Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

SAMSeq

RRID:SCR_011888
Type: Tool

Proper Citation

SAMSeq (RRID:SCR_011888)

Resource Information

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

Proper Citation: SAMSeq (RRID:SCR_011888)

Description: A nonparametric approach for identifying differential expression in RNA-Seq data.

Abbreviations: SAMSeq

Resource Type: software resource

Resource Name: SAMSeq

Resource ID: SCR_011888

Alternate IDs: OMICS_01314

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260903T235121+0000

Ratings and Alerts

No rating or validation information has been found for SAMSeq.

No alerts have been found for SAMSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 140 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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).

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).

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.

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

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.

Tiklová 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.

Baik B, et al. (2020) Benchmarking RNA-seq differential expression analysis methods using spike-in and simulation data. PloS one, 15(4), e0232271.

Tiklová K, et al. (2019) Single-cell RNA sequencing reveals midbrain dopamine neuron diversity emerging during mouse brain development. Nature communications, 10(1), 581.

Wang F, et al. (2019) Gene Expression Profiling Reveals Distinct Molecular Subtypes of Esophageal Squamous Cell Carcinoma in Asian Populations. Neoplasia (New York, N.Y.), 21(6), 571.

Perofsky AC, et al. (2019) Terrestriality and bacterial transfer: a comparative study of gut microbiomes in sympatric Malagasy mammals. The ISME journal, 13(1), 50.

Zhu A, et al. (2019) Nonparametric expression analysis using inferential replicate counts. Nucleic acids research, 47(18), e105.

Bae M, et al. (2019) Astaxanthin attenuates the increase in mitochondrial respiration during the activation of hepatic stellate cells. The Journal of nutritional biochemistry, 71, 82.

Phi JH, et al. (2019) NPM1 as a potential therapeutic target for atypical teratoid/rhabdoid tumors. BMC cancer, 19(1), 848.

Ricketts CJ, et al. (2018) The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell reports, 23(1), 313.

Tervaniemi MH, et al. (2018) Intracellular signalling pathways and cytoskeletal functions converge on the psoriasis candidate gene CCHCR1 expressed at P-bodies and centrosomes. BMC genomics, 19(1), 432.

Naor A, et al. (2018) MYR1-Dependent Effectors Are the Major Drivers of a Host Cell's Early Response to Toxoplasma, Including Counteracting MYR1-Independent Effects. mBio, 9(2).