Resource Summary Report

Generated by NIF on May 17, 2025

ShortFuse

RRID:SCR_001107
Type: Tool

Proper Citation

ShortFuse (RRID:SCR_001107)

Resource Information

URL: https://bitbucket.org/mckinsel/shortfuse

Proper Citation: ShortFuse (RRID:SCR_001107)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. A software package with tools for identifying fusion transcripts from RNA-Seq data. It is written in C++, and has dependencies on packages from Python 2.

Resource Type: software application, data analysis software, data processing software, sequence analysis software, software resource

Defining Citation: PMID:21330288

Keywords: fusion transcripts, rna, sequence data, python 2, c++, sequence analysis software, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ShortFuse

Resource ID: SCR_001107

Alternate IDs: biotools:shortfuse, OMICS_01355

Alternate URLs: https://bio.tools/shortfuse

Record Creation Time: 20220129T080205+0000

Record Last Update: 20250517T055455+0000

Ratings and Alerts

No rating or validation information has been found for ShortFuse.

No alerts have been found for ShortFuse.

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.

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