

Resource Summary Report

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[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

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: 20260903T235217+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 53 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Shah M, et al. (2025) Peptide-based therapeutics targeting the SLC39A14-PIWIL2 fusion in hepatocellular carcinoma. *Genomics & informatics*, 23(1), 28.

Jung DE, et al. (2024) PUM1-TRAF3 fusion protein activates non-canonical NF- κ 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.

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

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

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.

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.

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

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

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.

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

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.

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.