

Resource Summary Report

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Oncotator

RRID:SCR_005183

Type: Tool

Proper Citation

Oncotator (RRID:SCR_005183)

Resource Information

URL: <http://www.broadinstitute.org/cancer/cga/ncotator>

Proper Citation: Oncotator (RRID:SCR_005183)

Description: A tool for annotating human genomic point mutations and indels with data relevant to cancer researchers. Genomic Annotations, Protein Annotations, and Cancer Annotations are aggregated from many resources. A standalone version of Oncotator is being developed.

Abbreviations: Oncotator

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: annotate, genomic, point mutation, indel, mutation, genome, protein, variant

Related Condition: Cancer

Resource Name: Oncotator

Resource ID: SCR_005183

Alternate IDs: OMICS_00178

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260905T133128+0000

Ratings and Alerts

No rating or validation information has been found for Oncotator.

No alerts have been found for Oncotator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 223 mentions in open access literature.

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

Camp SY, et al. (2026) Single-cell epigenetic profiling reveals a tumor-intrinsic interferon response program in ccRCC tied to poor prognosis and BAP1 loss. *Science advances*, 12(8), eadv5457.

Kuo HH, et al. (2026) Patient-derived organoids across cancers reveal conserved tumor heterogeneity and actionable therapeutic vulnerabilities. *Science advances*, 12(26), eadz3351.

Ravillah D, et al. (2026) VSIG10L is a major determinant of esophageal homeostasis and inherited predisposition to Barrett's esophagus. *Nature communications*, 17(1).

Shi Y, et al. (2026) Genomic, Clinical, and Spatial Predictors of Durable Response to BRAF/MEK Inhibition in BRAF-Mutant Melanoma. *bioRxiv : the preprint server for biology*.

Lee EJ, et al. (2026) JIN-A02, a Mutant-Selective Fourth-Generation EGFR Inhibitor, Overcomes C797S-Mediated Resistance and Demonstrates Intracranial Activity in NSCLC. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1835.

Feng J, et al. (2026) Molecular and clinical characteristics of glioma patients with germline pathogenic mutations of Lynch syndrome genes: a large-scale multicenter study. *Journal of translational medicine*, 24(1).

Yang W, et al. (2026) Clinically actionable stratification of uncommon MET fusions: a precision oncology framework. *Journal of translational medicine*, 24(1).

Gentile C, et al. (2026) mSWI/SNF complex inhibition sensitizes KRAS-mutant lung cancers to targeted therapies via epithelial-mesenchymal subversion. *bioRxiv : the preprint server for biology*.

Oh SY, et al. (2025) The potential of lazertinib and amivantamab combination therapy as a treatment strategy for uncommon EGFR-mutated NSCLC. *Cell reports. Medicine*, 6(2), 101929.

Ghosh A, et al. (2025) Genomic hallmarks of endocrine therapy resistance in ER/PR+HER2- breast tumours. *Communications biology*, 8(1), 207.

Zhong S, et al. (2025) Genomic landscape and immunological profile of glioblastoma in East Asian patients. *Cell reports. Medicine*, 6(8), 102217.

K??bler K, et al. (2025) Tamoxifen induces PI3K activation in uterine cancer. *Nature genetics*, 57(9), 2192.

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

Zhang X, et al. (2025) Comprehensive molecular profiling of FH-deficient renal cell carcinoma identifies molecular subtypes and potential therapeutic targets. *Nature communications*, 16(1), 4398.

Feng EM, et al. (2025) Racial variation in the advanced prostate cancer genome. *Prostate cancer and prostatic diseases*, 28(4), 902.

Sun W, et al. (2025) A mutational process signature and genomic alterations associated with outcome and immunogenicity in cancers with brain metastasis. *Frontiers in immunology*, 16, 1607772.

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.

Wu M, et al. (2025) Genomic copy-number variants drive apoptotic evasion underlying acquired resistance to immune checkpoint inhibitors. *Immunity*, 58(11), 2864.

Knight AD, et al. (2025) Melanoma to rhabdomyosarcoma plasticity in the setting of immunotherapy. *medRxiv : the preprint server for health sciences*.

Wang H, et al. (2025) Genome-Wide Association Analysis of Flavor Precursor Traits in Chengkou Mountain Chicken. *Animals : an open access journal from MDPI*, 15(12).