Resource Summary Report

Generated by RRID on Apr 10, 2025

GeneScissors

RRID:SCR_003146
Type: Tool

Proper Citation

GeneScissors (RRID:SCR_003146)

Resource Information

URL: http://csbio.unc.edu/genescissors/

Proper Citation: GeneScissors (RRID:SCR_003146)

Description: Software for detecting and correcting spurious transcriptome inference due to RNAseq reads misalignment.

Synonyms: Gene Scissors

Resource Type: software application, data processing software, software resource, data analysis software, sequence analysis software

Defining Citation: PMID:23812996

Keywords: transcriptome inference, read misalignment, rna seq

Funding:

Availability: Available for download, Supported by Linux

Resource Name: GeneScissors

Resource ID: SCR_003146

Alternate IDs: OMICS_01232

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250410T064944+0000

Ratings and Alerts

No rating or validation information has been found for GeneScissors.

No alerts have been found for GeneScissors.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Crowley JJ, et al. (2015) Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nature genetics, 47(4), 353.