Resource Summary Report

Generated by NIF on May 25, 2025

pysam

RRID:SCR_021017
Type: Tool

Proper Citation

pysam (RRID:SCR_021017)

Resource Information

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

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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

Funding:

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: 20250525T032556+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 85 mentions in open access literature.

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

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

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).

Doud MB, et al. (2024) Competition-driven eco-evolutionary feedback reshapes bacteriophage lambda's fitness landscape and enables speciation. Nature communications, 15(1), 863.

Muyas F, et al. (2024) The ALT pathway generates telomere fusions that can be detected in the blood of cancer patients. Nature communications, 15(1), 82.

Tan L, et al. (2024) Analysis of bacterial transcriptome and epitranscriptome using nanopore direct RNA sequencing. Nucleic acids research, 52(15), 8746.

Chen Y, et al. (2024) Haplotype-resolved assembly of diploid and polyploid genomes using quantum computing. Cell reports methods, 4(5), 100754.

Ho DV, et al. (2024) Post-meiotic mechanism of facultative parthenogenesis in gonochoristic whiptail lizard species. eLife, 13.

Angelis N, et al. (2024) Loss of ARID3A perturbs intestinal epithelial proliferation-differentiation ratio and regeneration. The Journal of experimental medicine, 221(10).

Breunig H, et al. (2024) Achieving gigawatt-scale green hydrogen production and seasonal storage at industrial locations across the U.S. Nature communications, 15(1), 9049.

Ozturk K, et al. (2024) Interface-guided phenotyping of coding variants in the transcription factor RUNX1. Cell reports, 43(7), 114436.

O'Reilly RL, et al. (2024) Saliva-derived DNA is suitable for the detection of clonal

haematopoiesis of indeterminate potential. Scientific reports, 14(1), 18917.

Kohabir KAV, et al. (2024) Synthetic mismatches enable specific CRISPR-Cas12a-based detection of genome-wide SNVs tracked by ARTEMIS. Cell reports methods, 4(12), 100912.

Giordano N, et al. (2024) Genome-scale community modelling reveals conserved metabolic cross-feedings in epipelagic bacterioplankton communities. Nature communications, 15(1), 2721.

Lanza A, et al. (2024) Transcriptome analysis of Edwardsiella piscicida during intracellular infection reveals excludons are involved with the activation of a mitochondrion-like energy generation program. mBio, 15(3), e0352623.

Yoshimi K, et al. (2024) Genome editing using type I-E CRISPR-Cas3 in mice and rat zygotes. Cell reports methods, 4(8), 100833.

Thatikonda V, et al. (2024) Co-targeting SOS1 enhances the antitumor effects of KRASG12C inhibitors by addressing intrinsic and acquired resistance. Nature cancer, 5(9), 1352.

Morgan IL, et al. (2024) Highly sensitive mapping of in vitro type II topoisomerase DNA cleavage sites with SHAN-seq. bioRxiv : the preprint server for biology.

Nesta A, et al. (2024) Alternative splicing of transposable elements in human breast cancer. bioRxiv : the preprint server for biology.

Allentoft ME, et al. (2024) Population genomics of post-glacial western Eurasia. Nature, 625(7994), 301.

Zolfo M, et al. (2024) Discovering and exploring the hidden diversity of human gut viruses using highly enriched virome samples. bioRxiv : the preprint server for biology.