

# Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

## Parseq

RRID:SCR\_003464

Type: Tool

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### Proper Citation

Parseq (RRID:SCR\_003464)

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### Resource Information

**URL:** <http://www.lgm.upmc.fr/parseq/>

**Proper Citation:** Parseq (RRID:SCR\_003464)

**Description:** Statistical software for transcription landscape reconstruction at a basepair resolution from RNA Seq read counts. It is based on a state-space model which describes, in terms of abrupt shifts and more progressive drifts, the transcription level dynamics along the genome. Alongside variations of transcription level, it incorporates a component of short-range variation to pull apart local artifacts causing correlated dispersion. Reconstruction of the transcription level relies on a conditional sequential Monte Carlo approach that is combined with parameter estimation in a Markov chain Monte Carlo algorithm known as particle Gibbs. The method allows to estimate the local transcription level, to call transcribed regions, and to identify the transcript borders.

**Abbreviations:** Parseq

**Resource Type:** software resource

**Defining Citation:** [PMID:24470570](#)

**Keywords:** rna-seq, genome, transcription, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** Parseq

**Resource ID:** SCR\_003464

**Alternate IDs:** biotools:parseq, OMICS\_02302

**Alternate URLs:** <https://bio.tools/parseq>

**Record Creation Time:** 20220129T080219+0000

**Record Last Update:** 20260725T190540+0000

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## Ratings and Alerts

No rating or validation information has been found for Parseq.

No alerts have been found for Parseq.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Palyanova NV, et al. (2023) The Development of the SARS-CoV-2 Epidemic in Different Regions of Siberia in the 2020-2022 Period. Viruses, 15(10).

Oliveira PH, et al. (2020) Epigenomic characterization of Clostridioides difficile finds a conserved DNA methyltransferase that mediates sporulation and pathogenesis. Nature microbiology, 5(1), 166.