

# Resource Summary Report

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## CiLiQuant

RRID:SCR\_019319

Type: Tool

### Proper Citation

CiLiQuant (RRID:SCR\_019319)

### Resource Information

**URL:** <https://github.com/almorlio/CiLiQuant>

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**Description:** Software tool to separate junction reads based on their linear or circular origin. Only non ambiguous junction reads are used to compare relative linear and circular transcript abundance.

**Resource Type:** data processing software, software application, software resource

**Keywords:** RNA, splicing, circular origin, separate junction reads, circular transcript abundance, linear transcript abundance, compare, bio.tools

**Funding:** European Union's Horizon 2020 ;  
FWO ;  
Kom Op Tegen Kanker (Stand Up To Cancer) ;  
Special Research Fund UGent ;  
Stichting Tegen Kanker

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

**Resource Name:** CiLiQuant

**Resource ID:** SCR\_019319

**Alternate IDs:** biotools:ciliquant

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

**License:** BSD 3-Clause License

**Record Creation Time:** 20220129T080344+0000

**Record Last Update:** 20260912T200108+0000

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## Ratings and Alerts

No rating or validation information has been found for CiLiQuant.

No alerts have been found for CiLiQuant.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.