

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

## IsoformEx

RRID:SCR\_005235

Type: Tool

### Proper Citation

IsoformEx (RRID:SCR\_005235)

### Resource Information

**URL:** <http://bioinformatics.wistar.upenn.edu/isoformex>

**Proper Citation:** IsoformEx (RRID:SCR\_005235)

**Description:** Software that estimates transcript expression levels and gene expression levels from mRNA-Seq data. Technically speaking, IsoformEx parses bowtie alignment files in a project directory (e.g. ~yourid/isoformex/xxx, where xxx is the project name) and generates two files: (1) xxx/xxx\_transcript\_1.txt: expression levels of all transcripts, (2) xxx/xxx\_gene\_1.txt: expression levels of all genes.

**Synonyms:** IsoformEx: Isoform level gene expression estimation using non-negative least squares from mRNA-Seq data

**Resource Type:** software resource

**Availability:** Free for academic use, Commercial use with permission

**Resource Name:** IsoformEx

**Resource ID:** SCR\_005235

**Alternate IDs:** OMICS\_01260

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

**Record Last Update:** 20260725T190601+0000

### Ratings and Alerts

No rating or validation information has been found for IsoformEx.

No alerts have been found for IsoformEx.

### Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Dapas M, et al. (2017) Comparative evaluation of isoform-level gene expression estimation algorithms for RNA-seq and exon-array platforms. Briefings in bioinformatics, 18(2), 260.

Kim H, et al. (2011) IsoformEx: isoform level gene expression estimation using weighted non-negative least squares from mRNA-Seq data. BMC bioinformatics, 12, 305.