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: A 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: Resource, software resource

References: PMID:24812344

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

Parent Organization: University of Virginia; Virginia; USA

Availability: MIT License

Website Status: Last checked up

Resource Name: SAMBLASTER

Resource ID: SCR_000468

Alternate IDs: OMICS_04682, biotools:samblaster

Alternate URLs: https://bio.tools/samblaster
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 4 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


