

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 30, 2026

CIRIquant

RRID:SCR_021661

Type: Tool

Proper Citation

CIRIquant (RRID:SCR_021661)

Resource Information

URL: <https://github.com/bioinfo-biols/CIRIquant>

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Description: Software Python package for accurate circRNA quantification and differential expression analysis. Comprehensive analysis pipeline for circRNA detection and quantification in RNA-Seq data. Accurate quantification of circular RNAs identifies extensive circular isoform switching events.

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

Defining Citation: [DOI:10.1038/s41467-019-13840-9](https://doi.org/10.1038/s41467-019-13840-9)

Keywords: circRNA quantification, differential expression analysis, RNA-Seq data, circular RNA, circular isoform switching events

Funding: National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: CIRIquant

Resource ID: SCR_021661

Alternate URLs: <https://sourceforge.net/projects/ciri/files/>, https://ciri-cookbook.readthedocs.io/en/latest/CIRIquant_0_home.html#

License: MIT

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260829T182723+0000

Ratings and Alerts

No rating or validation information has been found for CIRIquant.

No alerts have been found for CIRIquant.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Yang G, et al. (2026) The Whole Transcriptome Sequencing Profile of Serum-Derived Exosomes and Potential Pathophysiology of Age-Related Hearing Loss. *Diagnostics* (Basel, Switzerland), 16(2).

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Li P, et al. (2026) Global mapping of circRNA-target RNA interactions reveal P-body-mediated translational repression. *Molecular cell*, 86(5), 868.

Rebolledo C, et al. (2023) Computational approaches for circRNAs prediction and in silico characterization. *Briefings in bioinformatics*, 24(3).