SAM
RRID:SCR_010951
Type: Tool

Proper Citation

SAM (RRID:SCR_010951)

Resource Information

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

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

Resource Type: Resource, software resource

Parent Organization: Stanford University; Stanford; California

Related resources: pysam

Availability: Commercial use requires license, Registration required

Website Status: Last checked up

Abbreviations: SAM

Resource Name: SAM

Resource ID: SCR_010951

Alternate IDs: OMICS_00779

Ratings and Alerts

No rating or validation information has been found for SAM.

No alerts have been found for SAM.
Usage and Citation Metrics

We found 83 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](http://FDI Lab - SciCrunch.org).

Eriksson J, et al. (2020) Prolyl 4-hydroxylase subunit alpha 1 (P4HA1) is a biomarker of poor prognosis in primary melanomas, and its depletion inhibits melanoma cell invasion and disrupts tumor blood vessel walls. Molecular oncology.


Liu BW, et al. (2017) Altered expression of target genes of spinal cord in different itch models compared with capsaicin assessed by RT-qPCR validation. Oncotarget, 8(43), 74423-74433.


Zhu P, et al. (2016) Phosphohistone H3 (pHH3) is a prognostic and epithelial to mesenchymal transition marker in diffuse gliomas. Oncotarget, 7(29), 45005-45014.


Shi L, et al. (2015) miR-483-5p and miR-486-5p are down-regulated in cumulus cells of metaphase II oocytes from women with polycystic ovary syndrome. Reproductive biomedicine online, 31(4), 565-72.