

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: 20260912T200331+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 [NIF](#) .

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.

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.

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

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.

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.

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

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.

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.

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.

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.