Resource Summary Report

Generated by T1D on Sep 5, 2026

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

Availability: Free, Available for download, Freely available

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/

License: MIT License

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260903T234341+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 19 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. GigaScience, 14.

Liu Y, et al. (2025) DNA hypomethylation promotes UHRF1-and SUV39H1/H2-dependent crosstalk between H3K18ub and H3K9me3 to reinforce heterochromatin states. Molecular cell, 85(2), 394.

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in Bos indicus. Journal of animal science and biotechnology, 16(1), 21.

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.

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

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

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

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

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

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

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

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.