Resource Summary Report

Generated by dkNET on Apr 30, 2025

chimerascan

RRID:SCR_013298
Type: Tool

Proper Citation

chimerascan (RRID:SCR_013298)

Resource Information

URL: http://code.google.com/p/chimerascan/

Proper Citation: chimerascan (RRID:SCR_013298)

Description: Software package that detects gene fusions in paired-end RNA sequencing (RNA-Seq) datasets. Used for detection of chimeric transcripts in high-throughput sequencing data.

Abbreviations: chimerascan

Resource Type: software resource

Keywords: Gene fusion detection, paired-end RNA sequencing data, RNA sequencing data, chimeric transcripts detection, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: chimerascan

Resource ID: SCR_013298

Alternate IDs: biotools:chimerascan, OMICS_01343

Alternate URLs: https://bio.tools/chimerascan

License: GNU GPL v3

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250420T014640+0000

Ratings and Alerts

No rating or validation information has been found for chimerascan.

No alerts have been found for chimerascan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 52 mentions in open access literature.

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

Jung DE, et al. (2024) PUM1-TRAF3 fusion protein activates non-canonical NF-?B signaling via rescued NIK in biliary tract cancer. NPJ precision oncology, 8(1), 170.

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

Qiu Q, et al. (2021) Integrated analysis of virus and host transcriptomes in cervical cancer in Asian and Western populations. Genomics, 113(3), 1554.

Bae K, et al. (2021) A fusion of CD63-BCAR4 identified in lung adenocarcinoma promotes tumorigenicity and metastasis. British journal of cancer, 124(1), 290.

Wang MY, et al. (2021) Transcriptome Analysis Reveals MFGE8-HAPLN3 Fusion as a Novel Biomarker in Triple-Negative Breast Cancer. Frontiers in oncology, 11, 682021.

Liu Z, et al. (2021) Unraveling Gene Fusions for Drug Repositioning in High-Risk Neuroblastoma. Frontiers in pharmacology, 12, 608778.

Kovac M, et al. (2021) The early evolutionary landscape of osteosarcoma provides clues for targeted treatment strategies. The Journal of pathology, 254(5), 556.

Ameline B, et al. (2021) Overactivation of the IGF signalling pathway in osteosarcoma: a potential therapeutic target? The journal of pathology. Clinical research, 7(2), 165.

Cai Z, et al. (2020) Fcirc: A comprehensive pipeline for the exploration of fusion linear and circular RNAs. GigaScience, 9(6).

Tian L, et al. (2020) CICERO: a versatile method for detecting complex and diverse driver

fusions using cancer RNA sequencing data. Genome biology, 21(1), 126.

Lee E, et al. (2020) Genomic profile of MYCN non-amplified neuroblastoma and potential for immunotherapeutic strategies in neuroblastoma. BMC medical genomics, 13(1), 171.

Ameline B, et al. (2020) NTRK fusions in osteosarcoma are rare and non-functional events. The journal of pathology. Clinical research, 6(2), 107.

Yun JW, et al. (2020) Dysregulation of cancer genes by recurrent intergenic fusions. Genome biology, 21(1), 166.

Urbini M, et al. (2020) Gene duplication, rather than epigenetic changes, drives FGF4 overexpression in KIT/PDGFRA/SDH/RAS-P WT GIST. Scientific reports, 10(1), 19829.

Kim SC, et al. (2019) Identification of a Novel Fusion Gene, FAM174A-WWC1, in Early-Onset Colorectal Cancer: Establishment and Characterization of Four Human Cancer Cell Lines from Early-Onset Colorectal Cancers. Translational oncology, 12(9), 1185.

Pfeifer A, et al. (2019) Novel TG-FGFR1 and TRIM33-NTRK1 transcript fusions in papillary thyroid carcinoma. Genes, chromosomes & cancer, 58(8), 558.

Padella A, et al. (2019) Novel and Rare Fusion Transcripts Involving Transcription Factors and Tumor Suppressor Genes in Acute Myeloid Leukemia. Cancers, 11(12).

Jang JE, et al. (2019) NFATC3-PLA2G15 Fusion Transcript Identified by RNA Sequencing Promotes Tumor Invasion and Proliferation in Colorectal Cancer Cell Lines. Cancer research and treatment, 51(1), 391.

Haile S, et al. (2019) Evaluation of protocols for rRNA depletion-based RNA sequencing of nanogram inputs of mammalian total RNA. PloS one, 14(10), e0224578.

L Abbate A, et al. (2018) MYC-containing amplicons in acute myeloid leukemia: genomic structures, evolution, and transcriptional consequences. Leukemia, 32(10), 2152.