Resource Summary Report

Generated by dkNET on Apr 18, 2025

MAPDISTO

RRID:SCR_009275
Type: Tool

Proper Citation

MAPDISTO (RRID:SCR_009275)

Resource Information

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

Proper Citation: MAPDISTO (RRID:SCR_009275)

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)

Abbreviations: MAPDISTO

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-excel

Funding:

Resource Name: MAPDISTO

Resource ID: SCR_009275

Alternate IDs: nlx_154456

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063542+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 112 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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

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

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

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.

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.

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

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.

Soler-Garzón A, et al. (2021) NAC Candidate Gene Marker for bgm-1 and Interaction With QTL for Resistance to Bean Golden Yellow Mosaic Virus in Common Bean. Frontiers in plant science, 12, 628443.

Kumawat G, et al. (2021) A Major and Stable Quantitative Trait Locus qSS2 for Seed Size and Shape Traits in a Soybean RIL Population. Frontiers in genetics, 12, 646102.

Arrieta M, et al. (2021) The effect of heat stress on sugar beet recombination. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 134(1), 81.