Resource Summary Report

Generated by RRID on Apr 28, 2025

SAMBLASTER

RRID:SCR_000468
Type: Tool

Proper Citation

SAMBLASTER (RRID:SCR_000468)

Resource Information

URL: https://github.com/GregoryFaust/samblaster

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Description: Software tool to mark duplicates and extract discordant and split reads from SAM files. This fast and flexible program for marking duplicates in read-id grouped paired-end SAM files can also optionally output discordant read pairs and/or split read mappings to separate SAM files, and/or unmapped/clipped reads to a separate FASTQ file. When marking duplicates, samblaster will require approximately 20MB of memory per 1M read pairs.

Resource Type: software resource

Defining Citation: PMID:24812344, DOI:10.1093/bioinformatics/btu314

Keywords: standalone software, c++, bio.tools

Funding:

Availability: MIT License

Resource Name: SAMBLASTER

Resource ID: SCR_000468

Alternate IDs: biotools:samblaster, OMICS_04682

Alternate URLs: https://bio.tools/samblaster, https://sources.debian.org/src/samblaster/

Record Creation Time: 20220129T080201+0000

Record Last Update: 20250420T013949+0000

Ratings and Alerts

No rating or validation information has been found for SAMBLASTER.

No alerts have been found for SAMBLASTER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Ferguson S, et al. (2024) Exploring the role of polymorphic interspecies structural variants in reproductive isolation and adaptive divergence in Eucalyptus. GigaScience, 13.

Booms A, et al. (2024) Parkinson's disease risk enhancers in microglia. iScience, 27(2), 108921.

Chomiak AA, et al. (2024) Select EZH2 inhibitors enhance viral mimicry effects of DNMT inhibition through a mechanism involving NFAT:AP-1 signaling. Science advances, 10(13), eadk4423.

Fuller T, et al. (2023) A reference assembly for the legume cover crop hairy vetch (Vicia villosa). GigaByte (Hong Kong, China), 2023, gigabyte98.

Griger J, et al. (2023) An integrated cellular and molecular model of gastric neuroendocrine cancer evolution highlights therapeutic targets. Cancer cell, 41(7), 1327.

Herliana L, et al. (2023) A chromosome-level genome assembly of Plantago ovata. Scientific reports, 13(1), 1528.

Aivalioti MM, et al. (2022) PU.1-Dependent Enhancer Inhibition Separates Tet2-Deficient Hematopoiesis from Malignant Transformation. Blood cancer discovery, 3(5), 444.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. GigaScience, 12.

Beale HC, et al. (2021) The case for using mapped exonic non-duplicate reads when

reporting RNA-sequencing depth: examples from pediatric cancer datasets. GigaScience, 10(3).

Brandies PA, et al. (2020) The first Antechinus reference genome provides a resource for investigating the genetic basis of semelparity and age-related neuropathologies. GigaByte (Hong Kong, China), 2020, gigabyte7.

Chen H, et al. (2020) Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs. GigaScience, 9(3).

Gabriel AAG, et al. (2020) A molecular map of lung neuroendocrine neoplasms. GigaScience, 9(11).

Barbosa M, et al. (2018) Identification of rare de novo epigenetic variations in congenital disorders. Nature communications, 9(1), 2064.

Aneichyk T, et al. (2018) Dissecting the Causal Mechanism of X-Linked Dystonia-Parkinsonism by Integrating Genome and Transcriptome Assembly. Cell, 172(5), 897.

Moriwaki M, et al. (2017) POLR2C Mutations Are Associated With Primary Ovarian Insufficiency in Women. Journal of the Endocrine Society, 1(3), 162.