

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

[sambamba](#)

RRID:SCR_024328

Type: Tool

Proper Citation

sambamba (RRID:SCR_024328)

Resource Information

URL: <https://github.com/biod/sambamba>

Proper Citation: sambamba (RRID:SCR_024328)

Description: Software tools for working with SAM/BAM data

Resource Type: software resource, software toolkit

Defining Citation: [PMID:25697820](#)

Keywords: working with SAM/BAM data,

Availability: Free, Available for download, Freely available,

Resource Name: sambamba

Resource ID: SCR_024328

Alternate IDs: OMICS_07586

Alternate URLs: <https://sources.debian.org/src/sambamba/>

License: GPL-2.0 license

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T042921+0000

Ratings and Alerts

No rating or validation information has been found for sambamba.

No alerts have been found for sambamba.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Patel UA, et al. (2026) CRISPR Screen Identifies HDAC3 as a Novel Radiosensitizing Target in Small Cell Lung Cancer. *Molecular cancer therapeutics*, 25(1), 183.

Xu Y, et al. (2026) From degraded to deciphered: Applying ATAC-seq to forensic molecular diagnosis under degradation conditions. *Forensic science international*, 379, 112789.

Nayarisseri A, et al. (2025) Whole genome sequence of petroleum hydrocarbon degrading novel strain *Microbacter* sp. EMBS2025 isolated from Chilika Lake, Odisha, India. *Scientific reports*, 15(1), 27961.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (*Leuciscidae*: *Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

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.

Kuklin A, et al. (2025) An Nrf2-NF- κ B Crosstalk Controls Hepatocyte Proliferation in the Normal and Injured Liver. *Cellular and molecular gastroenterology and hepatology*, 19(7), 101480.

Muffels IJJ, et al. (2025) Imaging flow cytometry-based cellular screening elucidates pathophysiology in individuals with Variants of Uncertain Significance. *Genome medicine*, 17(1), 12.

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. *Cancer discovery*, 15(6), 1203.

Struys I, et al. (2025) Prenatal Exposure to Chemotherapy Increases the Mutation Burden in Human Neonatal Hematopoietic Stem Cells. *Cancer discovery*, 15(5), 903.

Wu J, et al. (2025) Cell-free DNA testing for the detection and prognosis prediction of pancreatic cancer. *Nature communications*, 16(1), 6645.

Song C, et al. (2025) Chromatin accessibility and differentially expressed genes profiling in large yellow croaker (*Larimichthys crocea*) head kidney cells following iridovirus infection. *Frontiers in immunology*, 16, 1513966.

Jang H, et al. (2025) Structure and evolution of the Forsythieae genome elucidated by chromosome-level genome comparison of *Abeliophyllum distichum* and *Forsythia ovata* (Oleaceae). *Communications biology*, 8(1), 254.

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Humblin E, et al. (2025) The costimulatory molecule ICOS limits memory-like properties and function of exhausted PD-1+CD8+ T cells. *Immunity*, 58(8), 1966.

Wang C, et al. (2024) High-depth whole-genome sequencing identifies structure variants, copy number variants and short tandem repeats associated with Parkinson's disease. *NPJ Parkinson's disease*, 10(1), 134.

Harsono IW, et al. (2024) IDeRare: a lightweight and extensible open-source phenotype and exome analysis pipeline for germline rare disease diagnosis. *JAMIA open*, 7(2), ooae052.

Deng Y, et al. (2024) Neuronal miR-9 promotes HSV-1 epigenetic silencing and latency by repressing Oct-1 and One-cut family genes. *Nature communications*, 15(1), 1991.

Xiao Y, et al. (2024) Integrative Single Cell Atlas Revealed Intratumoral Heterogeneity Generation from an Adaptive Epigenetic Cell State in Human Bladder Urothelial Carcinoma. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(24), e2308438.

Pan JN, et al. (2024) AcornHRD: an HRD algorithm highly associated with anthracycline-based neoadjuvant chemotherapy in breast cancer in China. *European journal of medical research*, 29(1), 366.

Nebenführ M, et al. (2024) High-speed whole-genome sequencing of a Whippet: Rapid chromosome-level assembly and annotation of an extremely fast dog's genome. *GigaByte* (Hong Kong, China), 2024, gigabyte134.