

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 10, 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 toolkit, software resource

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: 20260810T040826+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 59 mentions in open access literature.

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

Müller J, et al. (2026) GLYATL1 is associated with metabolic and epigenetic changes and with endocrine resistance in luminal breast cancer. *Clinical epigenetics*, 18(1).

Abdolmaleki A, et al. (2026) Superabsorbent polymers seed coatings modulate transcriptomic and physiological responses to drought in rapeseed. *Frontiers in plant science*, 17, 1711479.

Abdolmaleki A, et al. (2026) Transcriptomic and physiological effects of superabsorbent polymer seed coating on maize under drought stress. *Frontiers in plant science*, 17, 1736004.

Nie Y, et al. (2026) Identification of sex chromosome, sex-biased gene expression and dosage compensation in the pygmy mole cricket *Xya riparia* (Orthoptera: Tridactyloidea). *BMC genomics*, 27(1).

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.

Adams NM, et al. (2026) Chromatin-mediated anticipatory control of type I interferon production in plasmacytoid dendritic cells. *Immunity*, 59(2), 270.

Ding C, et al. (2026) Glioblastoma-Secreted C1QL1 Orchestrates Tumor Microtubule Expansion and Neural Synaptic Pruning to Drive Malignant Synapse Formation and Recurrence. *Cancer discovery*, 16(6), 1176.

Wong H, et al. (2026) An Analytic Framework Characterizes the Biological Processes That Shape Copy Number-Based Genome Instability Patterns in Breast Cancer. *Cancer research*, 86(13), 3344.

Zhang L, et al. (2026) Bcl11a orchestrates multilineage integrity in aging hematopoiesis by regulating multipotent progenitor fate decisions. *Cell reports*, 45(7), 117716.

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.

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.

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.

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.

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.

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.

Gambardella G, et al. (2025) Joint processing of long- and short-read sequencing data with deep learning improves variant calling. *Cell reports methods*, 5(7), 101107.

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.