## SAMBLASTER

**RRID:** SCR_000468  
**Type:** Tool

### Proper Citation

SAMBLASTER (RRID:SCR_000468)

### Resource Information

**URL:** [https://github.com/GregoryFaust/samblaster](https://github.com/GregoryFaust/samblaster)

**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 Name:** SAMBLASTER  
**Proper Citation:** SAMBLASTER (RRID:SCR_000468)  
**Resource Type:** Resource, software resource  
**Keywords:** standalone software, c++  
**Resource ID:** SCR_000468  
**Parent Organization:** University of Virginia; Virginia; USA

**References:** [PMID: 24812344](https://www.ncbi.nlm.nih.gov/pubmed/24812344)

**Availability:** MIT License  
**Website Status:** Last checked up

**Alternate IDs:** OMICS_04682

**Mentions Count:** 4
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 Infrastructure](https://www.fdlab.org/scicrunch).


