

Resource Summary Report

Generated by SPARC SAWG on Aug 2, 2026

IsoformEx

RRID:SCR_005235

Type: Tool

Proper Citation

IsoformEx (RRID:SCR_005235)

Resource Information

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

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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: 20260801T190258+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](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.