

Resource Summary Report

Generated by [ASWG](#) on Sep 18, 2026

MAPDRAW

RRID:SCR_009276

Type: Tool

Proper Citation

MAPDRAW (RRID:SCR_009276)

Resource Information

URL: <http://www.nslj-genetics.org/soft/mapdraw.v2.2.xls>

Proper Citation: MAPDRAW (RRID:SCR_009276)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 11, 2023. Software application that draws genetic linkage maps on PC same as what MAPMAKER does on Mac. (entry from Genetic Analysis Software)

Abbreviations: MAPDRAW

Resource Type: software application, software resource

Defining Citation: [PMID:15639879](#)

Keywords: gene, genetic, genomic, microsoft visual basic, excel macro, ms-windows

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAPDRAW

Resource ID: SCR_009276

Alternate IDs: nlx_154457

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260912T200243+0000

Ratings and Alerts

No rating or validation information has been found for MAPDRAW.

No alerts have been found for MAPDRAW.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 98 mentions in open access literature.

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

Liu T, et al. (2025) Transcriptomic analysis reveals the crucial role of YABBY genes family in hormonal induced parthenocarp in *Cucumis sativus* L. *BMC plant biology*, 25(1), 45.

Zhang D, et al. (2024) The introgression of BjMYB113 from *Brassica juncea* leads to purple leaf trait in *Brassica napus*. *BMC plant biology*, 24(1), 735.

Yang Z, et al. (2024) QTL mapping for seed vigor-related traits under artificial aging in common wheat in two introgression line (IL) populations. *PeerJ*, 12, e17778.

Chen L, et al. (2024) Identification of a recessive gene RgM4G52 conferring red glume, stem, and rachis in a *Triticum boeoticum* mutant. *Frontiers in plant science*, 15, 1459505.

He N, et al. (2023) Fine Mapping and Cloning of a qRA2 Affect the Ratooning Ability in Rice (*Oryza sativa* L.). *International journal of molecular sciences*, 24(2).

Sun S, et al. (2022) Molecular Characterizations of the er1 Alleles Conferring Resistance to *Erysiphe pisi* in Three Chinese Pea (*Pisum sativum* L.) Landraces. *International journal of molecular sciences*, 23(19).

Zhao W, et al. (2021) Genome-Wide Analysis of MADS-Box Genes in Foxtail Millet (*Setaria italica* L.) and Functional Assessment of the Role of SiMADS51 in the Drought Stress Response. *Frontiers in plant science*, 12, 659474.

Zhang B, et al. (2021) Map-based cloning and promoter variation analysis of the lobed leaf gene BoLMI1a in ornamental kale (*Brassica oleracea* L. var. *acephala*). *BMC plant biology*, 21(1), 456.

Li M, et al. (2021) Genome-wide characterization and analysis of bHLH transcription factors related to anthocyanin biosynthesis in spine grapes (*Vitis davidii*). *Scientific reports*, 11(1), 6863.

Wang Y, et al. (2021) Molecular Mapping and Analysis of an Excellent Quantitative Trait Loci Conferring Adult-Plant Resistance to Stripe Rust in Chinese Wheat Landrace Gaoxianguangtoumai. *Frontiers in plant science*, 12, 756557.

Zhang X, et al. (2021) Genome-Wide Identification of PRP Genes in Apple Genome and the Role of MdPRP6 in Response to Heat Stress. *International journal of molecular sciences*, 22(11).

Li M, et al. (2021) Grape Small Auxin Upregulated RNA (SAUR) 041 Is a Candidate Regulator of Berry Size in Grape. *International journal of molecular sciences*, 22(21).

Wei C, et al. (2021) Genome-wide survey of the F-box/Kelch (FBK) members and molecular identification of a novel FBK gene TaAFR in wheat. *PloS one*, 16(7), e0250479.

Zhang H, et al. (2021) Transcriptomic analysis of salt tolerance-associated genes and diversity analysis using indel markers in yardlong bean (*Vigna unguiculata* ssp. *sesquipedialis*). *BMC genomic data*, 22(1), 34.

Zhang N, et al. (2020) Evaluation of leaf rust resistance in the Chinese wheat cultivar 'Een1'. *PeerJ*, 8, e8993.

Zhong C, et al. (2020) Fine Mapping, Candidate Gene Identification and Co-segregating Marker Development for the Phytophthora Root Rot Resistance Gene RpsYD25. *Frontiers in genetics*, 11, 799.

Ye J, et al. (2020) Fine mapping of the QTL cqSPDA2 for chlorophyll content in *Brassica napus* L. *BMC plant biology*, 20(1), 511.

Zhang Y, et al. (2020) Tracing the evolution of fatty acid-binding proteins (FABPs) in organisms with a heterogeneous fat distribution. *FEBS open bio*, 10(5), 861.

Guo B, et al. (2020) Characterization of the Nitrate Transporter gene family and functional identification of HvNRT2.1 in barley (*Hordeum vulgare* L.). *PloS one*, 15(4), e0232056.

Lhamo D, et al. (2020) Genome-Wide Analysis of the Five Phosphate Transporter Families in *Camelina sativa* and Their Expressions in Response to Low-P. *International journal of molecular sciences*, 21(21).