Resource Summary Report

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sRAP

RRID:SCR_001297
Type: Tool

Proper Citation

sRAP (RRID:SCR_001297)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/sRAP.html

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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

Funding:

Availability: GNU General Public License, v3

Resource Name: sRAP

Resource ID: SCR_001297

Alternate IDs: OMICS_02038

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250519T203123+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 dkNET.

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.

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.

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

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.