

Resource Summary Report

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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: 20260725T190446+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 18 mentions in open access literature.

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

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.

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.

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.

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.

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.