

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

[mrFAST](#)

RRID:SCR_005487

Type: Tool

Proper Citation

mrFAST (RRID:SCR_005487)

Resource Information

URL: <http://mrfast.sourceforge.net/>

Proper Citation: mrFAST (RRID:SCR_005487)

Description: Software designed to map short reads generated with the Illumina platform to reference genome assemblies; in a fast and memory-efficient manner. Currently Supported Features: * Output in SAM format * Indels up to 8 bp (4 bp deletions and 4 bp insertions) * Paired-end mapping ** Discordant option to generate mapping file ready for VariationHunter to detect structural variants. * One end anchored (OEA) map locations for novel sequence insertion detection with NovelSeq * Matepair library mapping (long inserts with RF orientation). Planned Features: * Multithreading

Abbreviations: mrFAST

Synonyms: mrFAST - Micro Read Fast Alignment Search Tool, Micro Read Fast Alignment Search Tool

Resource Type: software resource

Defining Citation: [PMID:19718026](#)

Keywords: next-generation sequencing, bio.tools

Resource Name: mrFAST

Resource ID: SCR_005487

Alternate IDs: biotools:mrfast, OMICS_00671

Alternate URLs: <https://bio.tools/mrfast>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260905T132536+0000

Ratings and Alerts

No rating or validation information has been found for mrFAST.

No alerts have been found for mrFAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Lopez JO, et al. (2024) Improved LINE-1 Detection through Pattern Matching by Increasing Probe Length. *Biology*, 13(4).

Aversano R, et al. (2024) Distinct structural variants and repeat landscape shape the genomes of the ancient grapes Aglianico and Falanghina. *BMC plant biology*, 24(1), 88.

Nuttle X, et al. (2024) Parallelized engineering of mutational models using piggyBac transposon delivery of CRISPR libraries. *Cell reports methods*, 4(1), 100672.

Warren WC, et al. (2018) Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. *Nature ecology & evolution*, 2(4), 669.

Zhernakova DV, et al. (2018) Analytical "bake-off" of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. *PloS one*, 13(7), e0200423.

Kim JS, et al. (2018) GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. *BMC genomics*, 19(Suppl 2), 89.

Serres-Armero A, et al. (2017) Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. *BMC genomics*, 18(1), 977.

Hintzsche JD, et al. (2016) A Survey of Computational Tools to Analyze and Interpret Whole Exome Sequencing Data. *International journal of genomics*, 2016, 7983236.

Drozdova PB, et al. (2016) Genome Sequencing and Comparative Analysis of *Saccharomyces cerevisiae* Strains of the Peterhof Genetic Collection. *PloS one*, 11(5), e0154722.

Rubin BE, et al. (2016) Comparative genomics reveals convergent rates of evolution in ant-plant mutualisms. *Nature communications*, 7, 12679.

Dobrynin P, et al. (2015) Genomic legacy of the African cheetah, *Acinonyx jubatus*. *Genome biology*, 16, 277.

Zhuang J, et al. (2014) TEMP: a computational method for analyzing transposable element polymorphism in populations. *Nucleic acids research*, 42(11), 6826.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. *Frontiers in genetics*, 5, 192.

Miyake K, et al. (2013) Comparison of Genomic and Epigenomic Expression in Monozygotic Twins Discordant for Rett Syndrome. *PloS one*, 8(6), e66729.

Itsara A, et al. (2012) Resolving the breakpoints of the 17q21.31 microdeletion syndrome with next-generation sequencing. *American journal of human genetics*, 90(4), 599.

Kidd JM, et al. (2010) A human genome structural variation sequencing resource reveals insights into mutational mechanisms. *Cell*, 143(5), 837.