Resource Summary Report

Generated by T1D on Aug 2, 2026

SAM format

RRID:SCR_012093
Type: Tool

Proper Citation

SAM format (RRID:SCR_012093)

Resource Information

URL: http://samtools.sourceforge.net/

Proper Citation: SAM format (RRID:SCR_012093)

Description: A generic alignment format for storing read alignments against reference sequences, supporting short and long reads (up to 128 Mbp) produced by different sequencing platforms.

Synonyms: Sequence Alignment/Map format

Resource Type: narrative resource, data or information resource, interchange format, standard specification

Defining Citation: PMID:19505943

Resource Name: SAM format

Resource ID: SCR_012093

Alternate IDs: OMICS_05115

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260801T190733+0000

Ratings and Alerts

No rating or validation information has been found for SAM format.

No alerts have been found for SAM format.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1204 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Zeng Y, et al. (2025) Mapping the chromothripsis landscape in urothelial carcinoma unravels great intratumoral and intertumoral heterogeneity. iScience, 28(1), 111510.

Chen T, et al. (2025) Temporal dynamics, microdiversity, and ecological functions of viral communities during cyanobacterial blooms in Lake Taihu. NPJ biofilms and microbiomes, 11(1), 178.

Zhang M, et al. (2025) Telomere-to-telomere genome assembly uncovers Wolbachia-driven recurrent male bottleneck effect and selection in a sawfly. Communications biology, 8(1), 1211.

Wu J, et al. (2025) Cell-free DNA testing for the detection and prognosis prediction of pancreatic cancer. Nature communications, 16(1), 6645.

Du R, et al. (2025) Comparative study of tools for copy number variation detection using next-generation sequencing data. Scientific reports, 15(1), 22145.

Zou J, et al. (2025) Genetic and clinical insights into acute kidney injury in maturity-onset diabetes of the young caused by the ABCC8 c.2500C>T mutation: Potential risk factors associated with SGLT2 inhibitors. Experimental and therapeutic medicine, 30(2), 164.

McCastlain K, et al. (2025) Somatic mtDNA mutations at intermediate levels of heteroplasmy are a source of functional heterogeneity among primary leukemic cells. Science advances, 11(37), eadt3873.

Zhang T, et al. (2025) Low-coverage whole-genome sequencing for differentiating cervical cancer from cervical intraepithelial neoplasia and benign diseases. Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology, 33(1), 12.

Li S, et al. (2025) Development of vascularized adipose organoids from PBMSCs and their application in evaluating Celastrol's effects. Adipocyte, 14(1), 2548787.

Qiu H, et al. (2025) Identification of PilD mutants reveals the iterative social evolution in Pseudomonas aeruginosa. Applied and environmental microbiology, 91(10), e0091525.

Broad Z, et al. (2025) Gravitropic Gene Expression Divergence Associated With Adaptation to Contrasting Environments in an Australian Wildflower. Molecular ecology, 34(15), e17543.

Leko V, et al. (2025) Utilization of primary tumor samples for cancer neoantigen discovery. Journal for immunotherapy of cancer, 13(1).

Lumbroso G, et al. (2025) The B-type cyclin Clb4 prevents meiosis I sister centromere separation in budding yeast. G3 (Bethesda, Md.), 15(9).

Fathi M, et al. (2025) Spectrum of genetic mutations in methylmalonic aciduria among Iranian patients. Scientific reports, 15(1), 16389.

Huang W, et al. (2025) Cryptosporidium parvum multidrug resistance protein confers resistance to toxic gut microbial metabolite. Cell host & microbe, 33(9), 1589.

Morovvati S, et al. (2025) The clinical and genetic spectrum of twenty-six individuals with hearing loss affected by MYO15A variants. Scientific reports, 15(1), 14320.

Zeeshan M, et al. (2025) A novel SUN1-ALLAN complex coordinates segregation of the bipartite MTOC across the nuclear envelope during rapid closed mitosis in Plasmodium berghei. eLife, 14.

Xu K, et al. (2025) ChromInSight: Revealing DNA Double-Strand Breaks Through Chromatin Structural Insights With an Interpretable Graph Neural Network Framework. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(36), e04571.

Kimball A, et al. (2025) Independent evolution of holocentric chromosomes in an early branching apicomplexan parasite. bioRxiv : the preprint server for biology.

Garrigue A, et al. (2025) Human oncostatin M deficiency underlies an inherited severe bone marrow failure syndrome. The Journal of clinical investigation, 135(6).