Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

The Cancer Genome Atlas

RRID:SCR_003193
Type: Tool

Proper Citation

The Cancer Genome Atlas (RRID:SCR_003193)

Resource Information

URL: http://cancergenome.nih.gov/

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Description: Project exploring the spectrum of genomic changes involved in more than 20 types of human cancer that provides a platform for researchers to search, download, and analyze data sets generated. As a pilot project it confirmed that an atlas of changes could be created for specific cancer types. It also showed that a national network of research and technology teams working on distinct but related projects could pool the results of their efforts, create an economy of scale and develop an infrastructure for making the data publicly accessible. Its success committed resources to collect and characterize more than 20 additional tumor types. Components of the TCGA Research Network: * Biospecimen Core Resource (BCR); Tissue samples are carefully cataloged, processed, checked for quality and stored, complete with important medical information about the patient. * Genome Characterization Centers (GCCs); Several technologies will be used to analyze genomic changes involved in cancer. The genomic changes that are identified will be further studied by the Genome Sequencing Centers. * Genome Sequencing Centers (GSCs); High-throughput Genome Sequencing Centers will identify the changes in DNA sequences that are associated with specific types of cancer. * Proteome Characterization Centers (PCCs); The centers, a component of NCI's Clinical Proteomic Tumor Analysis Consortium, will ascertain and analyze the total proteomic content of a subset of TCGA samples. * Data Coordinating Center (DCC); The information that is generated by TCGA will be centrally managed at the DCC and entered into the TCGA Data Portal and Cancer Genomics Hub as it becomes available. Centralization of data facilitates data transfer between the network and the research community, and makes data analysis more efficient. The DCC manages the TCGA Data Portal. * Cancer Genomics Hub (CGHub); Lower level sequence data will be deposited into a secure repository. This database stores cancer genome sequences and alignments. * Genome Data Analysis Centers (GDACs) - Immense amounts of data from array and second-generation sequencing technologies must be integrated across thousands of samples. These centers will provide novel informatics tools to the entire research community to facilitate broader use of TCGA data. TCGA is actively developing a network of collaborators who are able to provide

samples that are collected retrospectively (tissues that had already been collected and stored) or prospectively (tissues that will be collected in the future).

Abbreviations: TCGA

Synonyms: Cancer Genome Atlas

Resource Type: biomaterial supply resource, material resource

Keywords: genome, genome sequencing, breast, central nervous system, endocrine, gastrointestinal, gynecologic, head, neck, hematologic, skin, soft tissue, thoracic, urologic, clinical, genomic characterization, analysis, tumor genome, demographic, gene expression, copy number alteration, epigenetic, dna sequence, exome, snp, methylation, mrna, mirna, FASEB list

Related Condition: Cancer, Tumor, Normal, Breast cancer, Central Nervous System cancer, Endocrine cancer, Gastrointestinal cancer, Gynecologic cancer, Head cancer, Neck cancer, Hematologic cancer, Skin cancer, Soft tissue cancer, Thoracic cancer, Urologic cancer

Funding: NCI 261200800001E-12-0-1

Resource Name: The Cancer Genome Atlas

Resource ID: SCR_003193

Alternate IDs: nlx_156913

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260725T191227+0000

Ratings and Alerts

No rating or validation information has been found for The Cancer Genome Atlas.

No alerts have been found for The Cancer Genome Atlas.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6292 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Patra M, et al. (2026) SIRT2 mitigates radiation-induced oral mucositis by promoting homologous recombination-mediated DNA double-strand break repair in epithelial stem cells. Cancer letters, 640, 218239.

Chang LJ, et al. (2026) Assessment of Circulating Tumor DNA for Early Detection of Hepatocellular Carcinoma in Alpha-Fetoprotein-Negative Patients With Cirrhotic Nodules. JGH open : an open access journal of gastroenterology and hepatology, 10(1), e70331.

Cao Z, et al. (2026) Study on the mechanism of PSENEN in modulating cisplatin resistance in NSCLC through stromal cell interactions. International immunopharmacology, 169, 116037.

Pan K, et al. (2026) Lysine methylation-mediated SMYD2 degradation by casticin sensitizes non-small-cell lung cancer cells to osimertinib therapy. Biochemical pharmacology, 243(Pt 2), 117562.

Chen C, et al. (2026) Identifying myosin heavy chain 11 as a predictive biomarker of prostate cancer progression and antiandrogen resistance. Oncology letters, 31(2), 77.

Gou X, et al. (2026) Identification of a Two-Gene Biomarker Correlated with Sensitivity to Combined PARP7 Inhibition and AHR Activation in Cancer Cells. Cancer research communications, 6(1), 5.

Guo X, et al. (2026) HBx hijacks the miR-19a-3p/BAMBI/TGF-?1 axis to impair the anti-tumour activity of CD4+ T cells in diffuse large B-cell lymphoma. Clinical and translational medicine, 16(1), e70578.

House NC, et al. (2025) Profiling the Activity of the Potent and Highly Selective CDK2 Inhibitor BLU-222 Reveals Determinants of Response in CCNE1-Aberrant Ovarian and Endometrial Tumors. Cancer research, 85(7), 1297.

Benjamin JS, et al. (2025) 23ME-01473, an Fc Effector-Enhanced Anti-ULBP6/2/5 Antibody, Restores NK Cell-Mediated Antitumor Immunity through NKG2D and Fc?RIIIa Activation. Cancer research communications, 5(3), 476.

Woolley CE, et al. (2025) Coevolution of Atypical BRAF and KRAS Mutations in Colorectal Tumorigenesis. Molecular cancer research : MCR, 23(4), 300.

Ibrahim M, et al. (2025) NF1 Loss Promotes EGFR Activation and Confers Sensitivity to EGFR Inhibition in NF1-Mutant Melanoma. Cancer research, 85(17), 3348.

Huang Y, et al. (2025) A comparison of hepatitis B virus- and hepatitis C virus-related hepatocellular carcinoma: a bioinformatics analysis. Translational cancer research, 14(7), 4243.

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.

Oles AR, et al. (2025) MyoD is essential in rhabdomyosarcoma by promoting survival through differentiation and CYLD. iScience, 28(8), 113149.

Markey M, et al. (2025) Spatial Mapping of Gene Signatures in Hematoxylin and Eosin-Stained Images: A Proof of Concept for Interpretable Predictions Using Additive Multiple Instance Learning. Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc, 38(8), 100772.

Mateo-Victoriano B, et al. (2025) Oncogenic KRAS addiction states differentially influence MTH1 expression and 8-oxodGTPase activity in lung adenocarcinoma. Redox biology, 82, 103610.

Chávez LF, et al. (2025) GEF-H1 drives breast cancer cells to tumor progression. Biochimica et biophysica acta. Molecular basis of disease, 1871(5), 167816.

McDonald ES, et al. (2025) Ternary Complex Components Responsible for Rapid LDL Internalization as Biomarkers for Breast Cancer Associated with Proliferation and Early Recurrence. Cancer research communications, 5(2), 226.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

Ramchatesingh B, et al. (2025) Targeting PRAME directly or via EZH2 inhibition overcomes retinoid resistance and represents a novel therapy for keratinocyte carcinoma. Molecular oncology, 19(5), 1471.