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: MIT License

Resource Name: SAMBLASTER

Resource ID: SCR_000468

Alternate IDs: biotools:samblaster, OMICS_04682


Record Creation Time: 20220129T080201+0000

Record Last Update: 20240424T182710+0000
**Ratings and Alerts**

No rating or validation information has been found for SAMBLASTER.

No alerts have been found for SAMBLASTER.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 13 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](http://FDI-Lab-SiCruench.org).


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


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.


