

Resource Summary Report

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UCSC Cancer Genomics Browser

RRID:SCR_011796

Type: Tool

Proper Citation

UCSC Cancer Genomics Browser (RRID:SCR_011796)

Resource Information

URL: <https://genome-cancer.ucsc.edu/>

Proper Citation: UCSC Cancer Genomics Browser (RRID:SCR_011796)

Description: A suite of web-based tools to visualize, integrate and analyze cancer genomics and its associated clinical data. It is possible to display your own clinical data within one of their datasets.

Abbreviations: Cancer Genomics Browser

Resource Type: database, data or information resource, service resource

Defining Citation: [PMID:23109555](#), [PMID:21059681](#), [PMID:19333237](#)

Keywords: genome, genomics, clinical, next-generation sequencing, chromosome, gene, FASEB list

Related Condition: Cancer

Funding: NCI ;
NHGRI ;
American Association for Cancer Research ;
UCSF Comprehensive Cancer Center ;
California Institute for Quantitative Biosciences

Availability: Acknowledgement requested

Resource Name: UCSC Cancer Genomics Browser

Resource ID: SCR_011796

Alternate IDs: OMICS_00925

Record Creation Time: 20220129T080306+0000

Ratings and Alerts

No rating or validation information has been found for UCSC Cancer Genomics Browser.

No alerts have been found for UCSC Cancer Genomics Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 589 mentions in open access literature.

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

Park S, et al. (2026) Multi-modal molecular and spatial profiling reveals NNT as a prognostic biomarker in obesity-associated colorectal cancer. *Journal of gastroenterology*, 61(4), 435.

Moustafa RI, et al. (2026) SOX9 and TNFAIP3 dysregulation in HCV-associated HCC after DAA therapy: insights into post-viral oncogenic memory. *Infectious agents and cancer*, 21(1).

Huang J, et al. (2026) Increased IL4I1 expression predicts poor survival and modulates the immune microenvironment in acute myeloid leukemia. *Journal of translational medicine*, 24(1), 258.

He R, et al. (2026) Stromal ACTA2 Counteracts TCDD-Induced Hepatocarcinogenesis via Suppression of the PI3K-AKT-mTOR Pathway. *Journal of hepatocellular carcinoma*, 13, 586916.

Wang W, et al. (2026) Identification of TMEM59L as a potential diagnosis, prognosis and immunotherapy biomarker for colon adenocarcinoma. *Scientific reports*, 16(1), 5765.

Lee MK, et al. (2026) Keratinization-related gene signature predicting survival and response to radiation in patients with HPV-negative head and neck squamous cell carcinoma via regulation of cornification and integrin signaling. *Cellular & molecular biology letters*, 31(1).

Yan J, et al. (2026) Perspectives from machine learning and multi-omics to decoding the effects of VDAC2 malignant subsets on tumor evolution. *NPJ precision oncology*, 10(1).

Liu H, et al. (2026) AKAP7 is a prognostic biomarker involved in immune infiltration of bladder urothelial carcinoma and correlated with ferroptosis. *Discover oncology*, 17(1).

Zhai Z, et al. (2026) Unveiling the role of ANGPT2 in esophageal cancer: A prognostic factor and potential oncogene. *Oncology reports*, 55(5).

Zheng M, et al. (2025) The CYLD-PARP1 feedback loop regulates DNA damage repair and chemosensitivity in breast cancer cells. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2413890121.

You P, et al. (2025) Knockdown of RFC4 inhibits cell proliferation of oral squamous cell carcinoma in vitro and in vivo. *FEBS open bio*, 15(2), 346.

Liu L, et al. (2025) Multi-omics dissection of CPNE1 reveals its prognostic value and immune-regulatory function in liver cancer. *Discover oncology*, 16(1), 1499.

Lee MK, et al. (2025) Prognostic value of FLOT1-related gene signature in head and neck squamous cell carcinoma: insights into radioresistance mechanisms and clinical outcomes. *Cell death discovery*, 11(1), 224.

Chen C, et al. (2025) Predicting breast cancer prognosis based on a novel pathomics model through CHEK1 expression analysis using machine learning algorithms. *PloS one*, 20(5), e0321717.

Noh JK, et al. (2025) Inhibition of NR2F2 suppresses invasion ability and modulates EMT marker in head and neck squamous cell carcinoma. *Discover oncology*, 16(1), 1887.

Xu H, et al. (2025) CREB3L1 facilitates pancreatic tumor progression and reprograms intratumoral tumor-associated macrophages to shape an immunotherapy-resistance microenvironment. *Journal for immunotherapy of cancer*, 13(1).

Moazzam NF, et al. (2025) FoxM1 promotes TFAM expression and regulates Mitochondrial Dynamics in Glioblastoma cells. *Journal of Cancer*, 16(15), 4378.

Yuan S, et al. (2025) CLIC3 emerges as a novel prognostic biomarker and therapeutic target in triple-negative breast cancer through integrated multi-omics analysis. *BMC cancer*, 25(1), 1828.

Gu J, et al. (2025) SIGLEC1 has the potential to be an immune-related prognostic indicator in colon adenocarcinoma: a study based on transcriptomic data and Mendelian randomization analysis. *Discover oncology*, 16(1), 324.

Yan J, et al. (2025) Comprehensive pan-cancer analysis indicates key gene of p53-independent apoptosis is a novel biomarker for clinical application and chemotherapy in colorectal cancer. *Frontiers in immunology*, 16, 1571137.