

Resource Summary Report

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MAPCHART

RRID:SCR_009273

Type: Tool

Proper Citation

MAPCHART (RRID:SCR_009273)

Resource Information

URL: <http://www.biometris.wur.nl/uk/Software/MapChart/>

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Description: Software application that produces charts of genetic linkage and QTL data. The charts are composed of a sequence of vertical bars representing the linkage groups or chromosomes. On these bars the positions of loci are indicated, and next to the bars QTL intervals and QTL graphs can be shown. MapChart reads the linkage information (i.e. the locus and QTL names and their positions) from text files. Many options to adapt the charts to different purposes. Can produce graphic files (enhanced windows metafile format) which can be enhanced with other MS-Windows software. (entry from Genetic Analysis Software)

Abbreviations: MAPCHART

Synonyms: Windows software for the graphical presentation of linkage maps and QTLs

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, delphi, ms-windows, (95/98/me/nt4.0/2000)

Resource Name: MAPCHART

Resource ID: SCR_009273

Alternate IDs: nlx_154454

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260829T183109+0000

Ratings and Alerts

No rating or validation information has been found for MAPCHART.

No alerts have been found for MAPCHART.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1436 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Zhang Q, et al. (2026) Identification and characterization of the DREB family in Chinese yam and functional study of DoDREB28 under drought stress. BMC plant biology, 26(1).

Tong Y, et al. (2026) Genome-wide identification and expression analysis of stress-associated proteins (SAPs) containing A20/AN1 Zinc finger in Dendrobium officinale. BMC plant biology, 26(1).

Zeng Y, et al. (2026) Genome-Wide Identification and Characterization of the C2H2 Zinc Finger Gene Family in Pear (Pyrus bretschneideri) and Its Potential Role in Drought Stress Response. Biology, 15(4).

Liu J, et al. (2026) Genome-wide identification and immunological expression analysis of the C3HC4-type zinc finger protein genes in the silkworm, Bombyx Mori. BMC genomics, 27(1).

Chai X, et al. (2026) PFWRI1-10 transcription factor mediates lipid synthesis in Perilla frutescens through regulating PfBCCP1 gene transcription. BMC plant biology, 26(1).

Chavez J, et al. (2026) Seasonal Analysis of Candida auris Detection Rates at 80 Wastewater Monitoring Sites in the United States, December 2023-November 2024. Environmental microbiology reports, 18(3), e70376.

Lin Z, et al. (2026) Genome-wide analysis of HSP70 gene superfamily in kelp (Saccharina japonica): identification, characterization, and heat stress-responsive expression profiles. PeerJ, 14, e21451.

Yogeshwar SM, et al. (2026) Brain atrophy patterns in anti-IgLON5 disease. Brain : a journal of neurology, 149(3), 884.

Tovar-Herrera OE, et al. (2026) Core rumen microbes are functional generalists that sustain host metabolism and gut ecosystem function. Nature ecology & evolution, 10(1), 44.

Das S, et al. (2026) Genome-wide association analysis to identify QTLs and candidate genes associated with grain yield and its related traits under low light conditions in rice (Oryza sativa L.). The plant genome, 19(1), e70191.

Ren N, et al. (2026) Identifying candidate genes related to rice ML under salt-alkali tolerance. *BMC plant biology*, 26(1).

Ordine JVW, et al. (2026) Taxonomic and Functional Assessment of Microbial Communities in Urban Runoff-Contaminated Mangrove Sediments. *Current microbiology*, 83(6).

Pan L, et al. (2026) Genome-wide identification and expression analysis Pvrboh genes reveal their potential roles in salt tolerance and calcium signaling. *Plant & cell physiology*, 67(1), 8.

Koramutla MK, et al. (2026) Genome-wide identification of ethylene receptor protein-coding gene families in wheat and their regulated expression during development and under multiple abiotic stresses. *BMC plant biology*, 26(1), 347.

Davik J, et al. (2026) Development of a Flex-Seq SNP panel for raspberry (*Rubus idaeus* L.) and validation through linkage map construction and identification of QTL for several traits of agronomic importance to raspberry breeding. *PloS one*, 21(2), e0328606.

Huang X, et al. (2026) Genome-wide identification and functional analysis of the Caffeoylshikimate esterase (CSE) gene family in five fern species. *BMC plant biology*, 26(1).

Arango-Ibanez JP, et al. (2026) Comorbidity Clusters in Acute Heart Failure: Insights From the AMERICCAASS Registry. *Journal of the American Heart Association*, 15(9), e046820.

Bahmani K, et al. (2026) -Identification of QTL for steviol glycoside biosynthesis using a SNP-based genetic linkage map for *Stevia rebaudiana*. *G3 (Bethesda, Md.)*, 16(3).

Banda-Katha GW, et al. (2026) Implementation strategies and economic considerations for point-of-care ultrasound in Low- and Middle-Income Countries: A scoping review. *PLOS global public health*, 6(2), e0005852.

Feng Y, et al. (2026) Genome-Wide Analysis of the FAR1/FHY3 (FRS) Gene Family and Expression Responses of PbFRS Genes to PEG-Induced Osmotic Stress, Light, and Shade in *Phoebe bournei*. *International journal of molecular sciences*, 27(11).