Resource Summary Report

Generated by NIF on Sep 9, 2026

Human Tumor Atlas Network

RRID:SCR_023364
Type: Tool

Proper Citation

Human Tumor Atlas Network (RRID:SCR_023364)

Resource Information

URL: https://humantumoratlas.org

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Description: HTAN is National Cancer Institute funded Cancer Moonshot initiative to construct 3-dimensional atlases of dynamic cellular, morphological, and molecular features of human cancers as they evolve from precancerous lesions to advanced disease.Provides three dimensional atlases of cancer transitions for diverse set of tumor types. Efforts to map healthy organs and previous large-scale cancer genomics approaches focused on bulk sequencing at single point in time. Data portal for Human Tumor Atlas Network. Data available on HTAN Portal is open access. Certain data types with potential for re-identification are available in restricted access through dbGAP.

Abbreviations: HTAN

Resource Type: atlas, data or information resource, disease-related portal, portal, topical portal

Defining Citation: PMID:32302568

Keywords: Three dimensional atlases, cancer transitions, diverse set of tumor types, map healthy organs, cancer genomics approaches, bulk sequencing at single point in time, data, precancerous lesions to advanced disease,

Related Condition: cancer

Funding: National Cancer Institut Cancer Moonshot Initiative

Availability: Free, Freely available

Resource Name: Human Tumor Atlas Network

Resource ID: SCR_023364

Record Creation Time: 20230321T180026+0000

Record Last Update: 20260905T133023+0000

Ratings and Alerts

No rating or validation information has been found for Human Tumor Atlas Network.

No alerts have been found for Human Tumor Atlas Network.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Shin SK, et al. (2026) VISTA drives pancreatic tumor progression through modulation of the tumor-associated macrophage polarity. Nature communications, 17(1).

Oshinjo A, et al. (2026) MatriSpace: Identification and visualization of spatially resolved ECM gene expression patterns in health and disease. bioRxiv : the preprint server for biology.

Tu C, et al. (2026) Spatial multi-omics characterization of neuroblastoma reveals ferroptosis-associated metabolic features in high-risk tumors. Genome medicine, 18(1).

Redondo-Pedraza J, et al. (2026) Rank signaling drives basal cell-lineage infidelity leading to mammary tumorigenesis. Nature communications, 17(1).

Tong X, et al. (2026) A Single-Cell Atlas of Pan-Cancer Liver Metastasis Reveals Dynamic Cellular Programs Driving Metastatic Progression and Immune Modulation. Research (Washington, D.C.), 9, 1208.

Li G, et al. (2026) Spatial Multiomics Analyses Reveal That Diabetes Promotes Pancreatic Cancer Progression by Stimulating Cholesterol-Induced Neutrophil Extracellular Trap Formation. Cancer research, 86(10), 2327.

Santiago-Carvalho I, et al. (2025) Sensing of extracellular ATP via P2RX7 drives lung tumor growth through regulatory T cell suppressive function. bioRxiv : the preprint server for biology.

Gong Y, et al. (2025) Single-cell RNA profiling of colorectal granular-type laterally spreading tumor uncovers progression trajectory toward carcinoma and transcriptional signatures favoring lateral morphogenesis. Frontiers in oncology, 15, 1552841.

Seo Y, et al. (2025) Actin dysregulation induces neuroendocrine plasticity and immune evasion: a vulnerability of small cell lung cancer. Nature communications, 17(1), 386.

Qin X, et al. (2025) Single-Cell Expression Analysis of Ductal Carcinoma In Situ Identifies Complex Genotypic-Phenotypic Relationships Altering Epithelial Composition. Cancer research, 85(12), 2302.

Liu X, et al. (2025) CSI-GEP: A GPU-based unsupervised machine learning approach for recovering gene expression programs in atlas-scale single-cell RNA-seq data. Cell genomics, 5(1), 100739.

Le H, et al. (2025) Contrastive learning uncovers cellular interactions and morphologies in the tumor microenvironment of lung adenocarcinoma linked to immunotherapy response. Scientific reports, 15(1), 34373.

Gibbs DL, et al. (2025) Analysis of clinical, single cell, and spatial data from the Human Tumor Atlas Network (HTAN) with massively distributed cloud-based queries. Research square.

Wang K, et al. (2025) Toward universal immunofluorescence normalization for multiplex tissue imaging with UniFORM. Cell reports methods, 5(9), 101172.

Baker GJ, et al. (2025) Morphology-Aware Profiling of Highly Multiplexed Tissue Images using Variational Autoencoders. bioRxiv : the preprint server for biology.

Liu H, et al. (2025) IL1RA+ Myeloid-derived Suppressor Cells Activate Epithelial-mesenchymal Transition to Facilitate Lymphatic and Hepatic Metastasis in Pancreatic Ductal Carcinoma. Journal of clinical and translational hepatology, 13(11), 935.

Hori C, et al. (2025) Characterizing heterogeneous cis-regulatory elements in gene regulatory programs associated with breast cancer. Genome medicine, 17(1), 145.

Calder??n AS, et al. (2025) Ontogeny-specific induction of the KMT2A::AFF1-fusion drives development of a distinct CD24 positive pre-leukemic state. Leukemia, 39(9), 2099.

Forjaz A, et al. (2025) PIVOT: an open-source tool for multi-omic spatial data registration. bioRxiv : the preprint server for biology.

Heussner RT, et al. (2025) COEXIST: Coordinated single-cell integration of serial multiplexed tissue images. PLoS computational biology, 21(8), e1013325.