

# Resource Summary Report

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## 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:** sequence analysis software, data analysis software, software resource, software application, data processing software

**Defining Citation:** [PMID:23812996](#)

**Keywords:** transcriptome inference, read misalignment, rna seq

**Availability:** Free, Available for download, Freely available

**Resource Name:** GeneScissors

**Resource ID:** SCR\_003146

**Alternate IDs:** OMICS\_01232

**Record Creation Time:** 20220129T080217+0000

**Record Last Update:** 20260728T043141+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 2 mentions in open access literature.

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

Chen J, et al. (2025) CD146+ CAFs mediate immunosuppression in gastric cancer via COL4A1: potential therapeutic targets. Journal for immunotherapy of cancer, 13(12).

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.