

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## MiTie

RRID:SCR\_005228

Type: Tool

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### Proper Citation

MiTie (RRID:SCR\_005228)

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### 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:** 20260725T190600+0000

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### Ratings and Alerts

No rating or validation information has been found for MiTie.

No alerts have been found for MiTie.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.