

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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 analysis software, data processing software, sequence analysis software, software application, software resource

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: 20260905T132458+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 [Kravitz](#) .

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.