Resource Summary Report

Generated by ASWG on Aug 4, 2026

Oncofuse

RRID:SCR_011904
Type: Tool

Proper Citation

Oncofuse (RRID:SCR_011904)

Resource Information

URL: http://www.unav.es/genetica/oncofuse.html

Proper Citation: Oncofuse (RRID:SCR_011904)

Description: Software tool designed to predict the oncogenic potential of fusion genes found by Next-Generation Sequencing in cancer cells.

Abbreviations: Oncofuse

Resource Type: software resource

Defining Citation: DOI:10.1093/bioinformatics/btt445

Resource Name: Oncofuse

Resource ID: SCR_011904

Alternate IDs: OMICS_01406

Old URLs: https://sources.debian.org/src/oncofuse/

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190431+0000

Ratings and Alerts

No rating or validation information has been found for Oncofuse.

No alerts have been found for Oncofuse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Kyriazoglou A, et al. (2025) Exploring the impact of NGS on diagnostics and treatment of sarcoma: insights from real-world data across multiple institutions in Europe. ESMO open, 10(9), 105577.

Chen C, et al. (2024) Identification of a novel MEF2C::SS18L1 fusion in childhood acute B-lymphoblastic leukemia. Journal of cancer research and clinical oncology, 150(6), 314.

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

Pareja F, et al. (2020) Pleomorphic adenomas and mucoepidermoid carcinomas of the breast are underpinned by fusion genes. NPJ breast cancer, 6, 20.

Umbreit EC, et al. (2020) Origin of Subsequent Malignant Neoplasms in Patients with History of Testicular Germ Cell Tumor. Cancers, 12(12).

Basturk O, et al. (2020) Sclerosing epithelioid mesenchymal neoplasm of the pancreas - a proposed new entity. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 33(3), 456.

Kim SH, et al. (2020) Identification of recurrent FHL2-GLI2 oncogenic fusion in sclerosing stromal tumors of the ovary. Nature communications, 11(1), 44.

Elliott E, et al. (2020) Paired tumor sequencing and germline testing in breast cancer management: An experience of a single academic center. Cancer reports (Hoboken, N.J.), 3(6), e1287.

Leong TL, et al. (2019) Deep multi-region whole-genome sequencing reveals heterogeneity and gene-by-environment interactions in treatment-naive, metastatic lung cancer. Oncogene, 38(10), 1661.

Parris TZ, et al. (2018) Genome-wide multi-omics profiling of the 8p11-p12 amplicon in breast carcinoma. Oncotarget, 9(35), 24140.

Engqvist H, et al. (2018) Transcriptomic and genomic profiling of early-stage ovarian carcinomas associated with histotype and overall survival. Oncotarget, 9(80), 35162.

Ayars M, et al. (2017) IL2RG, identified as overexpressed by RNA-seq profiling of pancreatic intraepithelial neoplasia, mediates pancreatic cancer growth. Oncotarget, 8(48), 83370.

Gray PN, et al. (2016) TumorNext: A comprehensive tumor profiling assay that incorporates high resolution copy number analysis and germline status to improve testing

accuracy. Oncotarget, 7(42), 68206.

Koh Y, et al. (2015) Detection of a Distinctive Genomic Signature in Rhabdoid Glioblastoma, A Rare Disease Entity Identified by Whole Exome Sequencing and Whole Transcriptome Sequencing. Translational oncology, 8(4), 279.