

# Resource Summary Report

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## 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:** data or information resource, disease-related portal, portal, topical portal

**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:** 20260912T200500+0000

### Ratings and Alerts

No rating or validation information has been found for OncoTree.

No alerts have been found for OncoTree.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Saito Y, et al. (2026) Real-world clinical utility of comprehensive genomic profiling in advanced solid tumors. *Nature medicine*, 32(2), 690.

Yasuda T, et al. (2026) Refining Tumor Mutational Burden as a Predictive Biomarker for Pembrolizumab: A Real-World Analysis in Japanese Patients. *Cancer science*, 117(4), 1158.

Song X, et al. (2026) OncoRisk: a state-of-the-art web server for bridging the oncogenic databases and pan-cancer cohorts to the translational oncology. *Communications biology*, 9(1).

Uporey D, et al. (2026) Real-World Biomarker-Associated Therapy in Metastatic Carcinoma of Unknown Primary: Prevalence, Impact, and Outcomes. *Journal of the National Comprehensive Cancer Network : JNCCN*, 24(4).

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.

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.

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

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.

Kurz NS, et al. (2025) Onkopos: 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) TriDB: an integrated platform of knowledgebase and reporting system for cancer precision medicine. *Journal of translational medicine*, 21(1), 885.

Sobahy TM, et al. (2022) Clinically actionable cancer somatic variants (CACSV): a tumor interpreted dataset for analytical workflows. *BMC medical genomics*, 15(1), 95.

Wang S, et al. (2022) KRAS Mutation in Rare Tumors: A Landscape Analysis of 3453 Chinese Patients. *Frontiers in molecular biosciences*, 9, 831382.

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.