Resource Summary Report

Generated by NIF on Apr 27, 2025

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,

Funding:

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: 20250425T060605+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 30 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

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.

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.

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.

Silveira AB, et al. (2024) Base-excision repair pathway shapes 5-methylcytosine deamination signatures in pan-cancer genomes. Nature communications, 15(1), 9864.

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.

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.

He Q, et al. (2024) A genome-wide association study of neonatal metabolites. Cell genomics, 4(10), 100668.

Shen Y, et al. (2024) Genomic insights into endangerment and conservation of the garlic-fruit

tree (Malania oleifera), a plant species with extremely small populations. GigaScience, 13.

Knickmann J, et al. (2024) A simple method for rapid cloning of complete herpesvirus genomes. Cell reports methods, 4(2), 100696.

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish Entelurus aequoreus (Syngnathiformes: Syngnathidae). GigaByte (Hong Kong, China), 2024, gigabyte105.

Jang H, et al. (2024) Chromosome-level assemblies of the endemic Korean species Abeliophyllum distichum and Forsythia ovata. Scientific data, 11(1), 1372.

Yang YX, et al. (2024) The chromosome-level genome assembly of an endangered herb Bergenia scopulosa provides insights into local adaptation and genomic vulnerability under climate change. GigaScience, 13.

Wang C, et al. (2024) Next-generation variant exon screening: Moving forward in routine genetic disease investigations. Genetics in medicine open, 2, 101816.

Li M, et al. (2024) From degraded to deciphered: ATAC-seq's application potential in forensic diagnosis. International journal of legal medicine.

Lian Q, et al. (2023) Meiotic recombination is confirmed to be unusually high in the fission yeast Schizosaccharomyces pombe. iScience, 26(9), 107614.

Li G, et al. (2023) Integrative genomic analyses of promoter G-quadruplexes reveal their selective constraint and association with gene activation. Communications biology, 6(1), 625.

Brace S, et al. (2022) Genomes from a medieval mass burial show Ashkenazi-associated hereditary diseases pre-date the 12th century. Current biology : CB, 32(20), 4350.

Li Z, et al. (2022) Deciphering the distinct transcriptomic and gene regulatory map in adult macaque basal ganglia cells. GigaScience, 12.