Resource Summary Report

Generated by SPARC SAWG on Jul 29, 2026

pysam

RRID:SCR_021017
Type: Tool

Proper Citation

pysam (RRID:SCR_021017)

Resource Information

URL: https://pysam.readthedocs.io/en/latest/api.html

Proper Citation: pysam (RRID:SCR_021017)

Description: Software tool as interface for reading and writing SAM files. Python module to read and manipulate mapped short read sequence data stored in SAM/BAM files. Lightweight wrapper of htslib C-API.

Resource Type: software toolkit, software resource

Keywords: Interface, reading SAM files, writing SAM files, mapped short read sequence data, htslib C-API wrapper, SAM/BAM files

Availability: Free, Available for download, Freely available

Resource Name: pysam

Resource ID: SCR_021017

Alternate URLs: https://github.com/pysam-developers/pysam

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260729T044505+0000

Ratings and Alerts

No rating or validation information has been found for pysam.

No alerts have been found for pysam.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 122 mentions in open access literature.

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

Calderón-Osorno M, et al. (2025) The influence of depth on the global deep-sea plasmidome. Scientific reports, 15(1), 2959.

Seluzicki CM, et al. (2025) Regulation of translation elongation and integrated stress response in heat-shocked neurons. Cell reports, 44(5), 115639.

Viscardi MJ, et al. (2025) Endonucleolytic cleavage is the primary mechanism of decay elicited by C. elegans nonsense-mediated mRNA decay. Genome research, 35(6), 1337.

Kshatriya S, et al. (2025) TaRTLEt: Transcriptionally-active Riboswitch Tracer Leveraging Edge deTection. PeerJ, 13, e19418.

González A, et al. (2025) Multi-omic assessment of mRNA translation dynamics in liver cancer cell lines. Scientific data, 12(1), 1520.

Wenson L, et al. (2025) Precise mapping of single-stranded DNA breaks by sequence-templated erroneous DNA polymerase end-labelling. Nature communications, 16(1), 7130.

Schneider PG, et al. (2025) BEscreen: a versatile toolkit to design base editing libraries. Nucleic acids research, 53(W1), W68.

Webb MG, et al. (2025) Resolving spatial subclonal genomic heterogeneity of loss of heterozygosity and extrachromosomal DNA in gliomas. Nature communications, 16(1), 5290.

Kim JW, et al. (2025) Pairwise analysis of plasma cell-free DNA before and after palliative second-line paclitaxel plus ramucirumab treatment in patients with metastatic gastric cancer. Gastric cancer : official journal of the International Gastric Cancer Association and the Japanese Gastric Cancer Association, 28(4), 620.

Vendrell-Fernández S, et al. (2025) Incomplete lytic cycle of a widespread Bacteroides bacteriophage leads to the formation of defective viral particles. PLoS biology, 23(3), e3002787.

Momen-Roknabadi A, et al. (2025) Detection of Early-Stage Colorectal Cancer Using Cell-Free oncRNA Biomarkers and Artificial Intelligence. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(15), 3229.

Ho DV, et al. (2025) Ancestral Chromosome-Level Assemblies Reveal Posthybridization Genome Evolution in the New Mexico Whiptail Lizard (Aspidoscelis neomexicanus). Genome biology and evolution, 17(12).

Kolling FW, et al. (2025) Multi-site Assessment of Methods for Cell Preservation Upstream of Single Cell RNA Sequencing. bioRxiv : the preprint server for biology.

Van Deynze K, et al. (2025) Enhanced detection and genotyping of disease-associated tandem repeats using HMMSTR and targeted long-read sequencing. Nucleic acids research, 53(2).

Fonzino A, et al. (2025) REDInet: a temporal convolutional network-based classifier for A-to-I RNA editing detection harnessing million known events. Briefings in bioinformatics, 26(2).

Rubanova N, et al. (2025) An endogenous retroviral element co-opts an upstream regulatory sequence to achieve somatic expression and mobility. Nucleic acids research, 53(11).

Cuenca-Guardiola J, et al. (2025) Advanced analysis of retrotransposon variation in the human genome with nanopore sequencing using RetroInspector. Scientific reports, 15(1), 14489.

Guo Z, et al. (2025) Enhanced detection of RNA modifications in Escherichia coli utilizing direct RNA sequencing. Cell reports methods, 5(9), 101168.

Nesta A, et al. (2025) Alternative splicing of transposable elements in human breast cancer. Mobile DNA, 16(1), 6.

Dunker-Seidler F, et al. (2025) Recombinant AAV batch profiling by nanopore sequencing elucidates product-related DNA impurities and vector genome length distribution. Molecular therapy. Methods & clinical development, 33(1), 101417.