Resource Summary Report

Generated by NIF on May 13, 2025

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++

Funding:

Availability: Open source, Available for download

Resource Name: BreakFusion

Resource ID: SCR_001102

Alternate IDs: OMICS_01342

Record Creation Time: 20220129T080205+0000

Record Last Update: 20250420T014021+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

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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.