Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

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

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: 20260725T190600+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 88 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Liu Z, et al. (2025) Illuminating the FGFR fusion landscape in Chinese patients: unveiling novel molecular insights and clinical implications. The oncologist, 30(11).

Su D, et al. (2025) Molecular Subtyping and Genomic Profiling Expand Precision Medicine in KRAS Wild-Type Pancreatic Cancer. Cancer science, 116(4), 1094.

Yang Q, et al. (2025) Combined utility of genomic breakpoints and frame is a reliable predictor of ALK transcript function. Scientific reports, 15(1), 8437.

Vanacker H, et al. (2025) Assessing targetable NTRK1/2/3 fusions in mesenchymal tumors via whole-exome RNA sequencing. ESMO open, 10(9), 105555.

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.

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

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

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

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.

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.

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.

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.

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.

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

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.