

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 resource, software application

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: 20260801T191056+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 1380 mentions in open access literature.

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

Lima Cunha W, et al. (2026) Molecular mechanisms associated with rootstock-scion interactions in rubber trees. *The plant genome*, 19(1), e70147.

Liu S, et al. (2025) Development and application of the GenoBaits WheatSNP16K array to accelerate wheat genetic research and breeding. *Plant communications*, 6(1), 101138.

Khaskhali S, et al. (2025) Expression profile and characterization of respiratory burst oxidase homolog genes in rice under MeJA, SA and Xoo treatments. *Scientific reports*, 15(1), 5936.

Ohm H, et al. (2025) Comprehensive identification of the PEBP gene family in *Vicia faba* highlighting VtTFL1a variation and phenotypic insights into determinate growth. *Scientific reports*, 15(1), 28687.

Dumidae A, et al. (2025) Bithyniid snails (Gastropoda: Bithyniidae) infected with Xiphidiocercariae in Thailand include a new record of *Bithynia siamensis siamensis* as the intermediate host of *Plagiorchis* and *Paralecithodendrium*. *PloS one*, 20(2), e0317052.

Gonal B, et al. (2025) Discovery and validation of SSR marker-based QTL governing fresh pod yield in dolichos bean (*Lablab purpureus* L. Sweet). *Scientific reports*, 15(1), 8613.

Gu H, et al. (2025) Genome-wide analysis and functional validation of the cotton FAH gene family for salt stress. *BMC genomics*, 26(1), 271.

Peng C, et al. (2025) Epidemiology, Transmission, and Evolution of Japanese Encephalitis Virus. *Microorganisms*, 13(6).

Kellogg DS, et al. (2025) Practice Patterns of Graduates of a Rural Emergency Medicine Training Program. *The western journal of emergency medicine*, 26(1), 40.

Mar??n A, et al. (2025) Development and validation of versatile species-specific primer assays for eDNA monitoring and authentication of 10 commercially important Peruvian marine species. *PloS one*, 20(7), e0313181.

Tsehay Y, et al. (2025) Multi-locus genome-wide association study reveals genomic regions underlying root system architecture traits early growth stage of sorghum

germplasm. Scientific reports, 15(1), 31727.

Bellaloui N, et al. (2025) Genomic regions and candidate genes associated with seed nitrogen, phosphorus, and sulfur accumulation identified in the soybean 'Forrest' by 'Williams 82' RIL population. PloS one, 20(9), e0331214.

Zhang Y, et al. (2025) Rapid isolation of Yr9 via MutIsoSeq and QTL analysis of durable stripe rust resistance in wheat cultivar Xingzi 9104. Stress biology, 5(1), 29.

Fang H, et al. (2025) Unveiling the Role of GhP5CS1 in Cotton Salt Stress Tolerance: A Comprehensive Genomic and Functional Analysis of P5CS Genes. Plants (Basel, Switzerland), 14(2).

Huang X, et al. (2025) Genome-wide identification of the regulatory network of mitogen-activated protein kinase signaling cascades gene families in Hevea Brasiliensis. BMC plant biology, 25(1), 581.

Chen X, et al. (2025) Unveiling the genetic architecture of barley embryo: QTL mapping, candidate genes identification and its relationship with kernel size and early vigour. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(1), 32.

Turabi RY, et al. (2025) Weight-bearing and mobilisation timing after hip fracture surgery in older adults: an international survey of clinicians' perspectives. European geriatric medicine, 16(3), 909.

Luo Y, et al. (2025) Genetic mapping of the Fusarium head blight resistance gene in wheat Guixie 3. Journal of applied genetics, 66(4), 841.

Yuan M, et al. (2025) Wheat TaNADPO Promotes Spot Blotch Resistance. Molecular plant pathology, 26(6), e70103.

Pettit N, et al. (2025) Genetic and biochemical analyses identify a major locus, GH-PA1, underlying pollen carotenoid accumulation and pigmentation in upland cotton. Journal of experimental botany, 76(22), 6776.