

Resource Summary Report

Generated by NIF on Sep 9, 2026

ANTMAP

RRID:SCR_013426

Type: Tool

Proper Citation

ANTMAP (RRID:SCR_013426)

Resource Information

URL: <http://lbm.ab.a.u-tokyo.ac.jp/~iwata/antmap/>

Proper Citation: ANTMAP (RRID:SCR_013426)

Description: Software application based on the Ant Colony Optimization to solve the special case of the traveling salesman problem of ordering markers when the number of loci is large. ANYMAP performs segregation test, linkage grouping and locus ordering, and constructs a linkage map rapidly. (entry from Genetic Analysis Software)

Abbreviations: ANTMAP

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, java, ms-windows, macos, linux, unix, solaris

Resource Name: ANTMAP

Resource ID: SCR_013426

Alternate IDs: nlx_154226

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260905T133256+0000

Ratings and Alerts

No rating or validation information has been found for ANTMAP.

No alerts have been found for ANTMAP.

Data and Source Information

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Shioya N, et al. (2026) Loss-of-function allele of the soybean flowering/maturation gene TOF11 increases free amino acid content at the edamame stage and improves eating quality. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(4).

Horitani M, et al. (2024) Identification of Genes Responsible for the Synthesis of Glycitein Isoflavones in Soybean Seeds. Plants (Basel, Switzerland), 13(2).

Taura S, et al. (2023) Chromosomal Location of xa19, a Broad-Spectrum Rice Bacterial Blight Resistant Gene from XM5, a Mutant Line from IR24. Plants (Basel, Switzerland), 12(3).

Ogiso-Tanaka E, et al. (2023) Unique Salt-Tolerance-Related QTLs, Evolved in *Vigna riukuensis* (Na⁺ Includer) and *V. nakashimae* (Na⁺ Excluder), Shed Light on the Development of Super-Salt-Tolerant Azuki Bean (*V. angularis*) Cultivars. Plants (Basel, Switzerland), 12(8).

Takeshima R, et al. (2021) Targeted amplicon sequencing + next-generation sequencing-based bulked segregant analysis identified genetic loci associated with preharvest sprouting tolerance in common buckwheat (*Fagopyrum esculentum*). BMC plant biology, 21(1), 18.

Shimomura K, et al. (2021) Identification of quantitative trait loci for powdery mildew resistance in highly resistant cucumber (*Cucumis sativus* L.) using ddRAD-seq analysis. Breeding science, 71(3), 326.

Msami JA, et al. (2021) Linkage analysis of rice bacterial blight resistance gene xa20 in XM6, a mutant line from IR24. Breeding science, 71(2), 144.

Umeda M, et al. (2021) Detection of a major QTL related to smut disease resistance inherited from a Japanese wild sugarcane using GRAS-Di technology. Breeding science, 71(3), 365.

Yamaguchi N, et al. (2021) Identification and validation of quantitative trait loci associated with seed yield in soybean. Breeding science, 71(3), 396.

Sarkar MAR, et al. (2020) Single-base deletion in GmCHR5 increases the genistein-to-daidzein ratio in soybean seed. Breeding science, 70(3), 265.

Seki K, et al. (2020) A CIN-like TCP transcription factor (LsTCP4) having retrotransposon insertion associates with a shift from Salinas type to Empire type in crisphead lettuce (*Lactuca sativa* L.). Horticulture research, 7, 15.

Konishi A, et al. (2019) Detection of quantitative trait loci for capsanthin content in pepper (*Capsicum annuum* L.) at different fruit ripening stages. *Breeding science*, 69(1), 30.

Watanabe S, et al. (2019) Identification and characterization of a major QTL underlying soybean isoflavone malonylglycitin content. *Breeding science*, 69(4), 564.

Yamagata Y, et al. (2018) Selection criteria for SNP loci to maximize robustness of high-resolution melting analysis for plant breeding. *Breeding science*, 68(4), 488.

Murata J, et al. (2017) Oxidative rearrangement of (+)-sesamin by CYP92B14 co-generates twin dietary lignans in sesame. *Nature communications*, 8(1), 2155.

Edae EA, et al. (2017) Genotyping-by-Sequencing Facilitates a High-Density Consensus Linkage Map for *Aegilops umbellulata*, a Wild Relative of Cultivated Wheat. *G3 (Bethesda, Md.)*, 7(5), 1551.

Kanamori A, et al. (2016) A Genetic Map for the Only Self-Fertilizing Vertebrate. *G3 (Bethesda, Md.)*, 6(4), 1095.

Iwata H, et al. (2016) Genomics-assisted breeding in fruit trees. *Breeding science*, 66(1), 100.

Yamada T, et al. (2014) Major QTLs associated with green stem disorder insensitivity of soybean (*Glycine max* (L.) Merr.). *Breeding science*, 64(4), 331.

Yabe S, et al. (2014) Rapid genotyping with DNA micro-arrays for high-density linkage mapping and QTL mapping in common buckwheat (*Fagopyrum esculentum* Moench). *Breeding science*, 64(4), 291.