

# Resource Summary Report

Generated by [NIF](#) on Sep 16, 2026

## [seqpac](#)

RRID:SCR\_021079

Type: Tool

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### Proper Citation

seqpac (RRID:SCR\_021079)

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### 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:** 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:** 20260912T195950+0000

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### Ratings and Alerts

No rating or validation information has been found for seqpac.

No alerts have been found for seqpac.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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).