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: 82

Ratings and Alerts

No rating or validation information has been found for SAM.

No alerts have been found for SAM.
We found 82 mentions in open access literature.

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


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.


