Resource Summary Report

Generated by RRID on Aug 5, 2026

OncoTree

RRID:SCR_026218
Type: Tool

Proper Citation

OncoTree (RRID:SCR_026218)

Resource Information

URL: https://oncotree.mskcc.org/

Proper Citation: OncoTree (RRID:SCR_026218)

Description: Community-driven cancer classification platform encompassing rare and common cancers that provides clinically relevant and appropriately granular cancer classification for clinical decision support systems and oncology research. Cancer classification system for precision oncology.

Resource Type: topical portal, portal, disease-related portal, data or information resource

Defining Citation: PMID:33625877

Keywords: cancer classification platform, rare and common cancers, cancer classification, precision oncology,

Related Condition: cancer

Funding: NCI P30 CA008748

Availability: Free, Freely available

Resource Name: OncoTree

Resource ID: SCR_026218

Record Creation Time: 20250103T053333+0000

Record Last Update: 20260805T044556+0000

Ratings and Alerts

No rating or validation information has been found for OncoTree.

No alerts have been found for OncoTree.

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 RRID .

Ivanov M, et al. (2025) Analytical and Clinical Validation of Solo-Test Driver: A Targeted Amplicon-Based NGS Test-System for FFPE and cfDNA Analysis in Clinical Oncology Setting. Journal of clinical laboratory analysis, 39(6), e70008.

Elloumi F, et al. (2025) Protocol to set up the CellMinerCDB pharmacogenomics analysis web application with custom cell line data. STAR protocols, 6(4), 104076.

Starobova H, et al. (2025) Inhibition of the NLRP3 inflammasome using MCC950 reduces vincristine-induced adverse effects in an acute lymphoblastic leukemia patient-derived xenograft model. HemaSphere, 9(3), e70092.

Breen KE, et al. (2025) Paired tumor-normal sequencing provides insights into the CDKN2A-associated tumor spectrum. NPJ precision oncology, 9(1), 363.

Kurz NS, et al. (2025) Onkopus: precise interpretation and prioritization of sequence variants for biomedical research and precision medicine. Nucleic acids research, 53(W1), W431.

Taniguchi SH, et al. (2025) Impact of genetic mutations on prognosis and chemotherapy efficacy in advanced appendiceal carcinoma: insights from the nationwide Japanese comprehensive genomic profiling test database. International journal of clinical oncology, 30(5), 914.

Ghani H, et al. (2025) GPSai: A Clinically Validated AI Tool for Tissue of Origin Prediction during Routine Tumor Profiling. Cancer research communications, 5(9), 1477.

Zheng S, et al. (2023) Integrating POLE/POLD1 mutated for immunotherapy treatment planning of advanced stage non-small cell lung cancer. Thoracic cancer, 14(23), 2269.

Jiang W, et al. (2023) Tri??DB: an integrated platform of knowledgebase and reporting system for cancer precision medicine. Journal of translational medicine, 21(1), 885.

Pugh TJ, et al. (2022) AACR Project GENIE: 100,000 Cases and Beyond. Cancer discovery, 12(9), 2044.

Reisle C, et al. (2022) A platform for oncogenomic reporting and interpretation. Nature communications, 13(1), 756.

Zhang Y, et al. (2021) Pan-cancer circulating tumor DNA detection in over 10,000 Chinese patients. Nature communications, 12(1), 11.

Thomas S, et al. (2020) Linked Entity Attribute Pair (LEAP): A Harmonization Framework for Data Pooling. JCO clinical cancer informatics, 4, 691.

Gorelick AN, et al. (2020) Phase and context shape the function of composite oncogenic mutations. Nature, 582(7810), 100.