Resource Summary Report

Generated by SPARC SAWG on Sep 19, 2026

deFuse

RRID:SCR_003279
Type: Tool

Proper Citation

deFuse (RRID:SCR_003279)

Resource Information

URL: https://bitbucket.org/dranew/defuse

Proper Citation: deFuse (RRID:SCR_003279)

Description: Software package for gene fusion discovery using RNA-Seq data. It uses clusters of discordant paired end alignments to inform a split read alignment analysis for finding fusion boundaries.

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

Defining Citation: PMID:21625565

Keywords: rna sequencing, gene fusion, paired end alignment, split read, fusion boundary, bio.tools

Funding: British Columbia Cancer Foundation ;
Vancouver General Hospital Foundation ;
Genome Canada ;
Michael Smith Foundation for Health Research ;
Canadian Breast Cancer Foundation ;
Canadian Institutes of Health Research's Bioinformatics Training Program

Availability: Free, Available for download, Freely available

Resource Name: deFuse

Resource ID: SCR_003279

Alternate IDs: biotools:defuse, OMICS_01345

Alternate URLs: https://sourceforge.net/projects/defuse/, http://compbio.bccrc.ca/software/defuse/, https://bio.tools/defuse

Old URLs: http://sourceforge.net/apps/mediawiki/defuse/index.php?title=Main_Page

License: Creative Commons Attribution License

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260919T195016+0000

Ratings and Alerts

No rating or validation information has been found for deFuse.

No alerts have been found for deFuse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 95 mentions in open access literature.

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

Keck MK, et al. (2025) PLAG1 fusions define a third subtype of CNS embryonal tumor with PLAG family gene alteration. Acta neuropathologica, 150(1), 12.

Seo DH, et al. (2025) Radiotranscriptomics in papillary thyroid carcinoma complement current noninvasive risk stratification system. Science advances, 11(35), eadv6697.

Demeestere J, et al. (2025) Underestimation of Follow-Up Infarct Volume by Acute CT Perfusion Imaging. Neurology, 104(7), e213439.

Zhang Z, et al. (2024) Deviation From Personalized Blood Pressure Targets Correlates With Worse Outcome After Successful Recanalization. Journal of the American Heart Association, 13(7), e033633.

Anselmino N, et al. (2024) Integrative Molecular Analyses of the MD Anderson Prostate Cancer Patient-derived Xenograft (MDA PCa PDX) Series. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(10), 2272.

Lee J, et al. (2023) Comparative Analysis of Driver Mutations and Transcriptomes in Papillary Thyroid Cancer by Region of Residence in South Korea. Endocrinology and metabolism (Seoul, Korea), 38(6), 720.

Gentien D, et al. (2023) Multi-omics comparison of malignant and normal uveal melanocytes reveals molecular features of uveal melanoma. Cell reports, 42(9), 113132.

Fiore M, et al. (2023) Molecular Signature of Biological Aggressiveness in Clear Cell Sarcoma of the Kidney (CCSK). International journal of molecular sciences, 24(4).

D'Anna L, et al. (2023) Outcomes of mechanical thrombectomy in orally anticoagulated patients with anterior circulation large vessel occlusion: a propensity-matched analysis of the Imperial College Thrombectomy Registry. Journal of neurology, 270(12), 5827.

Stösser S, et al. (2023) Outcome of Stroke Patients with Unknown Onset and Unknown Time Last Known Well Undergoing Endovascular Therapy. Clinical neuroradiology, 33(1), 107.

Tsang ES, et al. (2023) Homologous recombination deficiency signatures in gastrointestinal and thoracic cancers correlate with platinum therapy duration. NPJ precision oncology, 7(1), 31.

de Traux de Wardin H, et al. (2023) Sequential genomic analysis using a multisample/multiplatform approach to better define rhabdomyosarcoma progression and relapse. NPJ precision oncology, 7(1), 96.

Ishino T, et al. (2023) Somatic mutations can induce a noninflamed tumour microenvironment via their original gene functions, despite deriving neoantigens. British journal of cancer, 128(6), 1166.

Bouchoucha Y, et al. (2022) Intra- and extra-cranial BCOR-ITD tumours are separate entities within the BCOR-rearranged family. The journal of pathology. Clinical research, 8(3), 217.

Reisle C, et al. (2022) A platform for oncogenomic reporting and interpretation. Nature communications, 13(1), 756.

Kishigami F, et al. (2022) Exploration of predictive biomarkers for postoperative recurrence of stage II/III colorectal cancer using genomic sequencing. Cancer medicine, 11(18), 3457.

Lavoie JM, et al. (2022) Whole-genome and transcriptome analysis of advanced adrenocortical cancer highlights multiple alterations affecting epigenome and DNA repair pathways. Cold Spring Harbor molecular case studies, 8(3).

Schultheis AM, et al. (2022) Genomic characterization of small cell carcinomas of the uterine cervix. Molecular oncology, 16(4), 833.

Cyrta J, et al. (2022) Breast carcinomas with osteoclast-like giant cells: a comprehensive clinico-pathological and molecular portrait and evidence of RANK-L expression. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 35(11), 1624.

Shen Y, et al. (2022) Comparison between collateral status and DEFUSE 3 or DAWN criteria in patient selection for endovascular thrombectomy within 6-24 hours after stroke: a protocol for meta-analysis. BMJ open, 12(10), e059557.