

Resource Summary Report

Generated by SPARC SAWG on Sep 18, 2026

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](https://pubmed.ncbi.nlm.nih.gov/22745232/)

Keywords: cancer, genomics

Related Condition: Cancer

Availability: Free, Available for download, Freely available,

Resource Name: nFuse

Resource ID: SCR_000066

Alternate IDs: OMICS_01353

License: GNU General Public License, v3

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260912T195502+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 [SPARC SAWG](#) .

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.