

Resource Summary Report

Generated by [Kravitz](#) on Sep 18, 2026

MiTie

RRID:SCR_005228

Type: Tool

Proper Citation

MiTie (RRID:SCR_005228)

Resource Information

URL: <http://www.raetschlab.org/suppl/mitie>

Proper Citation: MiTie (RRID:SCR_005228)

Description: Software framework for simultaneous RNA-Seq-based Transcript Identification and Quantification in Multiple Samples. They define a likelihood function based on the negative binomial distribution, use a regularization approach to select a few transcripts collectively explaining the observed read data, and show how to find the optimal solution using Mixed Integer Programming. MiTie can a) take advantage of known transcripts, b) reconstruct and quantify transcripts simultaneously in multiple samples, as well as c) resolve the location of multi-mapping reads. It is designed for genome- and assembly-based transcriptome reconstruction.

Abbreviations: MiTie

Synonyms: MiTie: Simultaneous RNA-Seq-based Transcript Identification and Quantification in Multiple Samples

Resource Type: software resource

Keywords: c++, rna-seq, transcript

Resource Name: MiTie

Resource ID: SCR_005228

Alternate IDs: OMICS_01279

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260912T195623+0000

Ratings and Alerts

No rating or validation information has been found for MiTie.

No alerts have been found for MiTie.

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 [Kravitz](#) .

Hemati W, et al. (2019) LSTMVoter: chemical named entity recognition using a conglomerate of sequence labeling tools. Journal of cheminformatics, 11(1), 3.

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.

Bernard E, et al. (2015) A convex formulation for joint RNA isoform detection and quantification from multiple RNA-seq samples. BMC bioinformatics, 16, 262.

Bridge P, et al. (2014) The development and evaluation of a medical imaging training immersive environment. Journal of medical radiation sciences, 61(3), 159.