Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

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

Defining Citation: PMID:21330288

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

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: 20260808T185723+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 SPARC SAWG .

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