

Resource Summary Report

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FusionMap

RRID:SCR_005242

Type: Tool

Proper Citation

FusionMap (RRID:SCR_005242)

Resource Information

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

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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: 20260808T185836+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 89 mentions in open access literature.

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

Hamid F, et al. (2026) PFGPred: a stack ensemble classifier for the identification of fusion genes in plants. DNA research : an international journal for rapid publication of reports on genes and genomes, 33(3).

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

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

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.

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

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.

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.

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