Resource Summary Report

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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: material resource, biomaterial supply 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

Availability: Open unspecified license, Controlled access

Resource Name: The Cancer Genome Atlas

Resource ID: SCR_003193

Alternate IDs: nlx_156913

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250421T053346+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 5918 mentions in open access literature.

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

Sun X, et al. (2025) Targeting PRMT1 Reduces Cancer Persistence and Tumor Relapse in EGFR- and KRAS-Mutant Lung Cancer. Cancer research communications, 5(1), 119.

Abelman RO, et al. (2025) TOP1 Mutations and Cross-Resistance to Antibody-Drug Conjugates in Patients with Metastatic Breast Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research.

Shen X, et al. (2025) The genetic duet of concurrent RASAL1 and PTEN alterations promotes cancer aggressiveness by cooperatively activating the PI3K-AKT pathway. Molecular oncology, 19(1), 248.

Song L, et al. (2025) Integrin ?8 Facilitates Macrophage Infiltration and Polarization by Regulating CCL5 to Promote LUAD Progression. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2406865.

Weber M, et al. (2025) Transcriptomic and proteomic profiling identifies feline fibrosarcoma as clinically amenable model for aggressive sarcoma subtypes. Neoplasia (New York, N.Y.), 60, 101104.

Würth R, et al. (2025) Circulating tumor cell plasticity determines breast cancer therapy resistance via neuregulin 1-HER3 signaling. Nature cancer, 6(1), 67.

Zhang S, et al. (2025) Integrative single-cell and multi-omics analyses reveal ferroptosis-associated gene expression and immune microenvironment heterogeneity in gastric cancer. Discover oncology, 16(1), 57.

Zhang J, et al. (2025) The suppression of the SPHK1/S1P/S1PR3 signaling pathway diminishes EGFR activation and increases the sensitivity of non-small cell lung cancer to gefitinib. Current research in pharmacology and drug discovery, 8, 100212.

Li J, et al. (2025) ALDH1L2 drives HCC progression through TAM polarization. JHEP reports : innovation in hepatology, 7(1), 101217.

Wu T, et al. (2025) E2F1 and E2F7 regulate gastric cancer cell proliferation, respectively, through transcriptional activation and transcriptional repression of MYBL2. The Journal of biological chemistry, 301(1), 108027.

Yan R, et al. (2025) SLC35A2 is a novel prognostic biomarker and promotes cell proliferation and metastasis via Wnt/?-catenin/EMT signaling pathway in breast cancer. Scientific reports, 15(1), 130.

Liu H, et al. (2025) Titin gene mutations enhance radiotherapy efficacy via modulation of tumour immune microenvironment in rectum adenocarcinoma. Clinical and translational medicine, 15(1), e70123.

Lu X, et al. (2025) Self-assembled PROTACs enable protein degradation to reprogram the tumor microenvironment for synergistically enhanced colorectal cancer immunotherapy. Bioactive materials, 43, 255.

Guo Q, et al. (2025) Identification of GBN5 as a molecular biomarker of pan-cancer species by integrated multi-omics analysis. Discover oncology, 16(1), 85.

Iida N, et al. (2025) Systematically developing a registry of splice-site creating variants utilizing massive publicly available transcriptome sequence data. Nature communications, 16(1), 426.

Zhao H, et al. (2025) High expression of nucleotide-binding oligomerization domain protein 1 correlates with poor prognosis and immune cell infiltration in Glioblastoma Multiforme patients. Discover oncology, 16(1), 32.

Yuan H, et al. (2025) Identification of critical biomarkers and immune landscape patterns in glioma based on multi-database. Discover oncology, 16(1), 35.

Yang H, et al. (2025) Gram-Negative Microflora Dysbiosis Facilitates Tumor Progression and Immune Evasion by Activating the CCL3/CCL5-CCR1-MAPK-PD-L1 Pathway in Esophageal Squamous Cell Carcinoma. Molecular cancer research : MCR, 23(1), 71.

Du W, et al. (2025) Integrated bioinformatics and experimental analysis of CHAF1B as a novel biomarker and immunotherapy target in LUAD. Discover oncology, 16(1), 43.

Liao W, et al. (2025) Comprehensive analysis of heat shock protein 110, 90, 70, 60 families and tumor immune microenvironment characterization in clear cell renal cell carcinoma. Scientific reports, 15(1), 469.