Aviv Regev

List of Publications by Year
in descending order

277 papers	136,430 citations	317 138 h-index	374 281 g-index
379 all docs	379 docs citations	379 times ranked	137791 citing authors

#	Article	IF	Citations
1	<i>Smarca4</i> Inactivation Promotes Lineage-Specific Transformation and Early Metastatic Features in the Lung. Cancer Discovery, 2022, 12, 562-585.	9.4	48
2	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. Nature Biotechnology, 2022, 40, 374-381.	17.5	31
3	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	17.5	127
4	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	1.3	37
5	Single‐Cell, Single‐Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. Hepatology Communications, 2022, 6, 821-840.	4.3	98
6	MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. Nature Methods, 2022, 19, 311-315.	19.0	102
7	Disruption of the IL-33-ST2-AKT signaling axis impairs neurodevelopment by inhibiting microglial metabolic adaptation and phagocytic function. Immunity, 2022, 55, 159-173.e9.	14.3	52
8	Colon stroma mediates an inflammation-driven fibroblastic response controlling matrix remodeling and healing. PLoS Biology, 2022, 20, e3001532.	5.6	41
9	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	1.4	14
10	Massively parallel phenotyping of coding variants in cancer with Perturb-seq. Nature Biotechnology, 2022, 40, 896-905.	17.5	44
11	Autism genes converge on asynchronous development of shared neuron classes. Nature, 2022, 602, 268-273.	27.8	180
12	Spatial components of molecular tissue biology. Nature Biotechnology, 2022, 40, 308-318.	17.5	148
13	SM-Omics is an automated platform for high-throughput spatial multi-omics. Nature Communications, 2022, 13, 795.	12.8	73
14	Three-dimensional spatial transcriptomics uncovers cell type localizations in the human rheumatoid arthritis synovium. Communications Biology, 2022, 5, 129.	4.4	35
15	A single-cell atlas of human and mouse white adipose tissue. Nature, 2022, 603, 926-933.	27.8	277
16	Tim-3 adapter protein Bat3 acts as an endogenous regulator of tolerogenic dendritic cell function. Science Immunology, 2022, 7, eabm0631.	11.9	22
17	The evolution, evolvability and engineering of gene regulatory DNA. Nature, 2022, 603, 455-463.	27.8	126
18	Single-cell RNA-seq reveals cell type–specific molecular and genetic associations to lupus. Science, 2022, 376, eabf1970.	12.6	156

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19	CAR T cell killing requires the IFNÎ³R pathway in solid but not liquid tumours. Nature, 2022, 604, 563-570.	27.8	150
20	Genome-wide CRISPR screen identifies PRC2 and KMT2D-COMPASS as regulators of distinct EMT trajectories that contribute differentially to metastasis. Nature Cell Biology, 2022, 24, 554-564.	10.3	53
21	Stepwise-edited, human melanoma models reveal mutationsâ€™ effect on tumor and microenvironment. Science, 2022, 376, eabi8175.	12.6	24
22	Traversing industry and academia in biomedicine: the best of both worlds?. Nature Reviews Genetics, 2022, 23, 461-466.	16.3	2
23	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. Science, 2022, 376, eabl4290.	12.6	180
24	DIALOGUE maps multicellular programs in tissue from single-cell or spatial transcriptomics data. Nature Biotechnology, 2022, 40, 1467-1477.	17.5	42
25	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. Cancer Cell, 2022, 40, 524-544.e5.	16.8	23
26	A human breast atlas integrating single-cell proteomics and transcriptomics. Developmental Cell, 2022, 57, 1400-1420.e7.	7.0	50
27	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. Cell, 2022, 185, 2918-2935.e29.	28.9	113
28	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	17.5	150
29	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. Nature Medicine, 2021, 27, 289-300.	30.7	64
30	QRICH1 dictates the outcome of ER stress through transcriptional control of proteostasis. Science, 2021, 371, .	12.6	73
31	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. Science, 2021, 371, .	12.6	197
32	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. Nature Immunology, 2021, 22, 216-228.	14.5	116
33	Building a high-quality Human Cell Atlas. Nature Biotechnology, 2021, 39, 149-153.	17.5	48
34	Skin-resident innate lymphoid cells converge on a pathogenic effector state. Nature, 2021, 592, 128-132.	27.8	119
35	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. Nature Genetics, 2021, 53, 332-341.	21.4	112
36	Transcriptional mediators of treatment resistance in lethal prostate cancer. Nature Medicine, 2021, 27, 426-433.	30.7	90

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37	Î³Î´ T cells regulate the intestinal response to nutrient sensing. Science, 2021, 371, .	12.6	78
38	Inhibitory CD161 receptor identified in glioma-infiltrating TÂcells by single-cell analysis. Cell, 2021, 184, 1281-1298.e26.	28.9	210
39	Blockade of IL-22 signaling reverses erythroid dysfunction in stress-induced anemias. Nature Immunology, 2021, 22, 520-529.	14.5	11
40	Tim-3 adaptor protein Bat3 is a molecular checkpoint of T cell terminal differentiation and exhaustion. Science Advances, 2021, 7, .	10.3	18
41	Compressed sensing for highly efficient imaging transcriptomics. Nature Biotechnology, 2021, 39, 936-942.	17.5	33
42	Using viral load and epidemic dynamics to optimize pooled testing in resource-constrained settings. Science Translational Medicine, 2021, 13, .	12.4	42
43	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
44	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. Cancer Cell, 2021, 39, 649-661.e5.	16.8	263
45	A cellular and spatial map of the choroid plexus across brain ventricles and ages. Cell, 2021, 184, 3056-3074.e21.	28.9	150
46	Deep generative model embedding of single-cell RNA-Seq profiles on hyperspheres and hyperbolic spaces. Nature Communications, 2021, 12, 2554.	12.8	48
47	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. Cancer Cell, 2021, 39, 779-792.e11.	16.8	245
48	L1CAM is not associated with extracellular vesicles in human cerebrospinal fluid or plasma. Nature Methods, 2021, 18, 631-634.	19.0	118
49	Molecular logic of cellular diversification in the mouse cerebral cortex. Nature, 2021, 595, 554-559.	27.8	212
50	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. Nature, 2021, 595, 101-106.	27.8	169
51	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. Nature Biotechnology, 2021, 39, 1246-1258.	17.5	244
52	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. Cell, 2021, 184, 3205-3221.e24.	28.9	73
53	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. Nature Biotechnology, 2021, 39, 1556-1562.	17.5	46
54	Towards a Human Cell Atlas: Taking Notes from the Past. Trends in Genetics, 2021, 37, 625-630.	6.7	59

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55	OTME-7. Cancer - immune cell interactions drive transitions to mesenchymal-like state in glioblastoma. Neuro-Oncology Advances, 2021, 3, ii14-ii15.	0.7	0
56	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. Cell, 2021, 184, 4168-4185.e21.	28.9	203
57	Cycling cancer persister cells arise from lineages with distinct programs. Nature, 2021, 596, 576-582.	27.8	236
58	The CD155/TIGIT axis promotes and maintains immune evasion in neoantigen-expressing pancreatic cancer. Cancer Cell, 2021, 39, 1342-1360.e14.	16.8	119
59	A cell-free nanobody engineering platform rapidly generates SARS-CoV-2 neutralizing nanobodies. Nature Communications, 2021, 12, 5506.	12.8	38
60	Antigen dominance hierarchies shape TCF1+ progenitor CD8 TÂcell phenotypes in tumors. Cell, 2021, 184, 4996-5014.e26.	28.9	84
61	Spatially organized multicellular immune hubs in human colorectal cancer. Cell, 2021, 184, 4734-4752.e20.	28.9	256
62	Dietary suppression of MHC class II expression in intestinal epithelial cells enhances intestinal tumorigenesis. Cell Stem Cell, 2021, 28, 1922-1935.e5.	11.1	67
63	Blood and immune development in human fetal bone marrow and Down syndrome. Nature, 2021, 598, 327-331.	27.8	73
64	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	27.8	114
65	A human liver cell-based system modeling a clinical prognostic liver signature for therapeutic discovery. Nature Communications, 2021, 12, 5525.	12.8	21
66	Conventional type I dendritic cells maintain a reservoir of proliferative tumor-antigen specific TCF-1+ CD8+ TÂcells in tumor-draining lymph nodes. Immunity, 2021, 54, 2338-2353.e6.	14.3	111
67	The legacy of the Human Genome Project. Science, 2021, 373, 1442-1443.	12.6	18
68	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. Nature Genetics, 2021, 53, 1469-1479.	21.4	100
69	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	17.5	96
70	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
71	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
72	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316

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73	A transcriptomic atlas of mouse cerebellar cortex comprehensivelyÂdefines cell types. Nature, 2021, 598, 214-219.	27.8	147
74	Joint single-cell measurements of nuclear proteins and RNA in vivo. Nature Methods, 2021, 18, 1204-1212.	19.0	69
75	Deep learning and alignment of spatially resolved single-cell transcriptomes with Tangram. Nature Methods, 2021, 18, 1352-1362.	19.0	276
76	Cell type ontologies of the Human Cell Atlas. Nature Cell Biology, 2021, 23, 1129-1135.	10.3	71
77	Stem-like intestinal Th17 cells give rise to pathogenic effector TÂcells during autoimmunity. Cell, 2021, 184, 6281-6298.e23.	28.9	99
78	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. Cell, 2021, 184, 6262-6280.e26.	28.9	125
79	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. Cell Genomics, 2021, 1, 100069.	6.5	15
80	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. Nature Biotechnology, 2020, 38, 56-65.	17.5	188
81	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	27.8	101
82	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. Cancer Cell, 2020, 38, 44-59.e9.	16.8	94
83	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. Cell Reports, 2020, 33, 108433.	6.4	54
84	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. Science, 2020, 370, .	12.6	155
85	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimerâ€™s disease. Nature Communications, 2020, 11, 6129.	12.8	371
86	A Distinct Transcriptional Program in Human CAR T Cells Bearing the 4-1BB Signaling Domain Revealed by scRNA-Seq. Molecular Therapy, 2020, 28, 2577-2592.	8.2	58
87	Purifying Selection against Pathogenic Mitochondrial DNA in Human T Cells. New England Journal of Medicine, 2020, 383, 1556-1563.	27.0	62
88	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. Cancer Cell, 2020, 38, 212-228.e13.	16.8	140
89	Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. Cancer Cell, 2020, 38, 229-246.e13.	16.8	210
90	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. Nature Methods, 2020, 17, 793-798.	19.0	134

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91	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. Cell, 2020, 183, 1103-1116.e20.	28.9	600
92	snRNA-seq reveals a subpopulation of adipocytes that regulates thermogenesis. Nature, 2020, 587, 98-102.	27.8	221
93	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. Nature Genetics, 2020, 52, 1208-1218.	21.4	226
94	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. Cell, 2020, 182, 1606-1622.e23.	28.9	287
95	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. Nature Communications, 2020, 11, 4296.	12.8	98
96	Endogenous Glucocorticoid Signaling Regulates CD8+ T Cell Differentiation and Development of Dysfunction in the Tumor Microenvironment. Immunity, 2020, 53, 658-671.e6.	14.3	98
97	T Follicular Regulatory Cell–Derived Fibrinogen-like Protein 2 Regulates Production of Autoantibodies and Induction of Systemic Autoimmunity. Journal of Immunology, 2020, 205, 3247-3262.	0.8	13
98	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	30.7	381
99	A single-cell landscape of high-grade serous ovarian cancer. Nature Medicine, 2020, 26, 1271-1279.	30.7	267
100	MAUDE: inferring expression changes in sorting-based CRISPR screens. Genome Biology, 2020, 21, 134.	8.8	18
101	Cell Atlas of The Human Fovea and Peripheral Retina. Scientific Reports, 2020, 10, 9802.	3.3	145
102	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	12.8	38
103	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	17.5	313
104	The network effect: studying COVID-19 pathology with the Human Cell Atlas. Nature Reviews Molecular Cell Biology, 2020, 21, 415-416.	37.0	12
105	ImmGen at 15. Nature Immunology, 2020, 21, 700-703.	14.5	55
106	A Synthesis Concerning Conservation and Divergence of Cell Types across Epithelia. Cold Spring Harbor Perspectives in Biology, 2020, 12, a035733.	5.5	6
107	Regenerative potential of prostate luminal cells revealed by single-cell analysis. Science, 2020, 368, 497-505.	12.6	165
108	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. Nature Biotechnology, 2020, 38, 737-746.	17.5	527

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109	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. Cell, 2020, 181, 1016-1035.e19.	28.9	1,956
110	Disease-associated astrocytes in Alzheimer's disease and aging. Nature Neuroscience, 2020, 23, 701-706.	14.8	525
111	Cell atlas of aqueous humor outflow pathways in eyes of humans and four model species provides insight into glaucoma pathogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10339-10349.	7.1	113
112	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
113	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. Immunity, 2020, 52, 1088-1104.e6.	14.3	79
114	Aging-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. Cell Reports, 2020, 33, 108566.	6.4	75
115	Abstract PR-007: Single-nucleus and spatial transcriptomics of archival pancreatic ductal adenocarcinoma reveals multi-compartment reprogramming after neoadjuvant treatment. Cancer Research, 2020, 80, PR-007-PR-007.	0.9	3
116	Integrated regulatory models for inference of subtype‐specific susceptibilities in glioblastoma. Molecular Systems Biology, 2020, 16, e9506.	7.2	5
117	EPEN-21. IMPAIRED NEURONAL-GLIAL FATE SPECIFICATION IN PEDIATRIC EPENDYMOMA REVEALED BY SINGLE-CELL RNA-SEQ. Neuro-Oncology, 2020, 22, iii311-iii312.	1.2	0
118	Anti-Tumor TCF1+ CD8 T Cells are Functionally Diverse and Evolve During Tumorigenesis and Progression. American Journal of Clinical Pathology, 2020, 154, S5-S6.	0.7	0
119	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. Nature Communications, 2019, 10, 3731.	12.8	45
120	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. Cell, 2019, 178, 1115-1131.e15.	28.9	231
121	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. Cell, 2019, 178, 835-849.e21.	28.9	1,408
122	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	27.8	273
123	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. Cell, 2019, 178, 714-730.e22.	28.9	806
124	DNA Microscopy: Optics-free Spatio-genetic Imaging by a Stand-Alone Chemical Reaction. Cell, 2019, 178, 229-241.e16.	28.9	77
125	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. Nature Communications, 2019, 10, 2907.	12.8	117
126	Calcitonin Gene-Related Peptide Negatively Regulates Alarmin-Driven Type 2 Innate Lymphoid Cell Responses. Immunity, 2019, 51, 709-723.e6.	14.3	144

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127	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide α-CGRP Modulates Group 2 Innate Lymphoid Cell Responses. Immunity, 2019, 51, 696-708.e9.	14.3	154
128	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	27.8	392
129	Combinatorial prediction of marker panels from single-cell transcriptomic data. Molecular Systems Biology, 2019, 15, e9005.	7.2	73
130	Distinct Tissue-Specific Roles for the Disease-Associated Autophagy Genes ATG16L2 and ATG16L1. Journal of Immunology, 2019, 203, 1820-1829.	0.8	18
131	High-definition spatial transcriptomics for in situ tissue profiling. Nature Methods, 2019, 16, 987-990.	19.0	708
132	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. Cell, 2019, 176, 1222-1237.e22.	28.9	347
133	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. Cell, 2019, 176, 928-943.e22.	28.9	411
134	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	6.4	122
135	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. Circulation, 2019, 140, 147-163.	1.6	231
136	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. Nature, 2019, 570, 523-527.	27.8	649
137	A Cellular Taxonomy of the Bone Marrow Stroma in Homeostasis and Leukemia. Cell, 2019, 177, 1915-1932.e16.	28.9	640
138	The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 31-41.	2.9	178
139	Streamlined Protocol for Deep Proteomic Profiling of FAC-sorted Cells and Its Application to Freshly Isolated Murine Immune Cells*. Molecular and Cellular Proteomics, 2019, 18, 995a-1009.	3.8	69
140	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
141	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	28.9	345
142	Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. Nature Communications, 2019, 10, 5462.	12.8	133
143	Integrative molecular and clinical modeling of clinical outcomes to PD1 blockade in patients with metastatic melanoma. Nature Medicine, 2019, 25, 1916-1927.	30.7	541
144	IL-33 Signaling Alters Regulatory T Cell Diversity in Support of Tumor Development. Cell Reports, 2019, 29, 2998-3008.e8.	6.4	53

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145	Single-Cell Profiles of Retinal Ganglion Cells Differing in Resilience to Injury Reveal Neuroprotective Genes. Neuron, 2019, 104, 1039-1055.e12.	8.1	396
146	Electrical and synaptic integration of glioma into neural circuits. Nature, 2019, 573, 539-545.	27.8	706
147	Single-cell transcriptomic profiling of the aging mouse brain. Nature Neuroscience, 2019, 22, 1696-1708.	14.8	432
148	Toward a Common Coordinate Framework for the Human Body. Cell, 2019, 179, 1455-1467.	28.9	81
149	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. Nature, 2019, 565, 234-239.	27.8	956
150	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1â̂'CD8+ Tumor-Infiltrating T Cells. Immunity, 2019, 50, 181-194.e6.	14.3	424
151	A quantitative framework for characterizing the evolutionary history of mammalian gene expression. Genome Research, 2019, 29, 53-63.	5.5	78
152	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	12.6	461
153	Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis. Science, 2018, 360, .	12.6	624
154	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell, 2018, 173, 90-103.e19.	28.9	296
155	Comprehensive Identification and Spatial Mapping of Habenular Neuronal Types Using Single-Cell RNA-Seq. Current Biology, 2018, 28, 1052-1065.e7.	3.9	139
156	Fas Promotes T Helper 17 Cell Differentiation and Inhibits T Helper 1 Cell Development by Binding and Sequestering Transcription Factor STAT1. Immunity, 2018, 48, 556-569.e7.	14.3	65
157	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of *ERAP2* transcripts under balancing selection. Genome Research, 2018, 28, 1812-1825.	5.5	66
158	Heterogeneous Responses of Hematopoietic Stem Cells to Inflammatory Stimuli Are Altered with Age. Cell Reports, 2018, 25, 2992-3005.e5.	6.4	127
159	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. Cell, 2018, 175, 984-997.e24.	28.9	892
160	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. Cell, 2018, 175, 1307-1320.e22.	28.9	388
161	Molecular, spatial, and functional single-cell profiling of the hypothalamic preoptic region. Science, 2018, 362, .	12.6	812
162	Regulation of Cellular Heterogeneity and Rates of Symmetric and Asymmetric Divisions in Triple-Negative Breast Cancer. Cell Reports, 2018, 24, 3237-3250.	6.4	31

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163	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimerâ€™s disease. Nature Neuroscience, 2018, 21, 811-819.	14.8	422
164	Genome-scale identification of transcription factors that mediate an inflammatory network during breast cellular transformation. Nature Communications, 2018, 9, 2068.	12.8	24
165	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. Nature, 2018, 560, 319-324.	27.8	878
166	BROCKMAN: deciphering variance in epigenomic regulators by k-mer factorization. BMC Bioinformatics, 2018, 19, 253.	2.6	38
167	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	21.4	139
168	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. Nature, 2018, 558, 454-459.	27.8	336
169	Scaling single-cell genomics from phenomenology to mechanism. Nature, 2017, 541, 331-338.	27.8	633
170	Critical role of IRF1 and BATF in forming chromatin landscape during type 1 regulatory cell differentiation. Nature Immunology, 2017, 18, 412-421.	14.5	103
171	Nucleic acid detection with CRISPR-Cas13a/C2c2. Science, 2017, 356, 438-442.	12.6	2,275
172	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. Science, 2017, 356, .	12.6	1,846
173	Inference and Evolutionary Analysis of Genome-Scale Regulatory Networks in Large Phylogenies. Cell Systems, 2017, 4, 543-558.e8.	6.2	40
174	PHF6 regulates phenotypic plasticity through chromatin organization within lineage-specific genes. Genes and Development, 2017, 31, 973-989.	5.9	50
175	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
176	RNA targeting with CRISPRâ€"Cas13. Nature, 2017, 550, 280-284.	27.8	1,442
177	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. Neuron, 2017, 96, 542-557.	8.1	235
178	Single-cell transcriptomics to explore the immune system in health and disease. Science, 2017, 358, 58-63.	12.6	440
179	Temporal Tracking of Microglia Activation in Neurodegeneration at Single-Cell Resolution. Cell Reports, 2017, 21, 366-380.	6.4	538
180	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764

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181	Anatomically and Functionally Distinct Lung Mesenchymal Populations Marked by Lgr5 and Lgr6. Cell, 2017, 170, 1149-1163.e12.	28.9	304
182	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. Nature, 2017, 549, 351-356.	27.8	460
183	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. Cell, 2017, 171, 1611-1624.e24.	28.9	1,656
184	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. Cell, 2017, 171, 1424-1436.e18.	28.9	95
185	A single-cell survey of the small intestinal epithelium. Nature, 2017, 551, 333-339.	27.8	1,197
186	IFNÎ³-Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. Cell, 2017, 170, 127-141.e15.	28.9	140
187	An Integrative Framework Reveals Signaling-to-Transcription Events in Toll-like Receptor Signaling. Cell Reports, 2017, 19, 2853-2866.	6.4	26
188	Massively parallel single-nucleus RNA-seq with DroNc-seq. Nature Methods, 2017, 14, 955-958.	19.0	859
189	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
190	The Human Cell Atlas: from vision to reality. Nature, 2017, 550, 451-453.	27.8	511
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