# **Resource Summary Report**

Generated by NIF on Apr 19, 2025

## **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 processing software, data analysis software, software resource, software application

Keywords: genotype, gene analysis

**Funding:** 

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: 20250417T065529+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**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 1491 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Thavornkanlapachai R, et al. (2025) Diverged Populations Admixture Bolsters Genetic Diversity of a New Island Dibbler (Parantechinus apicalis) Population, but Does Not Prevent Subsequent Loss of Genetic Variation. Evolutionary applications, 18(1), e70073.

Lamperty T, et al. (2025) Defaunation Increases Clustering and Fine-Scale Spatial Genetic Structure in a Small-Seeded Palm Despite Remaining Small-Bodied Frugivores. Molecular ecology, 34(2), e17620.

Broschewitz L, et al. (2025) Microsatellite/SSR dataset: characterization of apple cultivars of the German Fruit Genebank. Scientific data, 12(1), 75.

Méndez-Vidal C, et al. (2025) A genomic strategy for precision medicine in rare diseases: integrating customized algorithms into clinical practice. Journal of translational medicine, 23(1), 86.

Chen H, et al. (2025) Identification of a novel butenolide signal system to regulate high production of tylosin in Streptomyces fradiae. Applied microbiology and biotechnology, 109(1), 18.

Fameli A, et al. (2025) Relatedness of White-Tailed Deer from Culling Efforts Within Chronic Wasting Disease Management Zones in Minnesota. Pathogens (Basel, Switzerland), 14(1).

Jia X, et al. (2025) Genome-wide microsatellite characterization and their marker development and transferability in Broussonetia Species. BMC genomics, 26(1), 61.

Zhou X, et al. (2024) Tremor-associated short tandem repeat intermediate and pathogenic expansions in familial essential tremor. Brain communications, 6(4), fcae217.

Li J, et al. (2024) Phylogeographic analysis reveals extensive genetic variation of native grass Elymus nutans (Poaceae) on the Qinghai-Tibetan plateau. Frontiers in plant science, 15, 1349641.

Albuja-Quintana M, et al. (2024) Preliminary insights of the genetic diversity and invasion

pathways of Cedrela odorata in the Galapagos Islands, Ecuador. Ecology and evolution, 14(7), e11723.

Andraca-Gómez G, et al. (2024) Climatic and soil characteristics account for the genetic structure of the invasive cactus moth Cactoblastis cactorum, in its native range in Argentina. PeerJ, 12, e16861.

Backes A, et al. (2024) Shades of white: The Petunia long corolla tube clade evolutionary history. Genetics and molecular biology, 47(1), e20230279.

Mao ML, et al. (2024) Isolation and characterisation of 17 microsatellite DNA loci from RAD reduced-representation genomes for Asian warty newts, genus Paramesotriton (Caudata: Salamandridae). Biodiversity data journal, 12, e113979.

Wang Q, et al. (2024) Paternity bias and cryptic female choice in chickens. Poultry science, 103(6), 103744.

Ouadhene MA, et al. (2024) Structure of Aspergillus flavus populations associated with maize in Greece, Spain, and Serbia: Implications for aflatoxin biocontrol on a regional scale. Environmental microbiology reports, 16(2), e13249.

Beránková D, et al. (2024) Striking variation in chromosome structure within Musa acuminata subspecies, diploid cultivars, and F1 diploid hybrids. Frontiers in plant science, 15, 1387055.

Hwang S, et al. (2024) Genotype-phenotype correlation of ocular von Hippel-Lindau disease in Koreans. PloS one, 19(10), e0311665.

Mwesigwa A, et al. (2024) Temporal changes in Plasmodium falciparum genetic diversity and multiplicity of infection across three areas of varying malaria transmission intensities in Uganda. Tropical medicine and health, 52(1), 103.

Yang Y, et al. (2024) Application of a Multiplex Ligation-Dependent Probe Amplification-Based Next-Generation Sequencing Approach for the Detection of Pathogenesis of Duchenne Muscular Dystrophy and Spinal Muscular Atrophy Caused by Copy Number Aberrations. Molecular neurobiology, 61(1), 200.

Liu C, et al. (2024) Genetic diversities in wild and cultivated populations of the two closely-related medical plants species, Tripterygium Wilfordii and T. Hypoglaucum (Celastraceae). BMC plant biology, 24(1), 195.