

Resource Summary Report

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MAPDISTO

RRID:SCR_009275

Type: Tool

Proper Citation

MAPDISTO (RRID:SCR_009275)

Resource Information

URL: <http://mapdisto.free.fr/>

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Description: Software program for mapping genetic markers in experimental segregating populations like backcross, doubled haploids, single-seed descent. Its specificity is to propose recombination fraction estimates in case of segregation distortion. It can (1) compute and draw genetic maps easily and quickly through a graphical interface; (2) facilitate the analysis of marker data showing segregation distortion due to differential viability of gametes or zygotes. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: MAPDISTO

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, ms-excel

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAPDISTO

Resource ID: SCR_009275

Alternate IDs: nlx_154456

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260805T044220+0000

Ratings and Alerts

No rating or validation information has been found for MAPDISTO.

No alerts have been found for MAPDISTO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 115 mentions in open access literature.

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

Szabo-Hever A, et al. (2025) Identification and mapping of quantitative trait loci for Fusarium head blight resistance in a synthetic hexaploid × hard red spring wheat population. The plant genome, 18(3), e70073.

Neupane A, et al. (2025) Genetic improvement of FHB and DON resistance by combining the Fhb1 gene with additional resistance QTL in winter wheat population. The plant genome, 18(3), e70084.

Soler-Garzón A, et al. (2025) Mapping resistance to Sclerotinia white mold in two pinto bean recombinant inbred line populations. The plant genome, 18(1), e20538.

Jun S, et al. (2025) Mapping QTLs for PHS resistance and development of a deep learning model to measure PHS rate in japonica rice. The plant genome, 18(3), e70109.

Burridge AJ, et al. (2024) Development of a next generation SNP genotyping array for wheat. Plant biotechnology journal, 22(8), 2235.

Sharma JS, et al. (2024) Identification of Sr67, a new gene for stem rust resistance in KU168-2 located close to the Sr13 locus in wheat. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(1), 30.

Peñuela M, et al. (2024) Methylomes as key features for predicting recombination in some plant species. Plant molecular biology, 114(2), 25.

Jamison DR, et al. (2024) Identification of Quantitative Trait Loci (QTL) for Sucrose and Protein Content in Soybean Seed. Plants (Basel, Switzerland), 13(5).

Cavalet-Giorsa E, et al. (2024) Origin and evolution of the bread wheat D genome. Nature, 633(8031), 848.

Clare SJ, et al. (2024) High resolution mapping of a novel non-transgressive hybrid susceptibility locus in barley exploited by P. teres f. maculata. BMC plant biology, 24(1), 622.

Neupane A, et al. (2024) QTL analysis of native Fusarium head blight and deoxynivalenol resistance in 'D8006W'/Superior', soft white winter wheat population. BMC plant biology, 24(1), 852.

Chen HJ, et al. (2024) Reverse Mutations in Pigmentation Induced by Sodium Azide in the IR64 Rice Variety. *Current issues in molecular biology*, 46(12), 13328.

Peñuela M, et al. (2023) Prediction of crossover recombination using parental genomes. *PloS one*, 18(2), e0281804.

Sharma JS, et al. (2023) Fine mapping and marker development for the wheat leaf rust resistance gene Lr32. *G3 (Bethesda, Md.)*, 13(2).

Mandour H, et al. (2023) Identifying physiological and genetic determinants of faba bean transpiration response to evaporative demand. *Annals of botany*, 131(3), 533.

Silva A, et al. (2023) Genetic bases of resistance to the rice hoja blanca disease deciphered by a quantitative trait locus approach. *G3 (Bethesda, Md.)*, 13(12).

Sharma JS, et al. (2022) Origin and genetic analysis of stem rust resistance in wheat line Tr129. *Scientific reports*, 12(1), 4585.

Athiyannan N, et al. (2022) Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. *Nature genetics*, 54(3), 227.

Kandel R, et al. (2021) Identification and mapping of quantitative trait loci for resistance to *Liriomyza trifolii* in romaine lettuce cultivar 'Valmaine'. *Scientific reports*, 11(1), 998.

Shen C, et al. (2021) *Gossypium tomentosum* genome and interspecific ultra-dense genetic maps reveal genomic structures, recombination landscape and flowering depression in cotton. *Genomics*, 113(4), 1999.