

Resource Summary Report

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SAM

RRID:SCR_010951

Type: Tool

Proper Citation

SAM (RRID:SCR_010951)

Resource Information

URL: <http://www-stat.stanford.edu/~tibs/SAM/>

Proper Citation: SAM (RRID:SCR_010951)

Description: Software for genomic expression data mining using a statistical technique for finding significant genes in a set of microarray experiments.

Synonyms: SAM: Significance Analysis of Microarrays, Significance Analysis of Microarrays

Resource Type: software resource

Keywords: genomic expression, data mining, finding significant genes, microarray experiments,

Availability: Commercial use requires license, Registration required

Resource Name: SAM

Resource ID: SCR_010951

Alternate IDs: OMICS_01314, OMICS_00779, SCR_011888

Alternate URLs: <https://sources.debian.org/src/r-cran-samr/>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260804T043454+0000

Ratings and Alerts

No rating or validation information has been found for SAM.

No alerts have been found for SAM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 235 mentions in open access literature.

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

Watters CR, et al. (2025) Resistance signatures to oncolytic vesiculoviruses in pancreatic ductal adenocarcinoma. *Molecular therapy. Oncology*, 33(1), 200937.

Xue J, et al. (2024) Comparative study on differential expression analysis methods for single-cell RNA sequencing data with small biological replicates: Based on single-cell transcriptional data of PBMCs from COVID-19 severe patients. *PloS one*, 19(3), e0299358.

Lam N, et al. (2023) Development of a bicistronic anti-CD19/CD20 CAR construct including abrogation of unexpected nucleic acid sequence deletions. *Molecular therapy oncolytics*, 30, 132.

Zhang H, et al. (2023) Longitudinal study of 2 patients with cyclic thrombocytopenia, STAT3 and MPL mutations. *Blood advances*, 7(1), 190.

Mehta P, et al. (2023) SARS-CoV-2 infection severity and mortality is modulated by repeat-mediated regulation of alternative splicing. *Microbiology spectrum*, 11(5), e0135123.

Buratin A, et al. (2023) Systematic benchmarking of statistical methods to assess differential expression of circular RNAs. *Briefings in bioinformatics*, 24(1).

Xu-Monette ZY, et al. (2023) Tumor-Infiltrating Normal B Cells Revealed by Immunoglobulin Repertoire Clonotype Analysis Are Highly Prognostic and Crucial for Antitumor Immune Responses in DLBCL. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(23), 4808.

Sun W, et al. (2022) GFI1 Cooperates with IKZF1/IKAROS to Activate Gene Expression in T-cell Acute Lymphoblastic Leukemia. *Molecular cancer research : MCR*, 20(4), 501.

Bang D, et al. (2022) A Survey on Computational Methods for Investigation on ncRNA-Disease Association through the Mode of Action Perspective. *International journal of molecular sciences*, 23(19).

Maumus M, et al. (2021) Neuromedin B promotes chondrocyte differentiation of mesenchymal stromal cells via calcineurin and calcium signaling. *Cell & bioscience*, 11(1), 183.

Tolwani A, et al. (2021) Prognostic relevance of the hexosamine biosynthesis pathway activation in leiomyosarcoma. *NPJ genomic medicine*, 6(1), 30.

Hui W, et al. (2021) Alterations of Signaling Pathways in Essential Thrombocythemia with Calreticulin Mutation. *Cancer management and research*, 13, 6231.

Hildebrand KM, et al. (2021) The KrasG12D;Trp53fl/fl murine model of undifferentiated pleomorphic sarcoma is macrophage dense, lymphocyte poor, and resistant to immune checkpoint blockade. *PloS one*, 16(7), e0253864.

Saddozai UAK, et al. (2021) Identification of Clinical Relevant Molecular Subtypes of Pheochromocytoma. *Frontiers in endocrinology*, 12, 605797.

Wallen ZD, et al. (2021) Comparison study of differential abundance testing methods using two large Parkinson disease gut microbiome datasets derived from 16S amplicon sequencing. *BMC bioinformatics*, 22(1), 265.

Sheng LP, et al. (2021) Identification of potential serum exosomal microRNAs involved in acinar-ductal metaplasia that is a precursor of pancreatic cancer associated with chronic pancreatitis. *Medicine*, 100(18), e25753.

Brykczynska U, et al. (2020) Distinct Transcriptional Responses across Tissue-Resident Macrophages to Short-Term and Long-Term Metabolic Challenge. *Cell reports*, 30(5), 1627.

Tiklov K, et al. (2020) Single cell transcriptomics identifies stem cell-derived graft composition in a model of Parkinson's disease. *Nature communications*, 11(1), 2434.

Prakash S, et al. (2020) Unique molecular signatures of antiviral memory CD8+ T cells associated with asymptomatic recurrent ocular herpes. *Scientific reports*, 10(1), 13843.

Gadaleta E, et al. (2020) Characterization of four subtypes in morphologically normal tissue excised proximal and distal to breast cancer. *NPJ breast cancer*, 6, 38.