

# Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

## Hadoop-BAM

RRID:SCR\_005516

Type: Tool

---

### Proper Citation

Hadoop-BAM (RRID:SCR\_005516)

---

### Resource Information

**URL:** <http://sourceforge.net/projects/hadoop-bam/>

**Proper Citation:** Hadoop-BAM (RRID:SCR\_005516)

**Description:** A Java library for the manipulation of files in common bioinformatics formats using the Hadoop MapReduce framework with the Picard SAM JDK, and command line tools similar to SAMtools. The file formats currently supported are BAM, SAM, FASTQ, FASTA, QSEQ, BCF, and VCF.

**Abbreviations:** Hadoop-BAM

**Resource Type:** software library, software resource, software toolkit

**Defining Citation:** [PMID:22302568](#)

**Keywords:** mapreduce/hadoop, java, next generation sequencing data, cloud

**Availability:** MIT License

**Resource Name:** Hadoop-BAM

**Resource ID:** SCR\_005516

**Alternate IDs:** OMICS\_01051

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20260912T200011+0000

---

### Ratings and Alerts

No rating or validation information has been found for Hadoop-BAM.

No alerts have been found for Hadoop-BAM.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 7 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Wiewiórka M, et al. (2023) Cloud-native distributed genomic pileup operations. *Bioinformatics* (Oxford, England), 39(1).

Maarala AI, et al. (2021) Distributed hybrid-indexing of compressed pan-genomes for scalable and fast sequence alignment. *PloS one*, 16(8), e0255260.

Tahir M, et al. (2020) A Fast and Scalable Workflow for SNPs Detection in Genome Sequences Using Hadoop Map-Reduce. *Genes*, 11(2).

Expósito RR, et al. (2018) HSRA: Hadoop-based spliced read aligner for RNA sequencing data. *PloS one*, 13(7), e0201483.

Decap D, et al. (2017) Halvade-RNA: Parallel variant calling from transcriptomic data using MapReduce. *PloS one*, 12(3), e0174575.

Yu P, et al. (2016) Single-cell Transcriptome Study as Big Data. *Genomics, proteomics & bioinformatics*, 14(1), 21.

Decap D, et al. (2015) Halvade: scalable sequence analysis with MapReduce. *Bioinformatics* (Oxford, England), 31(15), 2482.