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, software application, software resource, sequence analysis software, data processing software

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

Availability: Restricted

Resource Name: GeneMapper

Resource ID: SCR_014290

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%2FLSG%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

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Record Last Update: 20260801T042730+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 5231 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

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.

Mearelli M, et al. (2026) C9orf72 Repeat Expansion Induces Metabolic Dysfunction in Human iPSC-Derived Microglia and Modulates Glial-Neuronal Crosstalk. Glia, 74(1), e70080.

Su R, et al. (2026) Early screening, diagnosis and recurrence monitoring of hepatocellular carcinoma in patients with chronic hepatitis B based on serum N-glycomics analysis: A cohort study. Hepatology (Baltimore, Md.), 83(1), 40.

Chen KH, et al. (2025) Mapping fitness landscapes to interpret sex allocation in hermaphrodites. Current biology : CB, 35(10), 2354.

D'Ignazio L, et al. (2025) A hexamer tandem repeat RNA embedded within an SVA retrotransposon drives R-loop formation and neurodegeneration. Cell reports, 44(7), 115812.

I??k Kalpar R, et al. (2025) Microsatellite-based genetic diversity and population structure of local goat breeds in Cyprus. Research in veterinary science, 200, 106033.

Maza AM, et al. (2025) MSH3 is a genetic modifier of somatic repeat instability in X-linked dystonia parkinsonism. bioRxiv : the preprint server for biology.

Iwasaki Y, et al. (2025) Bidirectional disruption of GNAS transcripts causes broad methylation defects in pseudohypoparathyroidism type 1B. Proceedings of the National

Academy of Sciences of the United States of America, 122(16), e2423271122.

Awata D, et al. (2025) Circular RNA profiling identifies circ_0001522, circ_0001278, and circ_0001801 as predictors of unfavorable prognosis and drivers of triple-negative breast cancer hallmarks. Cell death discovery, 11(1), 316.

Zheng F, et al. (2025) Ecological Isolation Maintains the Species Boundaries Between Two Sympatric Cycas From Southwest China. Ecology and evolution, 15(7), e71769.

Wang H, et al. (2025) Diagnostic yield of expanded carrier screening of a multi-ethnic population in yunnan, China. Scientific reports, 15(1), 23590.

Zhen X, et al. (2025) Parallel sequencing of 170 STR and 132 SNP markers using the FGID forensic four-in-one DNA typing kit on the DNBSEQ-G99RS platform. Forensic sciences research, 10(3), owae050.

Wei R, et al. (2025) Analysis of chromosomal aberrations in early pregnancy loss using high-throughput ligation-dependent probe amplification and single tandem repeats. Molecular cytogenetics, 18(1), 19.

Vychodilova L, et al. (2025) Genetic susceptibility to sarcoid in Arabian horses: associations with MHC class II and compound MHC class I/KLRA genotypes. Veterinary research communications, 49(3), 184.

da Costa AJM, et al. (2025) Analysis of genomic ancestry and characterization of a new variant in MPS type VII. Orphanet journal of rare diseases, 20(1), 198.

Siavrien? E, et al. (2025) A novel missense variant at the site of interaction between RLIM and E2 ubiquitin-conjugating enzymes causes Tønne-Kalscheuer syndrome. BMC pediatrics, 25(1), 797.

Nieminen TT, et al. (2025) Non-truncating BMPR1A variants associated with familial colorectal cancer and adenomatous polyps. BMC cancer, 25(1), 1435.

Lee E, et al. (2025) Huntington's disease LIG1 modifier variant increases ligase fidelity and suppresses somatic CAG repeat expansion. bioRxiv : the preprint server for biology.

Varella K, et al. (2025) Genetic analysis of Schistosoma mansoni in a low-transmission area in Brazil suggests population sharing between wild-hosts and humans and geographical isolation. PLoS neglected tropical diseases, 19(8), e0013379.

Xu X, et al. (2025) Molecular epidemiology of Nakaseomyces glabrata associated with vulvovaginal candidiasis revealed high genetic variability and the presence of novel genotypes in China. Virulence, 16(1), 2543058.