SAM
RRID:SCR_010951
Type: Tool

Proper Citation

SAM (RRID:SCR_010951)

Resource Information

URL: http://www-stat.stanford.edu/~tibs/SAM/
Proper Citation: SAM (RRID:SCR_010951)
Description: Software for genomic expression data mining using a statistical technique for finding significant genes in a set of microarray experiments.
Synonyms: SAM: Significance Analysis of Microarrays, Significance Analysis of Microarrays
Resource Type: software resource
Keywords: genomic expression, data mining, finding significant genes, microarray experiments,
Availability: Commercial use requires license, Registration required
Resource Name: SAM
Resource ID: SCR_010951
Alternate IDs: OMICS_01314, OMICS_00779, SCR_011888
Alternate URLs: https://sources.debian.org/src/r-cran-samr/
Record Creation Time: 20220129T080301+0000
Record Last Update: 20240705T053911+0000
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 232 mentions in open access literature.

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


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.


Sheng LP, et al. (2021) Identification of potential serum exosomal microRNAs involved in acinar-ductal metaplasia that is a precursor of pancreatic cancer associated with chronic pancreatitis. Medicine, 100(18), e25753.


