

# Resource Summary Report

Generated by [T1D](#) on Jul 29, 2026

## BreakFusion

RRID:SCR\_001102

Type: Tool

### Proper Citation

BreakFusion (RRID:SCR\_001102)

### Resource Information

**URL:** <http://bioinformatics.mdanderson.org/main/BreakFusion>

**Proper Citation:** BreakFusion (RRID:SCR\_001102)

**Description:** Software package written in Perl and C++ that provides a computational pipeline for identifying gene fusions from RNA-seq data.

**Abbreviations:** BreakFusion

**Resource Type:** software resource

**Defining Citation:** [PMID:22563071](#), [DOI:10.1093/bioinformatics/bts272](#)

**Keywords:** computational pipeline, gene fusions, rna, sequence, data, perl, c++

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

**Resource Name:** BreakFusion

**Resource ID:** SCR\_001102

**Alternate IDs:** OMICS\_01342

**Record Creation Time:** 20220129T080205+0000

**Record Last Update:** 20260725T190454+0000

### Ratings and Alerts

No rating or validation information has been found for BreakFusion.

No alerts have been found for BreakFusion.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Kumar S, et al. (2016) Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data. Scientific reports, 6, 21597.

Latysheva NS, et al. (2016) Discovering and understanding oncogenic gene fusions through data intensive computational approaches. Nucleic acids research, 44(10), 4487.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.