Resource Summary Report

Generated by RRID on Apr 28, 2025

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

Funding:

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: 20250420T014635+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 RRID.

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.

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