Resource Summary Report

Generated by NIF on May 16, 2025

FusionMap

RRID:SCR_005242
Type: Tool

Proper Citation

FusionMap (RRID:SCR_005242)

Resource Information

URL: http://www.omicsoft.com/fusionmap/

Proper Citation: FusionMap (RRID:SCR_005242)

Description: An efficient fusion aligner which aligns reads spanning fusion junctions directly to the genome without prior knowledge of potential fusion regions. It detects and characterizes fusion junctions at base-pair resolution. FusionMap can be applied to detect fusion junctions in both single- and paired-end dataset from either gDNA-Seq or RNA-Seq studies. FusionMap runs under both Windows and Linux (requiring MONO) environments. Although it can run on 32 bit machine, it is recommended to run on 64-bit machine with 8GB RAM or more. If you have an ArrayStudio License, you can run the fusion detection easily through its GUI.

Abbreviations: FusionMap

Resource Type: software resource

Defining Citation: PMID:21593131

Keywords: windows, linux, c#, fusion gene, next-generation sequencing, gene, reference indexing, read filtering, fusion alignment, reporting, alignment, bio.tools

Funding:

Availability: Free, Non-commercial

Resource Name: FusionMap

Resource ID: SCR_005242

Alternate IDs: biotools:fusionmap, OMICS_00316

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

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014247+0000

Ratings and Alerts

No rating or validation information has been found for FusionMap.

No alerts have been found for FusionMap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Feng J, et al. (2024) Clinical relevance and druggability of sole reciprocal kinase fusions: A large-scale study. Cancer medicine, 13(17), e70191.

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.

Kebede AM, et al. (2024) Comprehensive genomic characterization of hematologic malignancies at a pediatric tertiary care center. Frontiers in oncology, 14, 1498409.

DiPeri TP, et al. (2024) Utilizing Patient-derived Xenografts to Model Precision Oncology for Biliary Tract Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research.

Kou FR, et al. (2024) Analysis of actionable gene fusions in a large cohort of Chinese patients with colorectal cancer. Gastroenterology report, 12, goae092.

Zhou S, et al. (2023) Novel insights into molecular patterns of ROS1 fusions in a large Chinese NSCLC cohort: a multicenter study. Molecular oncology, 17(10), 2200.

Chen H, et al. (2023) A unified DNA- and RNA-based NGS strategy for the analysis of multiple types of variants at the dual nucleic acid level in solid tumors. Journal of clinical

laboratory analysis, 37(19-20), e24977.

Wang Z, et al. (2023) Molecular characterization of genomic breakpoints of ALK rearrangements in non-small cell lung cancer. Molecular oncology, 17(5), 765.

Lipplaa A, et al. (2023) A novel colony-stimulating factor 1 (CSF1) translocation involving human endogenous retroviral element in a tenosynovial giant cell tumor. Genes, chromosomes & cancer, 62(4), 223.

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.

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).

Tauziède-Espariat A, et al. (2022) An integrative histopathological and epigenetic characterization of primary intracranial mesenchymal tumors, FET:CREB-fused broadening the spectrum of tumor entities in comparison with their soft tissue counterparts. Brain pathology (Zurich, Switzerland), 32(1), e13010.

Vasella M, et al. (2022) Novel RGAG1-BCOR gene fusion revealed in a somatic soft tissue sarcoma with a long follow-up. Virchows Archiv : an international journal of pathology, 480(5), 1107.

Shi M, et al. (2022) Identification of RET fusions in a Chinese multicancer retrospective analysis by next-generation sequencing. Cancer science, 113(1), 308.

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.

Zhang L, et al. (2022) Novel read-through fusion transcript Bcl2l2-Pabpn1 in glioblastoma cells. Journal of cellular and molecular medicine, 26(17), 4686.

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.

Liu D, et al. (2021) Identification of Chimeric RNAs in Pig Skeletal Muscle and Transcriptomic Analysis of Chimeric RNA TNNI2-ACTA1 V1. Frontiers in veterinary science, 8, 742593.

Wang P, et al. (2021) The Presence of Genomic Instability in Cerebrospinal Fluid in Patients with Meningeal Metastasis. Cancer management and research, 13, 4853.

Si X, et al. (2021) Genomic characteristics of driver genes in Chinese patients with non-small cell lung cancer. Thoracic cancer, 12(3), 357.