

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 resource, software application

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: 20260801T191047+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 1049 mentions in open access literature.

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

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

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.

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.

Wu D, et al. (2025) High-resolution genetic and physical mapping reveals a peanut spotted wilt disease resistance locus, PSWDR-1, to Tomato spotted wilt virus (TSWV), within a recombination cold-spot on chromosome A01. *BMC genomics*, 26(1), 224.

Lee D, et al. (2025) QTL mapping and whole-genome sequencing analysis for novel genetic resources associated with sucrose content in soybean [*Glycine max* (L.) Merr.]. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(2), 43.

Parajuli S, et al. (2025) Genetic architecture of anthocyanin pigment traits and purple spot (*Stemphylium vesicarium*) resistance in an F1 pseudo-testcross population of asparagus. *The plant genome*, 18(2), e70028.

Ruud AK, et al. (2025) Quantitative trait loci mapping of resistance to pre-harvest sprouting in the Norwegian spring wheat breeding line T7347. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(7), 159.

Ji X, et al. (2025) Mapping and identification of QTLs for low light tolerance traits in grapevine. *BMC plant biology*, 25(1), 927.

Behling W, et al. (2025) Genetic basis for broad interspecific compatibility in *Solanum verrucosum*. *The Plant journal : for cell and molecular biology*, 123(4), e70426.

Mitchell AA, et al. (2025) Genetic mapping of novel QTL for seed protein stability in food-grade soybean (*Glycine max*). *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(12), 304.

Rodríguez MV, et al. (2025) Introgression of dwarfing allele *dw1* reduced seed dormancy and increased pre-harvest sprouting susceptibility in grain sorghum converted lines. *Plant biotechnology journal*, 23(5), 1783.

Yamazaki H, et al. (2025) QTL-Based Evidence of Population Genetic Divergence in Male Territorial Aggressiveness of the Japanese Freshwater Threespine Stickleback. *Ecology and evolution*, 15(1), e70795.

Yang X, et al. (2025) Novel candidate genes and genetic basis analysis of kernel starch content in tropical maize. *BMC plant biology*, 25(1), 105.

Feng C, et al. (2025) Genomic and genetic insights into Mendel's pea genes. *Nature*, 642(8069), 980.

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.

Bohorquez-Chaux A, et al. (2025) Genetic mapping and validation of QTL for whitefly resistance in cassava (*Manihot esculenta* Crantz). *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(7), 160.

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.

Karim MM, et al. (2025) Identification of three novel QTL for resistance to highly aggressive Canadian strains of *Plasmodiophora brassicae* in rutabaga cultivar ECD10. *Frontiers in plant science*, 16, 1588460.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Zhuang L, et al. (2025) Joint linkage and association analysis identifies genomic regions and candidate genes for yield-related traits in wheat. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(5), 107.