Resource Summary Report

Generated by RRID on Apr 29, 2025

R-SAP

RRID:SCR_011907
Type: Tool

Proper Citation

R-SAP (RRID:SCR_011907)

Resource Information

URL: https://mcdonaldlab.biology.gatech.edu/r-sap/

Proper Citation: R-SAP (RRID:SCR_011907)

Description: An automated bioinformatics pipeline that analyzes and quantitates high-throughput RNA-Seq datasets.

Abbreviations: R-SAP

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: R-SAP

Resource ID: SCR_011907

Alternate IDs: OMICS_01409, biotools:r-sap

Alternate URLs: https://bio.tools/r-sap

Old URLs: http://www.mcdonaldlab.biology.gatech.edu/r-sap.htm

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014601+0000

Ratings and Alerts

No rating or validation information has been found for R-SAP.

No alerts have been found for R-SAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Mittal VK, et al. (2017) De novo assembly and characterization of breast cancer transcriptomes identifies large numbers of novel fusion-gene transcripts of potential functional significance. BMC medical genomics, 10(1), 53.

Mittal VK, et al. (2015) Integrated sequence and expression analysis of ovarian cancer structural variants underscores the importance of gene fusion regulation. BMC medical genomics, 8, 40.

Mittal VK, et al. (2012) R-SAP: a multi-threading computational pipeline for the characterization of high-throughput RNA-sequencing data. Nucleic acids research, 40(9), e67.