

Resource Summary Report

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deFuse

RRID:SCR_003279

Type: Tool

Proper Citation

deFuse (RRID:SCR_003279)

Resource Information

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

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

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Record Creation Time: 20220129T080218+0000

Record Last Update: 20260729T044045+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 [dkNET](#) .

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.

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).

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.

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.

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).

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.

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

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.

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.