# **Resource Summary Report**

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## <u>seqpac</u>

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 application, software toolkit, data analysis software, data processing software, software resource

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: 20250525T031756+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 <u>NIF</u>.

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