Resource Summary Report

Generated by kravitz2 on Aug 1, 2026

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: * Mistmatches, No indels * Paired-end Mapping Mode * Discordant Paired-end Mapping Mode (to be used in conjuction 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: 20260725T190537+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 20 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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

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

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

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.

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

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

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

Steinberg KM, et al. (2014) Single haplotype assembly of the human genome from a hydatidiform mole. Genome research, 24(12), 2066.

Giannuzzi G, et al. (2013) Hominoid fission of chromosome 14/15 and the role of segmental duplications. Genome research, 23(11), 1763.