

Resource Summary Report

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GeneMarker

RRID:SCR_015661

Type: Tool

Proper Citation

GeneMarker (RRID:SCR_015661)

Resource Information

URL: <http://www.softgenetics.com/GeneMarker.php>

Proper Citation: GeneMarker (RRID:SCR_015661)

Description: Genotype analysis software which enhances the speed, accuracy, and ease of analysis. The software is an alternative to Applied BioSystems Genotyper®, GeneScan®, and other genotype analysis software.

Synonyms: GeneMarker: The Biologist Friendly Software

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: genotype, gene analysis

Availability: Commercially available, Trial available, Runs on Mac OS, Runs on Windows, Runs on Linux

Resource Name: GeneMarker

Resource ID: SCR_015661

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260912T195828+0000

Ratings and Alerts

No rating or validation information has been found for GeneMarker.

No alerts have been found for GeneMarker.

Data and Source Information

Usage and Citation Metrics

We found 1577 mentions in open access literature.

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

Braams M, et al. (2026) ABO: A 3D stroma-supported culture platform enabling full human B-lymphopoiesis for disease modeling and gene therapy development. *Cell reports. Medicine*, 7(7), 102879.

Fan PZ, et al. (2026) Genetic origins and climate-induced erosion in economically important Asian walnuts. *Conservation biology : the journal of the Society for Conservation Biology*, 40(1), e70125.

Hachizovu S, et al. (2026) Severe malaria treatment with rectal artesunate and artemisinin-based combination therapy in remote settings: an effectiveness-implementation hybrid type 3 study protocol (SEMA ReACT). *Malaria journal*, 25(1).

Zhong Y, et al. (2026) Elucidating the mechanism of thiosulfate oxidation by a novel two-component system SulRS in deep-sea *Campylobacterota*. *iScience*, 29(3), 114901.

Darmis F, et al. (2026) Evidence for Environment-Specific Pace-of-Life Syndromes. *Ecology and evolution*, 16(3), e73234.

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

Zeng G, et al. (2026) Divergence of mating systems in *Primula oreodoxa*: Insights from transplant experiments and mating portfolios. *Plant diversity*, 48(1), 169.

Yang L, et al. (2026) SSR-Based Genetic Diversity, Population Structure, and Marker-Trait Associations for Popping-Related Traits in Popcorn Germplasm. *Genes*, 17(6).

Gwon LW, et al. (2026) Optimizing twin prime editing components for scalable genome editing and therapy in spinocerebellar ataxia type 3. *Molecular therapy. Nucleic acids*, 37(3), 102988.

Kim Y, et al. (2026) High-resolution Chromosomal Microarray with Diagnostic Potential for Detecting Exon-level Copy Number Variations Using Targeted and Non-targeted Approaches. *Annals of laboratory medicine*, 46(2), 190.

Hou X, et al. (2026) Genetic legacy and recent cross of two ancient lineages underlie the rebound of the world's rarest primate. *Science advances*, 12(7), eadw3298.

Liu J, et al. (2026) Genetic diversity of *Schima superba* based on physiological traits and SSR markers. *PloS one*, 21(4), e0344465.

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).

Chen W, et al. (2026) The spindlin gene as a universal marker for molecular sex identification in different poultry species. *Poultry science*, 105(2), 106281.

Zhao Y, et al. (2026) Phenotypic and genotypic differences between bloodstream and non-blood *Candida krusei* isolates: implications for invasiveness and antifungal susceptibility. *Microbiology spectrum*, 14(1), e0260825.

Zhao C, et al. (2026) Genetic Structure of Populations of *Rhizoctonia solani* Anastomosis Group (AG)-2-IIIB and AG-4HGI Causing Sugar Beet Root Diseases in China. *Journal of fungi* (Basel, Switzerland), 12(2).

Píšová S, et al. (2026) Wide diversity in narrow geographic space: genetic, morphological and ploidy variation in three Central European *Crataegus* species with emphasis on their reproductive modes. *AoB PLANTS*, 18(1), plaf067.

Broschewitz L, et al. (2026) Microsatellite/SSR dataset: characterization of pear cultivars of the German Fruit Genebank. *Scientific data*, 13(1).

He X, et al. (2026) Development of Chloroplast Microsatellite Markers and Assessment of Genetic Diversity and Population Structure of *Sophora tonkinensis* Gagnep. in Southwestern China. *Current issues in molecular biology*, 48(6).

Shen Y, et al. (2026) Frequent origins and unidirectional gene-flow sustain cytotype coexistence in a mixed-ploidy species. *BMC plant biology*, 26(1).