Resource Summary Report

Generated by NIF on Apr 17, 2025

rpkmforgenes.py

RRID:SCR_014938
Type: Tool

Proper Citation

rpkmforgenes.py (RRID:SCR_014938)

Resource Information

URL: http://sandberg.cmb.ki.se/media/data/rnaseq/rpkmforgenes.py

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Description: Python script which calculates gene expression for RNA-Sequencing data. It analyzes files in formats such as BED, BAM, and SAM to output data about RNA.

Resource Type: source code, sequence analysis software, data analysis software, software application, data processing software, software resource

Keywords: rna, sequencing, rna-seq, python, script, data analysis, genetic, gene analysis

Funding:

Availability: Free, Available for download

Resource Name: rpkmforgenes.py

Resource ID: SCR_014938

Alternate URLs: http://sandberg.cmb.ki.se/media/data/rnaseq/rpkmforgenes.py

Record Creation Time: 20220129T080323+0000

Record Last Update: 20250417T065504+0000

Ratings and Alerts

No rating or validation information has been found for rpkmforgenes.py.

No alerts have been found for rpkmforgenes.py.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Di Martino E, et al. (2024) Inflammatory, metabolic, and sex-dependent gene-regulatory dynamics of microglia and macrophages in neonatal hippocampus after hypoxia-ischemia. iScience, 27(4), 109346.

Chaparro V, et al. (2020) Translational profiling of macrophages infected with Leishmania donovani identifies mTOR- and eIF4A-sensitive immune-related transcripts. PLoS pathogens, 16(6), e1008291.