# SAM

**RRID:** SCR_010951  
**Type:** Tool

## Proper Citation

SAM (RRID:SCR_010951)

## Resource Information


**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.
Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 82 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


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.


