

Resource Summary Report

Generated by [T1D](#) on Aug 1, 2026

[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>

Proper Citation: rpkmforgenes.py (RRID:SCR_014938)

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

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

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: 20260801T042741+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 [T1D](#) .

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.