SAM
RRID:SCR_010951
Type: Tool

Proper Citation
SAM (RRID:SCR_010951)

Resource Information

URL: http://www-stat.stanford.edu/~tibs/SAM/
Description: Software for genomic expression data mining using a statistical technique for finding significant genes in a set of microarray experiments.

Resource Name: SAM
Proper Citation: SAM (RRID:SCR_010951)
Resource Type: Resource, software resource
Resource ID: SCR_010951
Parent Organization: Stanford University; Stanford; California
Availability: Commercial use requires license, Registration required
Website Status: Last checked up
Alternate IDs: OMICS_00779
Abbreviations: SAM
Mentions Count: 81

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 81 mentions in open access literature.

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


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.


