

Resource Summary Report

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GeneMapper

RRID:SCR_014290

Type: Tool

Proper Citation

GeneMapper (RRID:SCR_014290)

Resource Information

URL: <https://www.thermofisher.com/order/catalog/product/4475073>

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Description: Genotyping software package that provides DNA sizing and quality allele calls for all Applied Biosystems electrophoresis-based genotyping systems. GeneMapper specializes in multiapplication functionality, including amplified fragment length polymorphism, loss of heterozygosity, microsatellite, and SNP genotyping analysis. The software provides remote auto-analysis and command line operation, and allows for multiuser, client-server deployment.

Synonyms: , GeneMapper Software 5, GeneMapper Software 6, GeneMapper Software

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

Keywords: genotyping software, sequence analysis software, multiplication functionality, dna sizing, allele call, electrophoresis genotyping system

Availability: Restricted

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Alternate URLs: <https://www.thermofisher.com/order/catalog/product/de/en/4370784>, <https://www.thermofisher.com/document-connect/document-connect.html?url=https://assets.thermofisher.com/TFS-Assets%2FFLSG%2Fmanuals%2F4476603A.pdf>,

Old URLs:

<https://products.appliedbiosystems.com/ab/en/US/adirect/ab?cmd=catNavigate2&catID=600798&tab>

License URLs: <http://www.thermofisher.com/us/en/home/global/terms-and-conditions.html>

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260912T200016+0000

Ratings and Alerts

No rating or validation information has been found for GeneMapper .

No alerts have been found for GeneMapper .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5354 mentions in open access literature.

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

Manoukian P, et al. (2026) Estrogen Production in Pancreatic Cancer Shapes a Tumor-Suppressive Stromal Microenvironment. Cancer research, 86(3), 571.

Tun NNZ, et al. (2026) Low Testosterone in Men With Type 2 Diabetes: The Role of Estrogen Excess and Aromatase Activity. Clinical endocrinology, 104(4), 362.

Bonamici L, et al. (2026) Characterization of Copy Number Variants in Hereditary Cancer Patients Through NGS Shows a Distinctive PALB2 Contribution to the Diagnostic Yield. Human mutation, 2026, 6601291.

Trecourt A, et al. (2026) Primary Uterine Nongestational Placental Site Trophoblastic Tumor as a Distinct Entity: A Report of 5 Cases. The American journal of surgical pathology, 50(4), 435.

Lim MYT, et al. (2026) A programmable ribozyme for RNA signal transduction. Nature communications, 17(1), 1428.

Chen Z, et al. (2026) USP1 promotes hepatocellular carcinoma progression by modulating mitophagy via stabilizing MCM3 to regulate the Keap1-Nrf2 axis. iScience, 29(3), 114927.

Forsberg C, et al. (2026) In the trail of the crime scene dog: Processing of human DNA from outdoor samples. Forensic science international. Synergy, 12, 100664.

Eshetu FB, et al. (2026) A Century of Invasion: How Biosecurity Influenced Populations of Sirex noctilio and Its Fungal Symbiont in Australasia. Molecular ecology, 35(6), e70311.

Yang X, et al. (2026) Xq28 duplication not F8 inversion: integrated genetic reanalysis redefines prenatal carrier diagnosis. *Scientific reports*, 16(1).

Vural T, et al. (2026) Decomposition and medicolegal autopsy in geriatric in-home non-traumatic deaths: histopathological findings and a public health perspective. *BMC geriatrics*, 26(1).

Seto J, et al. (2026) Food poisoning from raw horse meat contaminated with Shiga toxin-producing *Escherichia coli* O157 linked to nationwide spread of closely related strains, Japan, 2023. *Microbiology spectrum*, 14(5), e0411525.

Alkaraki AK, et al. (2026) Genetic Diversity of 27 Y-STRs in Two Jordanian Subpopulations: Bedouins and Fellahin. *Genes*, 17(2).

Xin Y, et al. (2026) Development of a multiplex SNaPshot assay for simultaneous detection of multiple insecticide-resistance mutations in *Anopheles sinensis*. *Parasites & vectors*, 19(1).

Lee E, et al. (2026) Huntington's disease LIG1 modifier variant increases ligase fidelity and suppresses somatic CAG repeat expansion. *Proceedings of the National Academy of Sciences of the United States of America*, 123(10), e2518854123.

Arai H, et al. (2026) Linking genomic variation in *Spiroplasma* endosymbionts to male production and male-killing in the pea aphid. *BMC genomics*, 27(1).

Tian J, et al. (2026) Genetic diversity and breeding efficiency of a salt-tolerant strain of largemouth bass (*Micropterus salmoides*) revealed by microsatellite analysis and phenotypic evaluations. *Scientific reports*, 16(1).

Staadig A, et al. (2026) Swedish population data for 37 autosomal, 12 X-chromosomal and 23 Y-chromosomal STR loci. *International journal of legal medicine*, 140(4), 2041.

Roukoz-Diab Y, et al. (2026) Evaluation of the STANDARD M10 and Xpert C. difficile assays for the detection of toxigenic *Clostridioides difficile* in stools. *Microbiology spectrum*, 14(6), e0347025.

Ordoñez KM, et al. (2026) *Wickerhamomyces anomalus* Fungemia during Healthcare-Associated Outbreak, Pereira, Colombia, 2025. *Emerging infectious diseases*, 32(6), 941.

Dolande-Franco M, et al. (2026) Outbreak of *Wickerhamomyces anomalus* (formerly *Candida pelliculosa*) Bloodstream Infections, Venezuela, 2022-2023. *Emerging infectious diseases*, 32(6), 933.