

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 [RRID](#) .

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.