

# The Human Cell Atlas

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. <i>Neuron</i> , 2017, 96, 542-557.	3.8	235
2	Usage of cell nomenclature in biomedical literature. <i>BMC Bioinformatics</i> , 2017, 18, 561.	1.2	1
3	Big knowledge from big data in functional genomics. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 245-248.	1.1	4
4	Mapping the Mouse Cell Atlas by Microwell-Seq. <i>Cell</i> , 2018, 172, 1091-1107.e17.	13.5	1,068
5	Cell type atlas and lineage tree of a whole complex animal by single-cell transcriptomics. <i>Science</i> , 2018, 360, .	6.0	381
6	Exploring intermediate cell states through the lens of single cells. <i>Current Opinion in Systems Biology</i> , 2018, 9, 32-41.	1.3	65
7	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	15.2	124
8	Systems Immunology: Learning the Rules of the Immune System. <i>Annual Review of Immunology</i> , 2018, 36, 813-842.	9.5	70
9	Using single-cell genomics to understand developmental processes and cell fate decisions. <i>Molecular Systems Biology</i> , 2018, 14, e8046.	3.2	190
10	The Body-wide Transcriptome Landscape of Disease Models. <i>iScience</i> , 2018, 2, 238-268.	1.9	18
11	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387.	1.5	1,282
12	Defining Cell Identity with Single-cell Omics. <i>Proteomics</i> , 2018, 18, e1700312.	1.3	52
13	Crosstalk between YAP/TAZ and Notch Signaling. <i>Trends in Cell Biology</i> , 2018, 28, 560-573.	3.6	104
14	Statistical single cell multi-omics integration. <i>Current Opinion in Systems Biology</i> , 2018, 7, 54-59.	1.3	61
15	Microfluidic channel optimization to improve hydrodynamic dissociation of cell aggregates and tissue. <i>Scientific Reports</i> , 2018, 8, 2774.	1.6	33
16	Meet some code-breakers of noncoding RNAs. <i>Nature Methods</i> , 2018, 15, 103-106.	9.0	2
17	Mapping human development at single-cell resolution. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	30
18	Brain Transcriptome Databases: A User's Guide. <i>Journal of Neuroscience</i> , 2018, 38, 2399-2412.	1.7	68

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19	A general and flexible method for signal extraction from single-cell RNA-seq data. <i>Nature Communications</i> , 2018, 9, 284.	5.8	540
21	Strength in numbers from integrated single-cell neuroscience. <i>Nature Biotechnology</i> , 2018, 36, 41-42.	9.4	1
22	Methods and challenges in the analysis of single-cell RNA-sequencing data. <i>Current Opinion in Systems Biology</i> , 2018, 7, 47-53.	1.3	19
23	Somatic mutations in neurons during aging and neurodegeneration. <i>Acta Neuropathologica</i> , 2018, 135, 811-826.	3.9	35
24	bigSCale: an analytical framework for big-scale single-cell data. <i>Genome Research</i> , 2018, 28, 878-890.	2.4	76
25	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	13.5	545
26	The ontogeny, activation and function of the epicardium during heart development and regeneration. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	73
27	Integrating single-cell transcriptomic data across different conditions, technologies, and species. <i>Nature Biotechnology</i> , 2018, 36, 411-420.	9.4	8,878
28	scmap: projection of single-cell RNA-seq data across data sets. <i>Nature Methods</i> , 2018, 15, 359-362.	9.0	533
29	Entering the post-epigenomic age: back to epigenetics. <i>Open Biology</i> , 2018, 8, 180013.	1.5	5
30	Human bone marrow assessment by single-cell RNA sequencing, mass cytometry, and flow cytometry. <i>JCI Insight</i> , 2018, 3, .	2.3	135
31	Statistical Analysis Can Fail to Reveal Underlying True Biological Mechanism: A Demonstration of Expression Profile Generation. , 2018, , .		0
32	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018, 7, 1968.	0.8	16
33	Dissecting human disease with single-cell omics: application in model systems and in the clinic. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	39
34	Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. <i>Nature Protocols</i> , 2018, 13, 2742-2757.	5.5	153
35	Force Spectroscopy and Beyond: Innovations and Opportunities. <i>Biophysical Journal</i> , 2018, 115, 2279-2285.	0.2	16
36	Cell types behaving in their natural habitat. <i>Science</i> , 2018, 362, 749-750.	6.0	0
37	Revealing the Critical Regulators of Cell Identity in the Mouse Cell Atlas. <i>Cell Reports</i> , 2018, 25, 1436-1445.e3.	2.9	185

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38	An integrative approach for building personalized gene regulatory networks for precision medicine. <i>Genome Medicine</i> , 2018, 10, 96.	3.6	49
39	Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. <i>PLoS ONE</i> , 2018, 13, e0209648.	1.1	400
40	Promoter-enhancer looping and shadow enhancers of the mouse $\beta$ -crystallin locus. <i>Biology Open</i> , 2018, 7, .	0.6	6
41	Automated in situ chromatin profiling efficiently resolves cell types and gene regulatory programs. <i>Epigenetics and Chromatin</i> , 2018, 11, 74.	1.8	53
42	Cell Hashing with barcoded antibodies enables multiplexing and doublet detection for single cell genomics. <i>Genome Biology</i> , 2018, 19, 224.	3.8	674
43	Deep generative modeling for single-cell transcriptomics. <i>Nature Methods</i> , 2018, 15, 1053-1058.	9.0	1,227
44	Bayesian deep learning for single-cell analysis. <i>Nature Methods</i> , 2018, 15, 1009-1010.	9.0	21
45	Understanding dynamic tissue organization by studying the human body one cell at a time: the human cell atlas (HCA) project. <i>Cardiovascular Research</i> , 2018, 114, e93-e95.	1.8	4
46	Advanced model systems and tools for basic and translational human immunology. <i>Genome Medicine</i> , 2018, 10, 73.	3.6	68
47	A Single-Cell Sequencing Guide for Immunologists. <i>Frontiers in Immunology</i> , 2018, 9, 2425.	2.2	167
48	Modeling and analysis of RNA-seq data: a review from a statistical perspective. <i>Quantitative Biology</i> , 2018, 6, 195-209.	0.3	49
49	Spatial Reconstruction of Single Enterocytes Uncovers Broad Zonation along the Intestinal Villus Axis. <i>Cell</i> , 2018, 175, 1156-1167.e15.	13.5	282
50	Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , 2018, 361, 1336-1340.	6.0	469
51	Writing, Reading, and Translating the Clustered Protocadherin Cell Surface Recognition Code for Neural Circuit Assembly. <i>Annual Review of Cell and Developmental Biology</i> , 2018, 34, 471-493.	4.0	84
52	Single Cell Gene Expression to Understand the Dynamic Architecture of the Heart. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 167.	1.1	16
53	Multi-Omics Profiling of the Tumor Microenvironment: Paving the Way to Precision Immuno-Oncology. <i>Frontiers in Oncology</i> , 2018, 8, 430.	1.3	57
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57	A 2018 Reference Guide to the Banff Classification of Renal Allograft Pathology. Transplantation, 2018, 102, 1795-1814.	0.5	479
58	Bridging the Data Gap From in vitro Toxicity Testing to Chemical Safety Assessment Through Computational Modeling. Frontiers in Public Health, 2018, 6, 261.	1.3	54
59	Deciphering the Evolution of Vertebrate Immune Cell Types with Single-Cell RNA-Seq. , 2018, , 95-111.		1
60	Identification of the RNA polymerase I-RNA interactome. Nucleic Acids Research, 2018, 46, 11002-11013.	6.5	19
61	The impact of genome-wide association studies on biomedical research publications. Human Genomics, 2018, 12, 38.	1.4	11
62	CellAtlasSearch: a scalable search engine for single cells. Nucleic Acids Research, 2018, 46, W141-W147.	6.5	39
63	Interpretable dimensionality reduction of single cell transcriptome data with deep generative models. Nature Communications, 2018, 9, 2002.	5.8	271
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65	An artificial intelligent single cell is part of the cell dream world. Cell Biology and Toxicology, 2018, 34, 247-249.	2.4	19
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69	Prioritizing network communities. Nature Communications, 2018, 9, 2544.	5.8	37
70	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. Nature, 2018, 560, 319-324.	13.7	878
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73	Revealing routes of cellular differentiation by single-cell RNA-seq. Current Opinion in Systems Biology, 2018, 11, 9-17.	1.3	10

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74	From the Human Cell Atlas to dynamic immune maps in human disease. <i>Nature Reviews Immunology</i> , 2018, 18, 597-598.	10.6	23
75	Translating GWAS Findings to Novel Therapeutic Targets for Coronary Artery Disease. <i>Frontiers in Cardiovascular Medicine</i> , 2018, 5, 56.	1.1	21
76	5-Hydroxymethylcytosine (5hmC), or How to Identify Your Favorite Cell. <i>Epigenomes</i> , 2018, 2, 3.	0.8	17
77	Single-cell biology: resolving biological complexity, one cell at a time. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	7
78	NeuroSystematics and Periodic System of Neurons: Model vs Reference Species at Single-Cell Resolution. <i>ACS Chemical Neuroscience</i> , 2018, 9, 1884-1903.	1.7	31
79	Genomic mosaicism in the developing and adult brain. <i>Developmental Neurobiology</i> , 2018, 78, 1026-1048.	1.5	81
80	CRISPR-based reagents to study the influence of the epigenome on gene expression. <i>Clinical and Experimental Immunology</i> , 2018, 194, 9-16.	1.1	9
81	Single-Cell (Multi)omics Technologies. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 15-41.	2.5	149
82	SCANPY: large-scale single-cell gene expression data analysis. <i>Genome Biology</i> , 2018, 19, 15.	3.8	3,958
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84	Manipulating Macrophage Polarization to Fix the Broken Heart. <i>Journal of the American College of Cardiology</i> , 2018, 72, 905-907.	1.2	9
85	Co-expression in Single-Cell Analysis: Saving Grace or Original Sin?. <i>Trends in Genetics</i> , 2018, 34, 823-831.	2.9	34
86	Molecular Architecture of the Mouse Nervous System. <i>Cell</i> , 2018, 174, 999-1014.e22.	13.5	2,002
87	Neuro-evo-devo in the single cell sequencing era. <i>Current Opinion in Systems Biology</i> , 2018, 11, 32-40.	1.3	9
88	Single-cell RNA sequencing technologies and bioinformatics pipelines. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-14.	3.2	1,087
89	First Giant Steps Toward a Cell Atlas of Atherosclerosis. <i>Circulation Research</i> , 2018, 122, 1632-1634.	2.0	6
90	zUMIs - A fast and flexible pipeline to process RNA sequencing data with UMIs. <i>GigaScience</i> , 2018, 7, .	3.3	265
91	Generalizable and Scalable Visualization of Single-Cell Data Using Neural Networks. <i>Cell Systems</i> , 2018, 7, 185-191.e4.	2.9	49

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93	Expansion microscopy: enabling single cell analysis in intact biological systems. <i>FEBS Journal</i> , 2019, 286, 1482-1494.	2.2	31
94	Bioinformatic and biological avenues for understanding alcohol use disorder. <i>Alcohol</i> , 2019, 74, 65-71.	0.8	3
95	Landscape of Intercellular Crosstalk in Healthy and NASH Liver Revealed by Single-Cell Secretome Gene Analysis. <i>Molecular Cell</i> , 2019, 75, 644-660.e5.	4.5	488
96	A serum protein signature of <i>APOE</i> genotypes in centenarians. <i>Aging Cell</i> , 2019, 18, e13023.	3.0	27
97	Immuno-SABER enables highly multiplexed and amplified protein imaging in tissues. <i>Nature Biotechnology</i> , 2019, 37, 1080-1090.	9.4	301
98	TeraVR empowers precise reconstruction of complete 3-D neuronal morphology in the whole brain. <i>Nature Communications</i> , 2019, 10, 3474.	5.8	64
99	RNA sequencing: the teenage years. <i>Nature Reviews Genetics</i> , 2019, 20, 631-656.	7.7	1,192
100	scGen predicts single-cell perturbation responses. <i>Nature Methods</i> , 2019, 16, 715-721.	9.0	290
101	Global prediction of chromatin accessibility using small-cell-number and single-cell RNA-seq. <i>Nucleic Acids Research</i> , 2019, 47, e121-e121.	6.5	24
102	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2019, 18, 4098-4107.	1.8	41
103	Reconstructing complex lineage trees from scRNA-seq data using MERLoT. <i>Nucleic Acids Research</i> , 2019, 47, 8961-8974.	6.5	18
104	CellSIUS provides sensitive and specific detection of rare cell populations from complex single-cell RNA-seq data. <i>Genome Biology</i> , 2019, 20, 142.	3.8	41
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106	Deconvolution of autoencoders to learn biological regulatory modules from single cell mRNA sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 379.	1.2	22
107	Single-Cell Signature Explorer for comprehensive visualization of single cell signatures across scRNA-seq datasets. <i>Nucleic Acids Research</i> , 2019, 47, e133-e133.	6.5	96
108	Polled Digital Cell Sorter (p-DCS): Automatic identification of hematological cell types from single cell RNA-sequencing clusters. <i>BMC Bioinformatics</i> , 2019, 20, 369.	1.2	22
109	Genetic mapping of cell type specificity for complex traits. <i>Nature Communications</i> , 2019, 10, 3222.	5.8	212

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111	Pathobiology of cardiovascular diseases: an update. <i>Cardiovascular Pathology</i> , 2019, 42, 44-53.	0.7	26
112	Microfluidics towards single cell resolution protein analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 117, 2-12.	5.8	56
113	The evolving concept of cell identity in the single cell era. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	115
114	Best Practices for Illumina Library Preparation. <i>Current Protocols in Human Genetics</i> , 2019, 102, e86.	3.5	24
115	A periodic table of cell types. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	54
116	Concepts and limitations for learning developmental trajectories from single cell genomics. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	177
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121	Informing disease modelling with brain-relevant functional genomic annotations. <i>Brain</i> , 2019, 142, 3694-3712.	3.7	8
122	Integrative Analysis Reveals Across-Cancer Expression Patterns and Clinical Relevance of Ribonucleotide Reductase in Human Cancers. <i>Frontiers in Oncology</i> , 2019, 9, 956.	1.3	13
123	A Systems-Based Map of Human Brain Cell-Type Enriched Genes and Malignancy-Associated Endothelial Changes. <i>Cell Reports</i> , 2019, 29, 1690-1706.e4.	2.9	22
124	Modelling heterogeneous intracellular networks at the cellular scale. <i>Current Opinion in Systems Biology</i> , 2019, 16, 10-16.	1.3	0
125	Sequencing the Human Brain at Single-Cell Resolution. <i>Current Behavioral Neuroscience Reports</i> , 2019, 6, 197-208.	0.6	5
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131	The future of otology. <i>Journal of Laryngology and Otology</i> , 2019, 133, 747-758.	0.4	7
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134	Multiplexed laser particles for spatially resolved single-cell analysis. <i>Light: Science and Applications</i> , 2019, 8, 74.	7.7	28
135	Convergence of human cellular models and genetics to study neural stem cell signaling to enhance central nervous system regeneration and repair. <i>Seminars in Cell and Developmental Biology</i> , 2019, 95, 84-92.	2.3	4
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138	Spatial and temporal tools for building a human cell atlas. <i>Molecular Biology of the Cell</i> , 2019, 30, 2435-2438.	0.9	3
139	Single-Cell Transcriptomic Map of the Human and Mouse Bladders. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2159-2176.	3.0	90
140	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	9.0	200
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146	The Human Cell Atlas: making cell space™ for disease. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	9

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148	Integrative single-cell analysis. <i>Nature Reviews Genetics</i> , 2019, 20, 257-272.	7.7	932
149	Single-Cell RNA Sequencing to Understand Host-Pathogen Interactions. <i>ACS Infectious Diseases</i> , 2019, 5, 336-344.	1.8	36
150	Revolutionizing Cancer Immunology: The Power of Next-Generation Sequencing Technologies. <i>Cancer Immunology Research</i> , 2019, 7, 168-173.	1.6	10
151	Deep learning for cellular image analysis. <i>Nature Methods</i> , 2019, 16, 1233-1246.	9.0	754
153	Rational Reprogramming of Cellular States by Combinatorial Perturbation. <i>Cell Reports</i> , 2019, 27, 3486-3499.e6.	2.9	18
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155	CHETAH: a selective, hierarchical cell type identification method for single-cell RNA sequencing. <i>Nucleic Acids Research</i> , 2019, 47, e95-e95.	6.5	169
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157	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. <i>Circulation</i> , 2019, 140, 147-163.	1.6	231
158	Genomic Imprinting As a Window into Human Language Evolution. <i>BioEssays</i> , 2019, 41, 1800212.	1.2	5
159	A case study on the detailed reproducibility of a Human Cell Atlas project. <i>Quantitative Biology</i> , 2019, 7, 162-169.	0.3	6
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161	A review on the pathophysiology of asthma remission. , 2019, 201, 8-24.		36
162	diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering. <i>Communications Biology</i> , 2019, 2, 183.	2.0	162
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164	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019, 570, 77-82.	13.7	257
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167	Modeling Spatial Correlation of Transcripts with Application to Developing Pancreas. <i>Scientific Reports</i> , 2019, 9, 5592.	1.6	7
168	Biologically inspired approaches to enhance human organoid complexity. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	68
169	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , 2019, 20, 59.	3.8	911
170	The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019, 61, 31-41.	1.4	178
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172	Noninvasive Subcellular Imaging Using Atomic Force Acoustic Microscopy (AFAM). <i>Cells</i> , 2019, 8, 314.	1.8	6
173	A Bioinformatic Toolkit for Single-Cell mRNA Analysis. <i>Methods in Molecular Biology</i> , 2019, 1979, 433-455.	0.4	2
174	Single-Cell Tagged Reverse Transcription (STRT-Seq). <i>Methods in Molecular Biology</i> , 2019, 1979, 133-153.	0.4	21
175	Characterization of cell fate probabilities in single-cell data with Palantir. <i>Nature Biotechnology</i> , 2019, 37, 451-460.	9.4	393
176	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 63.	3.8	608
177	Cell composition analysis of bulk genomics using single-cell data. <i>Nature Methods</i> , 2019, 16, 327-332.	9.0	94
178	Expanding the CRISPR Toolbox in Zebrafish for Studying Development and Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 13.	1.8	102
179	“Building a perfect body”: control of vertebrate organogenesis by PBX-dependent regulatory networks. <i>Genes and Development</i> , 2019, 33, 258-275.	2.7	38
180	In situ 10-cell RNA sequencing in tissue and tumor biopsy samples. <i>Scientific Reports</i> , 2019, 9, 4836.	1.6	23
181	Simplified Drop-seq workflow with minimized bead loss using a bead capture and processing microfluidic chip. <i>Lab on A Chip</i> , 2019, 19, 1610-1620.	3.1	22
182	Systems immunology: Integrating multi-omics data to infer regulatory networks and hidden drivers of immunity. <i>Current Opinion in Systems Biology</i> , 2019, 15, 19-29.	1.3	32
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