

Resource Summary Report

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JOINMAP

RRID:SCR_009248

Type: Tool

Proper Citation

JOINMAP (RRID:SCR_009248)

Resource Information

URL: <http://www.joinmap.nl/>

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Description: Software application for construction of genetic linkage maps for several types of mapping populations: BC1, F2, RILs, (doubled) haploids, outbreeders full-sib family. Can combine ("join") data derived from several sources into an integrated map. Further: linkage group determination, automatic phase determination for outbreeders full-sib family, several diagnostics, and map charts. Everything available in an intuitive MS-Windows user interface. (entry from Genetic Analysis Software)

Abbreviations: JOINMAP

Synonyms: Software for the calculation of genetic linkage maps

Resource Type: software application, software resource

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

Resource Name: JOINMAP

Resource ID: SCR_009248

Alternate IDs: nlx_154416

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260815T182942+0000

Ratings and Alerts

No rating or validation information has been found for JOINMAP.

No alerts have been found for JOINMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1072 mentions in open access literature.

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

Wu B, et al. (2026) Natural variations in MdBPM2/MdRGLG3-MdNAC83 network controlling the quantitative segregation of apple fruit storability. *Journal of integrative plant biology*, 68(1), 169.

Zhu J, et al. (2026) Unlocking tropical adaptation: novel flowering time genes implicate JA and ROS signaling in maize. *BMC plant biology*, 26(1), 195.

Mohanty JK, et al. (2026) Trans-QTL Alliance of HKT1 and PHL7 Modulate Salinity Stress Tolerance and Enhance Crop Yield Endurance. *Plant biotechnology journal*, 24(3), 1166.

Hulsey CD, et al. (2026) Divergence at the IRX gene cluster underlies extreme trophic polymorphism in a cichlid fish (*Herichthys minckleyi*). *Communications biology*, 9(1).

Awais M, et al. (2026) Epistatic interaction of the genes Raw1 and Raw7 controls barb size and frequency in barley awn roughness. *bioRxiv : the preprint server for biology*.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Pfeifer M, et al. (2026) QTL analysis of *Malus baccata* 'Jackii'-derived offspring reveals a polygenic inheritance pattern of apple blotch resistance. *Frontiers in plant science*, 17, 1854916.

López-Girona E, et al. (2026) Fine-mapping, candidate gene identification, and marker development for the apple scab resistance gene Rvi2. *Journal of experimental botany*, 77(6), 1647.

Li Q, et al. (2026) Functional 5Bq allele is responsible for the compact spike phenotype in common wheat (*Triticum aestivum* L.). *BMC plant biology*, 26(1).

Clevinger EM, et al. (2026) RenSeq-derived SNPs used in mapping resistance to *Phytophthora sojae* and three *Pythium* spp. in multiple soybean RIL populations. *Molecular breeding : new strategies in plant improvement*, 46(6), 64.

Colas I, et al. (2026) The RAD51 paralogue HvXRCC2 affects meiosis and recombination in barley. *Journal of experimental botany*, 77(12), 3593.

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

Cao Z, et al. (2026) AhBWR15, A Novel RLK Gene, Confers Resistance to *Ralstonia solanacearum* in Peanut. *Plant biotechnology journal*, 24(6), 3861.

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.

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).

Gandhadmath SS, et al. (2026) Genome-wide exploration of bacterial leaf blight resistance and fine mapping of major resistance gene (Bb13) in upland cotton (*Gossypium hirsutum* L.). *The plant genome*, 19(1), e70214.

Jia M, et al. (2025) Identification of late blight resistance QTLs in an interspecific RIL population of tomato via genotyping-by-sequencing. *Molecular breeding : new strategies in plant improvement*, 45(4), 43.

Liu Y, et al. (2025) Identification of a gene conferring broad-spectrum orthotospovirus resistance in Solanaceae. *Science advances*, 11(25), eadw4333.

Gao L, et al. (2025) Construction of a genetic linkage map and QTL mapping of the agronomic traits in Foxtail millet (*Setaria italica*). *BMC genomics*, 26(1), 152.

Pfeifer M, et al. (2025) Genetic mapping, marker development, and identification of candidate genes for powdery mildew resistance in *Malus baccata* 'Jackii'. *Frontiers in plant science*, 16, 1716290.