3 (Bethesda, Md.), 3(4), 617.