

Resource Summary Report

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mrsFAST

RRID:SCR_003128

Type: Tool

Proper Citation

mrsFAST (RRID:SCR_003128)

Resource Information

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

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Description: A cache-oblivious algorithm designed to map short reads to reference genome assemblies in a fast and memory-efficient manner. It optimizes cache usage to get higher performance. Currently Supported Features: * Mismatches, No indels * Paired-end Mapping Mode * Discordant Paired-end Mapping Mode (to be used in conjunction with Variation Hunter)

Abbreviations: mrsFAST

Synonyms: mrsFAST: micro-read substitution-only Fast Alignment Search Tool, micro-read substitution-only Fast Alignment Search Tool

Resource Type: software resource

Defining Citation: [PMID:20676076](#)

Keywords: next-generation sequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: mrsFAST

Resource ID: SCR_003128

Alternate IDs: biotools:mrsfast, nlx_156780

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

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260821T193654+0000

Ratings and Alerts

No rating or validation information has been found for mrsFAST.

No alerts have been found for mrsFAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Scheer K, et al. (2026) Rapid adaptive increase of amylase gene copy number in Indigenous Andeans. *Nature communications*, 17(1).

Abuelanin M, et al. (2026) Single-library chromosome-scale diploid assemblies of vole genomes resolve a species-specific duplication implicated in pair bonding. *bioRxiv* : the preprint server for biology.

Nguyen AK, et al. (2024) Duplications and Retrogenes Are Numerous and Widespread in Modern Canine Genomic Assemblies. *Genome biology and evolution*, 16(7).

Porubsky D, et al. (2023) Gaps and complex structurally variant loci in phased genome assemblies. *Genome research*, 33(4), 496.

Batcher K, et al. (2023) Ancient segmentally duplicated LCORL retrocopies in equids. *PloS one*, 18(6), e0286861.

Noyes MD, et al. (2022) Familial long-read sequencing increases yield of de novo mutations. *American journal of human genetics*, 109(4), 631.

Hsieh P, et al. (2021) Evidence for opposing selective forces operating on human-specific duplicated TCAF genes in Neanderthals and humans. *Nature communications*, 12(1), 5118.

Cantsilieris S, et al. (2020) An evolutionary driver of interspersed segmental duplications in primates. *Genome biology*, 21(1), 202.

Maggiolini FAM, et al. (2020) Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. *Genome research*, 30(11), 1680.

Bi WX, et al. (2019) Sinopyrophorinae, a new subfamily of Elateridae (Coleoptera, Elateroidea) with the first record of a luminous click beetle in Asia and evidence for multiple origins of bioluminescence in Elateridae. *ZooKeys*, 864, 79.

Kruger AN, et al. (2019) A Neofunctionalized X-Linked Ampliconic Gene Family Is Essential for Male Fertility and Equal Sex Ratio in Mice. *Current biology : CB*, 29(21), 3699.

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

Dougherty ML, et al. (2017) The birth of a human-specific neural gene by incomplete duplication and gene fusion. *Genome biology*, 18(1), 49.

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.

Peter B, et al. (2016) Genetic Candidate Variants in Two Multigenerational Families with Childhood Apraxia of Speech. *PloS one*, 11(4), e0153864.

Paudel Y, et al. (2015) Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. *BMC genomics*, 16(1), 330.

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

Forni D, et al. (2015) Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. *BMC genomics*, 16, 891.

, et al. (2015) Copy number variant analysis from exome data in 349 patients with epileptic encephalopathy. *Annals of neurology*, 78(2), 323.

Huddleston J, et al. (2014) Reconstructing complex regions of genomes using long-read sequencing technology. *Genome research*, 24(4), 688.