

Resource Summary Report

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Human Cell Atlas

RRID:SCR_016530

Type: Tool

Proper Citation

Human Cell Atlas (RRID:SCR_016530)

Resource Information

URL: <https://www.humancellatlas.org>

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Description: Software tool as a catalog of comprehensive reference of human cells based on their stable properties, transient features, locations and abundances. Map to show the relationships among its elements. Open data international collaborative project involving diverse scientific communities to provide a framework for understanding cellular dysregulation in human disease.

Resource Type: data or information resource, image, atlas, catalog, database, map, portal

Defining Citation: [PMID:29206104](#)

Keywords: human, cell, line, atlas, catalog, map, open, data, international, project, FASEB list

Availability: Free, Available for download, Freely available

Resource Name: Human Cell Atlas

Resource ID: SCR_016530

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260808T190056+0000

Ratings and Alerts

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

No alerts have been found for Human Cell Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 127 mentions in open access literature.

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

Huang C, et al. (2026) Ochratoxin A and Clear Cell Renal Cell Carcinoma: Exploring Potential Molecular Links Through Network Toxicology and Machine Learning. International journal of molecular sciences, 27(7).

Zhou W, et al. (2026) EZH2-Mediated Epigenetic Modifications Induce Pyroptosis in Dental Pulp Endothelial Cells via Activation of NLRP6 Inflammasome During Pulpitis Development. Mediators of inflammation, 2026(1), e5876995.

Nguyen TDT, et al. (2026) Pan-Cancer Single-Cell RNA Sequencing Analysis Refines Multi-Origin Monocyte and Macrophage Lineages. Cancer immunology research, 14(2), 350.

Bai D, et al. (2026) scLong: a billion-parameter foundation model for capturing long-range gene context in single-cell transcriptomics. Nature communications, 17(1).

Takei S, et al. (2026) The CD4+ T cell population partners with Tpex CD8+ T cells to mediate antitumor immunity in the tumor microenvironment. Nature communications, 17(1).

Wrynn T, et al. (2026) A Mouthful of Genomic Data: Single-Cell Insights into Salivary Gland Biology and Disease. Biology, 15(8).

Guo F, et al. (2025) Foundation models in bioinformatics. National science review, 12(4), nwaf028.

Leir SH, et al. (2025) Cellular imbalance in proximal and distal lung of CFTR^{-/-} sheep in utero and at birth. Molecular medicine (Cambridge, Mass.), 31(1), 231.

Guo Z, et al. (2025) Cold Exposure Induces Swine Brown Adipocytes to Display an Island-like Distribution with Atypical Characteristics. International journal of molecular sciences, 26(20).

Shi M, et al. (2025) A resource for whole-body gene expression map of human tissues based on integration of single cell and bulk transcriptomics. Genome biology, 26(1), 152.

Hara Y, et al. (2025) Selective AMPK γ 1 activation induces fetal hemoglobin in human erythroid cells and sickle cell mice via the noncanonical NRF2 pathway. Science advances, 11(47), eadx1144.

Burge KY, et al. (2025) Spatial transcriptomics delineates potential differences in intestinal phenotypes of cardiac and classical necrotizing enterocolitis. iScience, 28(4), 112166.

Liu H, et al. (2025) Identification of immunogenic cell death signature genes in hepatocellular carcinoma: from single-cell transcriptomics to in vitro mechanistic validation and comprehensive prognostic modeling with hundreds of machine learning algorithms. *Frontiers in immunology*, 16, 1649618.

Wang W, et al. (2025) The potential role of BCL2A1⁺ tissue-resident macrophages in the prognosis of Wilms tumor. *European journal of medical research*, 30(1), 670.

Liu XH, et al. (2025) Multi-omics in immunotherapy research for HNSCC: present situation and future perspectives. *NPJ precision oncology*, 9(1), 93.

Moon Y, et al. (2025) PolyASite v3.0: a multi-species atlas of polyadenylation sites inferred from single-cell RNA-sequencing data. *Nucleic acids research*, 53(D1), D197.

Li Y, et al. (2025) UDA-seq: universal droplet microfluidics-based combinatorial indexing for massive-scale multimodal single-cell sequencing. *Nature methods*, 22(6), 1199.

Yin C, et al. (2025) Development and pan-cancer validation of an epigenetics-based random survival forest model for prognosis prediction and drug response in OS. *Frontiers in pharmacology*, 16, 1529525.

Xie Z, et al. (2025) DNA-guided transcription factor interactions extend human gene regulatory code. *Nature*, 641(8065), 1329.

Zheng J, et al. (2025) HMGB1-mediated macrophage polarization to M2 phenotype promotes ureteral stricture: therapeutic potential of HMGB1 inhibitors. *European journal of medical research*, 30(1), 893.