IsoEM

RRID:SCR_009993
Type: Tool

Proper Citation

IsoEM (RRID:SCR_009993)

Resource Information

URL: http://dna.engr.uconn.edu/?page_id=105

Proper Citation: IsoEM (RRID:SCR_009993)

Description: Software package that can be used to infer isoform and gene expression levels from high-throughput transcriptome sequencing (RNA-Seq) data.

Abbreviations: IsoEM

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: IsoEM

Resource ID: SCR_009993

Alternate IDs: biotools:isoem, OMICS_01278

Alternate URLs: https://bio.tools/isoem

Record Creation Time: 20220129T080256+0000

Record Last Update: 20250214T183131+0000

Ratings and Alerts

No rating or validation information has been found for IsoEM.

No alerts have been found for IsoEM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Igder S, et al. (2024) Circulating Nucleic Acids in Colorectal Cancer: Diagnostic and Prognostic Value. Disease markers, 2024, 9943412.

Knyazev S, et al. (2021) Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. Nucleic acids research, 49(17), e102.

Sang L, et al. (2021) Atlas of receptor genes expressed by the bovine morula and corresponding ligand-related genes expressed by uterine endometrium. Molecular reproduction and development, 88(10), 694.

Duan JE, et al. (2019) Methylome Dynamics of Bovine Gametes and in vivo Early Embryos. Frontiers in genetics, 10, 512.

Duan JE, et al. (2019) Dosage Compensation and Gene Expression of the X Chromosome in Sheep. G3 (Bethesda, Md.), 9(1), 305.

Duan JE, et al. (2019) Dosage Compensation of the X Chromosomes in Bovine Germline, Early Embryos, and Somatic Tissues. Genome biology and evolution, 11(1), 242.

Duan JE, et al. (2018) Effects of maternal nutrition on the expression of genomic imprinted genes in ovine fetuses. Epigenetics, 13(8), 793.

Karunakaran DK, et al. (2016) Network-based bioinformatics analysis of spatio-temporal RNA-Seq data reveals transcriptional programs underpinning normal and aberrant retinal development. BMC genomics, 17 Suppl 5(Suppl 5), 495.

Kanitz A, et al. (2015) Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. Genome biology, 16(1), 150.

Lee S, et al. (2015) EMSAR: estimation of transcript abundance from RNA-seq data by mappability-based segmentation and reclustering. BMC bioinformatics, 16, 278.