Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 15, 2025

nFuse

RRID:SCR_000066
Type: Tool

Proper Citation

nFuse (RRID:SCR_000066)

Resource Information

URL: https://code.google.com/p/nfuse/

Proper Citation: nFuse (RRID:SCR_000066)

Description: Software that predicts fusion transcripts and associated CGRs from matched RNA-seq and Whole Genome Shotgun Sequencing (WGSS).

Abbreviations: nFuse

Synonyms: nFuse: Discovery of Complex Genomic Rearrangements in Cancer

Resource Type: software resource

Defining Citation: PMID:22745232

Keywords: cancer, genomics

Related Condition: Cancer

Funding:

Availability: GNU General Public License, v3

Resource Name: nFuse

Resource ID: SCR_000066

Alternate IDs: OMICS_01353

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250410T064506+0000

Ratings and Alerts

No rating or validation information has been found for nFuse.

No alerts have been found for nFuse.

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 FDI Lab - SciCrunch.org.

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.