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: 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: 20260829T183042+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 7443 mentions in open access literature.

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

Liu Y, et al. (2026) C1QBP-STAT1 Interaction Promotes Activation of the c-Myc-CHK1/CHK2 Signaling Axis and Radioresistance in Lung Cancer. Molecular cancer research : MCR, 24(5), 315.

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.

Bai G, et al. (2026) LARS promotes osteosarcoma proliferation through leucine-dependent PRIM2 translation and DNA replication activation. Journal of experimental & clinical cancer research : CR, 45(1).

Gurjao C, et al. (2026) Germline Predisposition to Oncogenic Alkylating Damage in Colorectal Cancer. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(3), 420.

Stoiber S, et al. (2026) [18F]FDG PET/CT multiomics identifies Hedgehog-driven HPV-negative head and neck squamous cell carcinoma. Molecular cancer, 25(1).

Krusen BM, et al. (2026) Improving a Plasma Biomarker Panel for Early Detection of Pancreatic Ductal Adenocarcinoma with Aminopeptidase N (ANPEP) and Polymeric Immunoglobulin Receptor (PIGR). Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 756.

Tankka AT, et al. (2026) Integrative CRISPR Screening and RNA Analyses Discover an Essential Role for PUF60 Interactions with 3' Splice Sites in Cancer Progression. Cancer research, 86(7), 1586.

Liu SS, et al. (2026) Epigenetic regulation of NDGA and its synergistic inhibition with EZH2 inhibitors in prostate cancer via NRP1. Acta pharmacologica Sinica, 47(6), 1643.

Horvat NK, et al. (2026) Loss of miR-29a/b1 Cluster Reprograms the Tumor Microenvironment and Contributes to Immunosuppression in Lung Cancer. Cancer immunology research, 14(6), 974.

Wang G, et al. (2026) VGLL4 promotes hepatocellular carcinoma progression via the Wnt/??-catenin pathway. Tissue & cell, 100, 103391.

Foidart P, et al. (2026) Whole-genome doubling drives immune evasion by silencing antigen presentation. Cancer cell, 44(7), 1418.

Huang C, et al. (2026) Survival Genie 2: a next-generation web server for targeted and single-cell-based survival analyses. Genome medicine, 18(1).

Ziman B, et al. (2026) ETS1 Orchestrates a Hybrid EMT Program Driving Metastasis and Immune Evasion. Cancer research.

Lee H, et al. (2026) PLD1 and PLD2 promote an immunosuppressive tumor microenvironment via CCL19-dependent macrophage polarization and PD-L1 induction. Experimental & molecular medicine, 58(6), 1870.

Fidaleo AM, et al. (2026) LRRC8A-containing anion channels promote glioblastoma proliferation via a WNK1/mTORC2-dependent mechanism. The Journal of physiology, 604(5), 1995.

Tao Y, et al. (2026) TENT5A Maintains MYC mRNA Stability to Enhance Osteosarcoma Stemness. Cancer research, 86(9), 2161.

Gupta I, et al. (2026) Correlation of the differential expression of PIK3R1 and its spliced variant, p55??, in pan-cancer. Molecular oncology, 20(5), 1299.

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.

Hayward MK, et al. (2026) Tissue tension fosters macrophage-driven lipid peroxidation-induced DNA damage. Cancer cell, 44(6), 1255.

Zhou X, et al. (2026) Knowledge-enhanced pretraining for vision-language pathology foundation model on cancer diagnosis. Cancer cell, 44(4), 777.