Resource Summary Report

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POWERMARKER

RRID:SCR_009332
Type: Tool

Proper Citation

POWERMARKER (RRID:SCR_009332)

Resource Information

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

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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 resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: POWERMARKER

Resource ID: SCR_009332

Alternate IDs: nlx_154544

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250421T053726+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 607 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

Mekapogu M, et al. (2025) Evaluation of Genetic Diversity and Identification of Cultivars in Spray-Type Chrysanthemum Based on SSR Markers. Genes, 16(1).

Chi Y, et al. (2024) Population genetic variation and geographic distribution of suitable areas of Coptis species in China. Frontiers in plant science, 15, 1341996.

Yadav J, et al. (2024) Unravelling the novel genetic diversity and marker-trait associations of corn leaf aphid resistance in wheat using microsatellite markers. PloS one, 19(2), e0289527.

Yang W, et al. (2024) Utilizing SSR-based core collection development to improve conservation and utilization of Corylus L. genetic resources. PloS one, 19(10), e0312116.

Oladimeji JJ, et al. (2024) Extent and patterns of morphological and molecular genetic diversity and population structure of Nigerian Taro cultivars. BMC plant biology, 24(1), 1077.

Amouzoune M, et al. (2024) Genome wide association study of seedling and adult plant leaf rust resistance in two subsets of barley genetic resources. Scientific reports, 14(1), 15428.

Zewodu A, et al. (2024) Analysis of genetic diversity and population structure of some Ethiopian barley (Hordeum vulgare L.) accessions using SSR markers. PloS one, 19(6), e0305945.

Peng J, et al. (2024) Assessing population genetic structure and diversity and their driving factors in Phoebe zhennan populations. BMC plant biology, 24(1), 1091.

Ouma BO, et al. (2024) Integrating Morpho-Physiological, Biochemical, and Molecular

Genotyping for Selection of Drought-Tolerant Pigeon Pea (Cajanus cajan L.) Genotypes at Seedling Stage. Plants (Basel, Switzerland), 13(22).

Li F, et al. (2024) Assessing genetic diversity and geographical differentiation in a global collection of wild soybean (Glycine soja Sieb. et Zucc.) and assigning a mini-core collection. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(2).

Sehgal D, et al. (2024) Genomic wide association study and selective sweep analysis identify genes associated with improved yield under drought in Turkish winter wheat germplasm. Scientific reports, 14(1), 8431.

Zapata-Alvarez A, et al. (2024) Molecular, biochemical, and sensorial characterization of cocoa (Theobroma cacao L.) beans: A methodological pathway for the identification of new regional materials with outstanding profiles. Heliyon, 10(3), e24544.

Zhang S, et al. (2024) Identification and genetic diversity analysis of specific walnut F1 progeny based on SSR molecular markers: taking heart-shaped walnuts and Jinghong 1 as examples. Scientific reports, 14(1), 27869.

Diallo S, et al. (2024) Genetic diversity and population structure of cowpea mutant collection using SSR and ISSR molecular markers. Scientific reports, 14(1), 31833.

Di Pasquale GM, et al. (2024) Morphological and Genetic Characterization of Maize Landraces Adapted to Marginal Hills in North-West Italy. Plants (Basel, Switzerland), 13(7).

Brhane H, et al. (2024) Genetic diversity and population structure analysis of a diverse panel of pea (Pisum sativum). Frontiers in genetics, 15, 1396888.

Li C, et al. (2024) Genetic relationship analysis and core collection construction of Eucalyptus grandis from Dongmen improved variety base: the largest eucalypt germplasm resource in China. BMC plant biology, 24(1), 1240.

Azon CF, et al. (2024) Molecular Diversity and Agronomic Performance of Sesame (Sesamum indicum) Cultivars in Benin: Local Cultivars and Lines Introduced From China. Plant-environment interactions (Hoboken, N.J.), 5(6), e70024.