Resource Summary Report

Generated by NIF on Apr 19, 2025

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

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

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 Last Update: 20250419T054913+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 92 mentions in open access literature.

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

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.

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.

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.

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.

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.

Zhang Y, et al. (2021) Rearrangement-mediated cis-regulatory alterations in advanced

patient tumors reveal interactions with therapy. Cell reports, 37(7), 110023.

Yaghi S, et al. (2021) The Effect of Hyperglycemia on Infarct Growth after Reperfusion: An Analysis of the DEFUSE 3 trial. Journal of stroke and cerebrovascular diseases : the official journal of National Stroke Association, 30(1), 105380.

Rogounovitch TI, et al. (2021) Major Oncogenic Drivers and Their Clinicopathological Correlations in Sporadic Childhood Papillary Thyroid Carcinoma in Belarus. Cancers, 13(13).