

Resource Summary Report

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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: disease-related portal, data or information resource, atlas, topical portal, 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: 20260729T044554+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 27 mentions in open access literature.

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

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*.

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.

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

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.

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

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

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

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

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.

Sun H, et al. (2024) Expanding the coverage of spatial proteomics: a machine learning approach. *Bioinformatics* (Oxford, England), 40(2).

Klughammer J, et al. (2024) A multi-modal single-cell and spatial expression map of metastatic breast cancer biopsies across clinicopathological features. *Nature medicine*, 30(11), 3236.

Iglesia MD, et al. (2024) Differential chromatin accessibility and transcriptional dynamics define breast cancer subtypes and their lineages. *Nature cancer*, 5(11), 1713.

Pfeifer M, et al. (2024) Genome-wide CRISPR screens identify the YAP/TEAD axis as a driver of persister cells in EGFR mutant lung cancer. *Communications biology*, 7(1), 497.

Wang K, et al. (2024) UniFORM: Towards Universal Immunofluorescence Normalization for Multiplex Tissue Imaging. *bioRxiv : the preprint server for biology*.

Patel AG, et al. (2024) A spatial cell atlas of neuroblastoma reveals developmental, epigenetic and spatial axis of tumor heterogeneity. *bioRxiv : the preprint server for biology*.

Pot D, et al. (2024) NCI Cancer Research Data Commons: Cloud-Based Analytic Resources. *Cancer research*, 84(9), 1396.

Sims Z, et al. (2024) MIM-CyCIF: masked imaging modeling for enhancing cyclic immunofluorescence (CyCIF) with panel reduction and imputation. *Communications biology*, 7(1), 409.

Giuliani G, et al. (2024) Spatial organization and stochastic fluctuations of immune cells impact clinical responsiveness to immunotherapy in melanoma patients. *PNAS nexus*, 3(12), pgae539.

Zhu Y, et al. (2024) Global loss of promoter-enhancer connectivity and rebalancing of gene expression during early colorectal cancer carcinogenesis. *Nature cancer*, 5(11), 1697.

Coy S, et al. (2023) 2D and 3D multiplexed subcellular profiling of nuclear instability in human cancer. *bioRxiv : the preprint server for biology*.