Resource Summary Report

Generated by NIF on May 28, 2025

seqpac

RRID:SCR_021079
Type: Tool

Proper Citation

seqpac (RRID:SCR_021079)

Resource Information

URL: https://github.com/Danis102/seqpac

Proper Citation: seqpac (RRID:SCR_021079)

Description: Software R package for analysis of short sequenced reads. Framework for small RNA analysis in R using Sequence Based Counts.Can be applied on any type of data generated by large scale nucleotide sequencing, where user wish to maintain sequence integrity during whole analysis.

Resource Type: software toolkit, software resource, data analysis software, data processing software, software application

Defining Citation: DOI:10.1101/2021.03.19.436151

Keywords: sRNA-seq data analysis, RNA-seq, small RNA, short sequence reads analysis, sequence based counts, nucleotide sequencing data

Funding: The Swedish Research Council 2015-03141;
Knut and Alice Wallenberg Stiftelse ; 2015.0165;
Ragnar Söderberg ;
Formas - Swedish Research Council for Sustainable Development 2020-01042

Availability: Free, Available for download, Freely available

Resource Name: seqpac

Resource ID: SCR_021079

License: GNU GPL v3.0

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250528T061541+0000

Ratings and Alerts

No rating or validation information has been found for seqpac.

No alerts have been found for seqpac.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Skog S, et al. (2023) Seqpac: a framework for sRNA-seq analysis in R using sequence-based counts. Bioinformatics (Oxford, England), 39(4).