Resource Summary Report

Generated by NIF on Apr 19, 2025

SOAPfuse

RRID:SCR_000078
Type: Tool

Proper Citation

SOAPfuse (RRID:SCR_000078)

Resource Information

URL: http://soap.genomics.org.cn/soapfuse.html

Proper Citation: SOAPfuse (RRID:SCR_000078)

Description: THIS RESOURCE IS NO LONGER IN SERVICE.Documented on August 23,2022. An open source tool developed for genome-wide detection of fusion transcripts from human being paired-end RNA-Seq data. This tool is a part of a larger set of tools to efficiently align oligonucleotides onto reference sequences .

Abbreviations: SOAPfuse

Resource Type: software resource

Defining Citation: PMID:23409703

Keywords: software, resource, open license, DNA sequencing, genome, transcripts, RNA, oligonucleotide

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SOAPfuse

Resource ID: SCR_000078

Alternate IDs: OMICS_01357

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250410T064508+0000

Ratings and Alerts

No rating or validation information has been found for SOAPfuse.

No alerts have been found for SOAPfuse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Ou MY, et al. (2021) The CTNNBIP1-CLSTN1 fusion transcript regulates human neocortical development. Cell reports, 35(13), 109290.

Hsieh G, et al. (2017) Statistical algorithms improve accuracy of gene fusion detection. Nucleic acids research, 45(13), e126.

Latysheva NS, et al. (2016) Discovering and understanding oncogenic gene fusions through data intensive computational approaches. Nucleic acids research, 44(10), 4487.

Yu J, et al. (2016) Disruption of NCOA2 by recurrent fusion with LACTB2 in colorectal cancer. Oncogene, 35(2), 187.

Kumar S, et al. (2016) Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data. Scientific reports, 6, 21597.

Lee JR, et al. (2016) Transcriptome analysis of paired primary colorectal carcinoma and liver metastases reveals fusion transcripts and similar gene expression profiles in primary carcinoma and liver metastases. BMC cancer, 16, 539.

Jia W, et al. (2013) SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. Genome biology, 14(2), R12.