# **Resource Summary Report**

Generated by <u>NIF</u> on May 15, 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 <u>NIF</u>.

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.