

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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 resource, software toolkit

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: 20260905T133306+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

Usage and Citation Metrics

We found 164 mentions in open access literature.

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

Wäneskog M, et al. (2026) High-throughput methods enabling random duplications, deletions, or nucleotide-constrained mutagenesis of entire DNA motifs. *Nucleic acids research*, 54(6).

Chen L, et al. (2026) Animal-associated jumbo phages as widespread and active modulators of gut microbiome ecology and metabolism. *Science advances*, 12(6), eaeb6265.

Pastore S, et al. (2026) Mapping human pre-rRNA processing and modification at single nucleotide resolution using long read nanopore sequencing. *Nature communications*, 17(1).

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Hallast P, et al. (2026) Population-scale Y chromosome assemblies reveal recurrent remodeling within constrained architectures. *bioRxiv : the preprint server for biology*.

Rishik S, et al. (2026) SmallBARN 2026: a kingdom-wide bacterial sRNA resource. *Nucleic acids research*, 54(D1), D342.

Engin B, et al. (2026) Atlas of HIV cis-regulatory elements reveals extensive transcriptional variation across clades, isolates, and within individuals. *bioRxiv : the preprint server for biology*.

Jeong R, et al. (2026) Functional analysis of NPR2 variants supports the therapeutic rationale for CNP in short stature. *American journal of human genetics*, 113(1), 117.

Bucher P, et al. (2026) CAR-adapted PIK3CD base editing enhances T cell anti-tumor potency. *Nature cancer*, 7(2), 368.

Ben Chehida Y, et al. (2026) Genetic parallelism underpins convergent mimicry coloration in Lepidoptera across 120 million years of evolution. *PLoS biology*, 24(4), e3003742.

Kolling Iv FW, et al. (2026) Multisite Assessment of Methods for Cell Preservation Upstream of Single-Cell RNA Sequencing. *Journal of biomolecular techniques : JBT*, 37(2), 9.

Ji HJ, et al. (2026) Accurate serotype identification of *Streptococcus pneumoniae* using nanopore Cas9-targeted serotype identification (nCATSerotyping). *Journal of clinical microbiology*, 64(2), e0098425.

Jasnauskaitė M, et al. (2026) Structure and mechanism of antiphage retron Eco2. *Nature structural & molecular biology*, 33(2), 330.

Hunt M, et al. (2026) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. *Nature methods*, 23(3), 653.

Dziagwa C, et al. (2026) Disruption of tRNA threonylation triggers RIG-I mediated anti-tumour immune response. *Nature communications*, 17(1).

Choi JH, et al. (2026) Universal conditional knockout approach to multiple species, from fish to human induced pluripotent stem cells. *Nucleic acids research*, 54(9).

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

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.

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*.