

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

IsoLasso

RRID:SCR_013176

Type: Tool

Proper Citation

IsoLasso (RRID:SCR_013176)

Resource Information

URL: <http://alumni.cs.ucr.edu/~liw/isolasso.html>

Proper Citation: IsoLasso (RRID:SCR_013176)

Description: An algorithm to assemble transcripts and estimate their expression levels from RNA-Seq reads.

Abbreviations: IsoLasso

Resource Type: software resource

Keywords: bio.tools

Resource Name: IsoLasso

Resource ID: SCR_013176

Alternate IDs: OMICS_01320, biotools:isolasso

Alternate URLs: <https://bio.tools/isolasso>

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260912T195759+0000

Ratings and Alerts

No rating or validation information has been found for IsoLasso.

No alerts have been found for IsoLasso.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Canzar S, et al. (2016) CIDANE: comprehensive isoform discovery and abundance estimation. Genome biology, 17, 16.

Hayer KE, et al. (2015) Benchmark analysis of algorithms for determining and quantifying full-length mRNA splice forms from RNA-seq data. Bioinformatics (Oxford, England), 31(24), 3938.

Marett L, et al. (2014) Bayesian transcriptome assembly. Genome biology, 15(10), 501.