

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

POWERMARKER

RRID:SCR_009332

Type: Tool

Proper Citation

POWERMARKER (RRID:SCR_009332)

Resource Information

URL: <http://statgen.ncsu.edu/powermarker/>

Proper Citation: POWERMARKER (RRID:SCR_009332)

Description: A comprehensive set of statistical methods for genetic marker data analysis, designed especially for SSR/SNP data analysis. PowerMarker builds a powerful user interface around both new and traditional statistical methods for population genetic analysis. See analysis to check out the versatility of PowerMarker. PowerMarker is also a 2D Viewer - which was used intensively for visualizing linkage disequilibria results. (entry from Genetic Analysis Software)

Abbreviations: POWERMARKER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: POWERMARKER

Resource ID: SCR_009332

Alternate IDs: nlx_154544

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260905T133250+0000

Ratings and Alerts

No rating or validation information has been found for POWERMARKER.

No alerts have been found for POWERMARKER.

Data and Source Information

Usage and Citation Metrics

We found 639 mentions in open access literature.

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

Bilgen Y, et al. (2026) Unraveling genetic diversity in 'Fo?a' and 'Yomra' hazelnut accessions (*Corylus avellana* L.) using SSR markers and phenotypic analysis. Scientific reports, 16(1).

Zhang F, et al. (2026) Unveiling the genetic architecture of stripe rust resistance in wheat: a region-specific GWAS in Xinjiang, China. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(2), 51.

Prakash U, et al. (2026) Integrating morphological and molecular diversity to develop high-biomass fodder pearl millet composites. Frontiers in plant science, 17, 1767075.

Huang C, et al. (2026) Genome-Wide InDel Marker Development and Genetic Diversity Analysis of 52 Tomato Germplasm Accessions. Plants (Basel, Switzerland), 15(7).

Yang W, et al. (2026) Genetic diversity and core collection construction of glutinous rice landraces in 'He' cultivation zone of Guizhou using SSR sequencing. PloS one, 21(3), e0343623.

Wang H, et al. (2026) Development of KASP markers, SNP fingerprinting and population structure analysis of *Robinia pseudoacacia* and its closely related species. Frontiers in plant science, 17, 1761477.

Halilo?lu K, et al. (2026) Genetic diversity and population structure analysis of cotton (*Gossypium hirsutum* L.) genotypes using DArTseq technology. BMC genomics, 27(1).

Liu C, et al. (2026) Characterization of the genetic architecture of adult plant resistance to sharp eyespot in Chinese wheat germplasm. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(1), 38.

Li C, et al. (2026) Genetic diversity and population structure of the *Dermacentor nuttalli* in Northern China inferred from microsatellite markers. Parasites & vectors, 19(1).

Gao C, et al. (2026) Genomic divergence, introgression and KASP fingerprinting panel development in five cultivar groups of sweet osmanthus. BMC plant biology, 26(1).

Zhou K, et al. (2026) Core virome shapes adaptation of a phytopathogenic fungus to climate and cropping patterns. The ISME journal, 20(1).

Meheret F, et al. (2026) Genetic diversity and population structure in Ethiopian *Urochloa brizantha* genotypes uncovered using inter simple sequence repeat (ISSR) markers. PloS one, 21(1), e0340368.

Sztankóová Z, et al. (2026) Genetic Diversity and Population Structure Among Czech and Polish Goat Breeds Assessed Using Microsatellite Markers. *Animals : an open access journal from MDPI*, 16(11).

Gebre WT, et al. (2026) High-density single nucleotide polymorphism markers analysis reveals the genetic diversity and population structure in tropical highland maize (*Zea mays* L.) inbred lines. *PloS one*, 21(6), e0351845.

Huang M, et al. (2025) Genetic diversity, population structure and quality-trait associations in *Blumea balsamifera* revealed by EST-SSR markers. *PloS one*, 20(7), e0328403.

Tekle K, et al. (2025) RNA-Seq-based transcriptomics reveals differential gene expression between two *Pisum sativum* subspecies and uncovers their molecular marker profiles. *BMC genomics*, 27(1), 89.

Laribi M, et al. (2025) Genetic diversity and population structure of a core collection of Mediterranean durum wheat accessions using DArTseq markers. *BMC genomics*, 26(1), 1130.

Niu M, et al. (2025) Microsatellite and Mitochondrial COI Provide Novel Insights Into the Population Genetic Structure of White Prunicola Scale (*Pseudaulacaspis prunicola*) in China. *Ecology and evolution*, 15(1), e70865.

Galal AA, et al. (2025) Molecular diversity and genetic potential of new maize inbred lines across varying sowing conditions in arid environment. *Scientific reports*, 15(1), 2809.

Li Y, et al. (2025) Migration of wheat stripe rust from the primary oversummering region to neighboring regions in China. *Communications biology*, 8(1), 350.