

# Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

## iReckon

RRID:SCR\_005232

Type: Tool

### Proper Citation

iReckon (RRID:SCR\_005232)

### Resource Information

**URL:** <http://compbio.cs.toronto.edu/ireckon/>

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**Description:** An algorithm for the simultaneous isoform reconstruction and abundance estimation. In addition to modelling novel isoforms, multi-mapped reads and read duplicates, this method takes into account the possible presence of unspliced pre-mRNA and intron retention. iReckon only requires a set of transcription start and end sites, but can use known full isoforms to improve sensitivity. Starting from the set of nearly all possible isoforms, iReckon uses a regularized EM algorithm to determine those actually present in the sequenced sample, together with their abundances. iReckon is multi-threaded to increase efficiency in all its time consuming steps.

**Abbreviations:** iReckon

**Resource Type:** software resource

**Defining Citation:** [PMID:23204306](#)

**Resource Name:** iReckon

**Resource ID:** SCR\_005232

**Alternate IDs:** OMICS\_01277

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260829T182224+0000

### Ratings and Alerts

No rating or validation information has been found for iReckon.

No alerts have been found for iReckon.

## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Newman JRB, et al. (2018) Event Analysis: Using Transcript Events To Improve Estimates of Abundance in RNA-seq Data. G3 (Bethesda, Md.), 8(9), 2923.

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.

Merico D, et al. (2015) Compound heterozygous mutations in the noncoding RNU4ATAC cause Roifman Syndrome by disrupting minor intron splicing. Nature communications, 6, 8718.