Resource Summary Report

Generated by RRID on Apr 11, 2025

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

Funding:

Resource Name: SAM format

Resource ID: SCR_012093

Alternate IDs: OMICS_05115

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250411T055503+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 1182 mentions in open access literature.

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

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

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

Good JD, et al. (2025) Protocol for mitochondrial variant enrichment from single-cell RNA sequencing using MAESTER. STAR protocols, 6(1), 103564.

Wang J, et al. (2024) Transcriptome and Weighted Gene Co-Expression Network Analysis for Feather Follicle Density in a Chinese Indigenous Breed. Animals : an open access journal from MDPI, 14(1).

Shaikh SS, et al. (2024) Evidence of a genetic background predisposing to complex regional pain syndrome type 1. Journal of medical genetics, 61(2), 163.

Jiang B, et al. (2024) Uncovering the GacS-mediated role in evolutionary progression through trajectory reconstruction in Pseudomonas aeruginosa. Nucleic acids research, 52(7), 3856.

Tameni A, et al. (2024) HELLS regulates transcription in T-cell lymphomas by reducing unscheduled R-loops and by facilitating RNAPII progression. Nucleic acids research, 52(11), 6171.

Li X, et al. (2024) Genome-wide and cell-type-selective profiling of in vivo small noncoding RNA:target RNA interactions by chimeric RNA sequencing. Cell reports methods, 4(8), 100836.

Zhur KV, et al. (2024) Human DNA from the oldest Eneolithic cemetery in Nalchik points the spread of farming from the Caucasus to the Eastern European steppes. iScience, 27(11), 110963.

Wang B, et al. (2024) Population expansion from central plain to northern coastal China

inferred from ancient human genomes. iScience, 27(12), 111405.

Xu W, et al. (2024) Genetic diversity and population structure analysis of 418 tomato cultivars based on single nucleotide polymorphism markers. Frontiers in plant science, 15, 1445734.

Miri Karam Z, et al. (2024) Identification of a Novel Deletion Variant (c.2999_3005delTGTGTGT/p.Asn1000SerfsTer4) in NPHP4 Associated With Nephronophthisis-4. Journal of clinical laboratory analysis, 38(11-12), e25077.

Fu W, et al. (2024) Whole-genome resequencing identifies candidate genes and allelic variation in the MdNADP-ME promoter that regulate fruit malate and fructose contents in apple. Plant communications, 5(9), 100973.

Morozumi Y, et al. (2024) Rapamycin-sensitive mechanisms confine the growth of fission yeast below the temperatures detrimental to cell physiology. iScience, 27(1), 108777.

Sogari A, et al. (2024) Tolerance to colibactin correlates with homologous recombination proficiency and resistance to irinotecan in colorectal cancer cells. Cell reports. Medicine, 5(2), 101376.

McClain MT, et al. (2024) Epigenetic and transcriptional responses in circulating leukocytes are associated with future decompensation during SARS-CoV-2 infection. iScience, 27(1), 108288.

Yadav DK, et al. (2024) O-GlcNAc signaling increases neuron regeneration through one-carbon metabolism in Caenorhabditis elegans. eLife, 13.

Baptista CG, et al. (2024) The Toxoplasma gondii F-Box Protein L2 Functions as a Repressor of Stage Specific Gene Expression. PLoS pathogens, 20(5), e1012269.

Wang H, et al. (2024) Integrative analysis of single-nucleus RNA-seq and bulk RNA-seq reveals germline cells development dynamics and niches in the Pacific oyster gonad. iScience, 27(4), 109499.

Montaño J, et al. (2024) Transcriptional re-programming of liver-resident iNKT cells into T-regulatory type-1-like liver iNKT cells involves extensive gene de-methylation. Frontiers in immunology, 15, 1454314.