## **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

# **SL-quant**

RRID:SCR\_016205

Type: Tool

### **Proper Citation**

SL-quant (RRID:SCR\_016205)

#### **Resource Information**

URL: https://github.com/cyaguesa/SL-quant/

Proper Citation: SL-quant (RRID:SCR\_016205)

**Description:** Source code for a bash pipeline that quantifies splice-leader (SL) trans-splicing events by genes in the nematode C. elegans. It is designed to work downstream of read mapping and takes the reads left unmapped as primary input.

Abbreviations: SLQ

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

Keywords: RNA-seq, trans-splicing, pipeline, c elegans, bash, nematode, read, mapping,

gene

Funding: FNRS-FRIA

Availability: Free, Available for download

**Resource Name:** SL-quant

Resource ID: SCR\_016205

License: MIT License

**Record Creation Time:** 20220129T080329+0000

Record Last Update: 20250430T060052+0000

## **Ratings and Alerts**

No rating or validation information has been found for SL-quant.

No alerts have been found for SL-quant.

### **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 dkNET.

Yague-Sanz C, et al. (2018) SL-quant: a fast and flexible pipeline to quantify spliced leader trans-splicing events from RNA-seq data. GigaScience, 7(7).