

Resource Summary Report

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sRAP

RRID:SCR_001297

Type: Tool

Proper Citation

sRAP (RRID:SCR_001297)

Resource Information

URL: <https://rdrr.io/bioc/sRAP/>

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Description: Software package that provides a pipeline for gene expression analysis (primarily for RNA-Seq data). The normalization function is specific for RNA-Seq analysis, but all other functions (Quality Control Figures, Differential Expression and Visualization, and Functional Enrichment via BD-Func) will work with any type of gene expression data.

Abbreviations: sRAP

Synonyms: Simplified RNA-Seq Analysis

Resource Type: software resource

Keywords: gene expression, differential expression, go, gene set enrichment, microarray, preprocessing, quality control, rna-seq, statistical method, visualization

Availability: Free, Available for download, Freely available

Resource Name: sRAP

Resource ID: SCR_001297

Alternate IDs: OMICS_02038

Alternate URLs: <http://www.bioconductor.org/packages/release/bioc/html/sRAP.html>

License: GNU General Public License, v3

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260801T190137+0000

Ratings and Alerts

No rating or validation information has been found for sRAP.

No alerts have been found for sRAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Wagner MC, et al. (2023) Lrpap1 (RAP) Inhibits Proximal Tubule Clathrin Mediated and Clathrin Independent Endocytosis, Ameliorating Renal Aminoglycoside Nephrotoxicity. *Kidney360*, 4(5), 591.

Borchmann S, et al. (2021) An atlas of the tissue and blood metagenome in cancer reveals novel links between bacteria, viruses and cancer. *Microbiome*, 9(1), 94.

Kwiecinski JM, et al. (2019) Staphylococcus aureus adhesion in endovascular infections is controlled by the ArlRS-MgrA signaling cascade. *PLoS pathogens*, 15(5), e1007800.

Podyma W, et al. (2019) A multilevel exploration of Avena strigosa diversity as a prelude to promote alternative crop. *BMC plant biology*, 19(1), 291.

Chang CM, et al. (2019) Functional Effects of let-7g Expression in Colon Cancer Metastasis. *Cancers*, 11(4).

Blanchette KA, et al. (2018) Current therapies in treatment and prevention of fracture wound biofilms: why a multifaceted approach is essential for resolving persistent infections. *Journal of bone and joint infection*, 3(2), 50.

Wahba A, et al. (2018) Radiation-induced alternative transcripts as detected in total and polysome-bound mRNA. *Oncotarget*, 9(1), 691.

Van Grembergen O, et al. (2016) Portraying breast cancers with long noncoding RNAs. *Science advances*, 2(9), e1600220.

Liu S, et al. (2014) SRA regulates adipogenesis by modulating p38/JNK phosphorylation and stimulating insulin receptor gene expression and downstream signaling. *PloS one*, 9(4), e95416.

McKay DB, et al. (2014) Structure and function of steroid receptor RNA activator protein, the proposed partner of SRA noncoding RNA. *Journal of molecular biology*, 426(8), 1766.

Wong PS, et al. (2014) Tracking difference in gene expression in a time-course experiment using gene set enrichment analysis. *PloS one*, 9(9), e107629.

Pickett SR, et al. (2013) Environmental and parental influences on offspring health and growth in great tits (*Parus major*). *PloS one*, 8(7), e69695.

Yan Y, et al. (2009) Steroid Receptor RNA Activator Protein (SRAP): a potential new prognostic marker for estrogen receptor-positive/node-negative/younger breast cancer patients. *Breast cancer research : BCR*, 11(5), R67.

Yoon SR, et al. (2009) The ups and downs of mutation frequencies during aging can account for the Apert syndrome paternal age effect. *PLoS genetics*, 5(7), e1000558.

Qin J, et al. (2007) The molecular anatomy of spontaneous germline mutations in human testes. *PLoS biology*, 5(9), e224.