# **Resource Summary Report**

Generated by NIF on Apr 29, 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:** data processing software, sequence analysis software, data analysis

software, software resource, software application

**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: 20250429T054821+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 NIF.

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.