

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 25, 2026

[seqpac](#)

RRID:SCR_021079

Type: Tool

Proper Citation

seqpac (RRID:SCR_021079)

Resource Information

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

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

Defining Citation: [DOI:10.1101/2021.03.19.436151](https://doi.org/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: Formas - Swedish Research Council for Sustainable Development 2020-01042; Knut and Alice Wallenberg Stiftelse ; 2015.0165; Ragnar Söderberg ; The Swedish Research Council 2015-03141

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: 20260821T194149+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 [PRECISE-TBI](#) .

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