

Aviv Regev

List of Publications by Year in descending order

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Version: 2024-02-01

277
papers

136,430
citations

381

138
h-index

439

281
g-index

379
all docs

379
docs citations

379
times ranked

150889
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Smarca4</i> Inactivation Promotes Lineage-Specific Transformation and Early Metastatic Features in the Lung. <i>Cancer Discovery</i> , 2022, 12, 562-585.	7.7	48
2	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. <i>Nature Biotechnology</i> , 2022, 40, 374-381.	9.4	31
3	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217.	9.4	127
4	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2022, 162, 859-876.	0.6	37
5	Single-Cell, Single-Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. <i>Hepatology Communications</i> , 2022, 6, 821-840.	2.0	98
6	MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. <i>Nature Methods</i> , 2022, 19, 311-315.	9.0	102
7	Disruption of the IL-33-ST2-AKT signaling axis impairs neurodevelopment by inhibiting microglial metabolic adaptation and phagocytic function. <i>Immunity</i> , 2022, 55, 159-173.e9.	6.6	52
8	Colon stroma mediates an inflammation-driven fibroblastic response controlling matrix remodeling and healing. <i>PLoS Biology</i> , 2022, 20, e3001532.	2.6	41
9	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546.	0.6	14
10	Massively parallel phenotyping of coding variants in cancer with Perturb-seq. <i>Nature Biotechnology</i> , 2022, 40, 896-905.	9.4	44
11	Autism genes converge on asynchronous development of shared neuron classes. <i>Nature</i> , 2022, 602, 268-273.	13.7	180
12	Spatial components of molecular tissue biology. <i>Nature Biotechnology</i> , 2022, 40, 308-318.	9.4	148
13	SM-Omics is an automated platform for high-throughput spatial multi-omics. <i>Nature Communications</i> , 2022, 13, 795.	5.8	73
14	Three-dimensional spatial transcriptomics uncovers cell type localizations in the human rheumatoid arthritis synovium. <i>Communications Biology</i> , 2022, 5, 129.	2.0	35
15	A single-cell atlas of human and mouse white adipose tissue. <i>Nature</i> , 2022, 603, 926-933.	13.7	277
16	Tim-3 adapter protein Bat3 acts as an endogenous regulator of tolerogenic dendritic cell function. <i>Science Immunology</i> , 2022, 7, eabm0631.	5.6	22
17	The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463.	13.7	126
18	Single-cell RNA-seq reveals cell type-specific molecular and genetic associations to lupus. <i>Science</i> , 2022, 376, eabf1970.	6.0	156

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19	CAR T cell killing requires the IFN γ R pathway in solid but not liquid tumours. <i>Nature</i> , 2022, 604, 563-570.	13.7	150
20	Genome-wide CRISPR screen identifies PRC2 and KMT2D-COMPASS as regulators of distinct EMT trajectories that contribute differentially to metastasis. <i>Nature Cell Biology</i> , 2022, 24, 554-564.	4.6	53
21	Stepwise-edited, human melanoma models reveal mutations \hat{c} ™ effect on tumor and microenvironment. <i>Science</i> , 2022, 376, eabi8175.	6.0	24
22	Traversing industry and academia in biomedicine: the best of both worlds?. <i>Nature Reviews Genetics</i> , 2022, 23, 461-466.	7.7	2
23	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. <i>Science</i> , 2022, 376, eabl4290.	6.0	180
24	DIALOGUE maps multicellular programs in tissue from single-cell or spatial transcriptomics data. <i>Nature Biotechnology</i> , 2022, 40, 1467-1477.	9.4	42
25	An activation to memory differentiation trajectory of tumor-infiltrating lymphocytes informs metastatic melanoma outcomes. <i>Cancer Cell</i> , 2022, 40, 524-544.e5.	7.7	23
26	A human breast atlas integrating single-cell proteomics and transcriptomics. <i>Developmental Cell</i> , 2022, 57, 1400-1420.e7.	3.1	50
27	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. <i>Cell</i> , 2022, 185, 2918-2935.e29.	13.5	113
28	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021, 39, 451-461.	9.4	150
29	Opposing immune and genetic mechanisms shape oncogenic programs in synovial sarcoma. <i>Nature Medicine</i> , 2021, 27, 289-300.	15.2	64
30	QRICH1 dictates the outcome of ER stress through transcriptional control of proteostasis. <i>Science</i> , 2021, 371, .	6.0	73
31	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , 2021, 371, .	6.0	197
32	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. <i>Nature Immunology</i> , 2021, 22, 216-228.	7.0	116
33	Building a high-quality Human Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 149-153.	9.4	48
34	Skin-resident innate lymphoid cells converge on a pathogenic effector state. <i>Nature</i> , 2021, 592, 128-132.	13.7	119
35	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. <i>Nature Genetics</i> , 2021, 53, 332-341.	9.4	112
36	Transcriptional mediators of treatment resistance in lethal prostate cancer. <i>Nature Medicine</i> , 2021, 27, 426-433.	15.2	90

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37	Î³Î´ T cells regulate the intestinal response to nutrient sensing. <i>Science</i> , 2021, 371, .	6.0	78
38	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , 2021, 184, 1281-1298.e26.	13.5	210
39	Blockade of IL-22 signaling reverses erythroid dysfunction in stress-induced anemias. <i>Nature Immunology</i> , 2021, 22, 520-529.	7.0	11
40	Tim-3 adaptor protein Bat3 is a molecular checkpoint of T cell terminal differentiation and exhaustion. <i>Science Advances</i> , 2021, 7, .	4.7	18
41	Compressed sensing for highly efficient imaging transcriptomics. <i>Nature Biotechnology</i> , 2021, 39, 936-942.	9.4	33
42	Using viral load and epidemic dynamics to optimize pooled testing in resource-constrained settings. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	42
43	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	13.7	537
44	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 649-661.e5.	7.7	263
45	A cellular and spatial map of the choroid plexus across brain ventricles and ages. <i>Cell</i> , 2021, 184, 3056-3074.e21.	13.5	150
46	Deep generative model embedding of single-cell RNA-Seq profiles on hyperspheres and hyperbolic spaces. <i>Nature Communications</i> , 2021, 12, 2554.	5.8	48
47	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. <i>Cancer Cell</i> , 2021, 39, 779-792.e11.	7.7	245
48	L1CAM is not associated with extracellular vesicles in human cerebrospinal fluid or plasma. <i>Nature Methods</i> , 2021, 18, 631-634.	9.0	118
49	Molecular logic of cellular diversification in the mouse cerebral cortex. <i>Nature</i> , 2021, 595, 554-559.	13.7	212
50	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. <i>Nature</i> , 2021, 595, 101-106.	13.7	169
51	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. <i>Nature Biotechnology</i> , 2021, 39, 1246-1258.	9.4	244
52	B cell genomics behind cross-neutralization of SARS-CoV-2 variants and SARS-CoV. <i>Cell</i> , 2021, 184, 3205-3221.e24.	13.5	73
53	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. <i>Nature Biotechnology</i> , 2021, 39, 1556-1562.	9.4	46
54	Towards a Human Cell Atlas: Taking Notes from the Past. <i>Trends in Genetics</i> , 2021, 37, 625-630.	2.9	59

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55	OTME-7. Cancer - immune cell interactions drive transitions to mesenchymal-like state in glioblastoma. <i>Neuro-Oncology Advances</i> , 2021, 3, ii14-ii15.	0.4	0
56	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. <i>Cell</i> , 2021, 184, 4168-4185.e21.	13.5	203
57	Cycling cancer persister cells arise from lineages with distinct programs. <i>Nature</i> , 2021, 596, 576-582.	13.7	236
58	The CD155/TIGIT axis promotes and maintains immune evasion in neoantigen-expressing pancreatic cancer. <i>Cancer Cell</i> , 2021, 39, 1342-1360.e14.	7.7	119
59	A cell-free nanobody engineering platform rapidly generates SARS-CoV-2 neutralizing nanobodies. <i>Nature Communications</i> , 2021, 12, 5506.	5.8	38
60	Antigen dominance hierarchies shape TCF1+ progenitor CD8 T cell phenotypes in tumors. <i>Cell</i> , 2021, 184, 4996-5014.e26.	13.5	84
61	Spatially organized multicellular immune hubs in human colorectal cancer. <i>Cell</i> , 2021, 184, 4734-4752.e20.	13.5	256
62	Dietary suppression of MHC class II expression in intestinal epithelial cells enhances intestinal tumorigenesis. <i>Cell Stem Cell</i> , 2021, 28, 1922-1935.e5.	5.2	67
63	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	13.7	73
64	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
65	A human liver cell-based system modeling a clinical prognostic liver signature for therapeutic discovery. <i>Nature Communications</i> , 2021, 12, 5525.	5.8	21
66	Conventional type I dendritic cells maintain a reservoir of proliferative tumor-antigen specific TCF-1+ CD8+ T cells in tumor-draining lymph nodes. <i>Immunity</i> , 2021, 54, 2338-2353.e6.	6.6	111
67	The legacy of the Human Genome Project. <i>Science</i> , 2021, 373, 1442-1443.	6.0	18
68	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. <i>Nature Genetics</i> , 2021, 53, 1469-1479.	9.4	100
69	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	9.4	96
70	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
71	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
72	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316

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73	A transcriptomic atlas of mouse cerebellar cortex comprehensively defines cell types. <i>Nature</i> , 2021, 598, 214-219.	13.7	147
74	Joint single-cell measurements of nuclear proteins and RNA in vivo. <i>Nature Methods</i> , 2021, 18, 1204-1212.	9.0	69
75	Deep learning and alignment of spatially resolved single-cell transcriptomes with Tangram. <i>Nature Methods</i> , 2021, 18, 1352-1362.	9.0	276
76	Cell type ontologies of the Human Cell Atlas. <i>Nature Cell Biology</i> , 2021, 23, 1129-1135.	4.6	71
77	Stem-like intestinal Th17 cells give rise to pathogenic effector T cells during autoimmunity. <i>Cell</i> , 2021, 184, 6281-6298.e23.	13.5	99
78	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. <i>Cell</i> , 2021, 184, 6262-6280.e26.	13.5	125
79	GWAS of stool frequency provides insights into gastrointestinal motility and irritable bowel syndrome. <i>Cell Genomics</i> , 2021, 1, 100069.	3.0	15
80	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. <i>Nature Biotechnology</i> , 2020, 38, 56-65.	9.4	188
81	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. <i>Nature</i> , 2020, 586, 769-775.	13.7	101
82	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. <i>Cancer Cell</i> , 2020, 38, 44-59.e9.	7.7	94
83	An IL-27-Driven Transcriptional Network Identifies Regulators of IL-10 Expression across T Helper Cell Subsets. <i>Cell Reports</i> , 2020, 33, 108433.	2.9	54
84	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. <i>Science</i> , 2020, 370, .	6.0	155
85	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 6129.	5.8	371
86	A Distinct Transcriptional Program in Human CAR T Cells Bearing the 4-1BB Signaling Domain Revealed by scRNA-Seq. <i>Molecular Therapy</i> , 2020, 28, 2577-2592.	3.7	58
87	Purifying Selection against Pathogenic Mitochondrial DNA in Human T Cells. <i>New England Journal of Medicine</i> , 2020, 383, 1556-1563.	13.9	62
88	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. <i>Cancer Cell</i> , 2020, 38, 212-228.e13.	7.7	140
89	Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. <i>Cancer Cell</i> , 2020, 38, 229-246.e13.	7.7	210
90	Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. <i>Nature Methods</i> , 2020, 17, 793-798.	9.0	134

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91	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. <i>Cell</i> , 2020, 183, 1103-1116.e20.	13.5	600
92	snRNA-seq reveals a subpopulation of adipocytes that regulates thermogenesis. <i>Nature</i> , 2020, 587, 98-102.	13.7	221
93	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. <i>Nature Genetics</i> , 2020, 52, 1208-1218.	9.4	226
94	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. <i>Cell</i> , 2020, 182, 1606-1622.e23.	13.5	287
95	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020, 11, 4296.	5.8	98
96	Endogenous Glucocorticoid Signaling Regulates CD8+ T Cell Differentiation and Development of Dysfunction in the Tumor Microenvironment. <i>Immunity</i> , 2020, 53, 658-671.e6.	6.6	98
97	T Follicular Regulatory Cell-Derived Fibrinogen-like Protein 2 Regulates Production of Autoantibodies and Induction of Systemic Autoimmunity. <i>Journal of Immunology</i> , 2020, 205, 3247-3262.	0.4	13
98	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. <i>Nature Medicine</i> , 2020, 26, 792-802.	15.2	381
99	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , 2020, 26, 1271-1279.	15.2	267
100	MAUDE: inferring expression changes in sorting-based CRISPR screens. <i>Genome Biology</i> , 2020, 21, 134.	3.8	18
101	Cell Atlas of The Human Fovea and Peripheral Retina. <i>Scientific Reports</i> , 2020, 10, 9802.	1.6	145
102	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. <i>Nature Communications</i> , 2020, 11, 1237.	5.8	38
103	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	9.4	313
104	The network effect: studying COVID-19 pathology with the Human Cell Atlas. <i>Nature Reviews Molecular Cell Biology</i> , 2020, 21, 415-416.	16.1	12
105	ImmGen at 15. <i>Nature Immunology</i> , 2020, 21, 700-703.	7.0	55
106	A Synthesis Concerning Conservation and Divergence of Cell Types across Epithelia. <i>Cold Spring Harbor Perspectives in Biology</i> , 2020, 12, a035733.	2.3	6
107	Regenerative potential of prostate luminal cells revealed by single-cell analysis. <i>Science</i> , 2020, 368, 497-505.	6.0	165
108	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	9.4	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. <i>Cell</i> , 2020, 181, 1016-1035.e19.	13.5	1,956
110	Disease-associated astrocytes in Alzheimer's disease and aging. <i>Nature Neuroscience</i> , 2020, 23, 701-706.	7.1	525
111	Cell atlas of aqueous humor outflow pathways in eyes of humans and four model species provides insight into glaucoma pathogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10339-10349.	3.3	113
112	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	13.5	334
113	Integrated scRNA-Seq Identifies Human Postnatal Thymus Seeding Progenitors and Regulatory Dynamics of Differentiating Immature Thymocytes. <i>Immunity</i> , 2020, 52, 1088-1104.e6.	6.6	79
114	Aging-Associated Alterations in Mammary Epithelia and Stroma Revealed by Single-Cell RNA Sequencing. <i>Cell Reports</i> , 2020, 33, 108566.	2.9	75
115	Abstract PR-007: Single-nucleus and spatial transcriptomics of archival pancreatic ductal adenocarcinoma reveals multi-compartment reprogramming after neoadjuvant treatment. <i>Cancer Research</i> , 2020, 80, PR-007-PR-007.	0.4	3
116	Integrated regulatory models for inference of subtype-specific susceptibilities in glioblastoma. <i>Molecular Systems Biology</i> , 2020, 16, e9506.	3.2	5
117	EPEN-21. IMPAIRED NEURONAL-GLIAL FATE SPECIFICATION IN PEDIATRIC EPENDYMOMA REVEALED BY SINGLE-CELL RNA-SEQ. <i>Neuro-Oncology</i> , 2020, 22, iii311-iii312.	0.6	0
118	Anti-Tumor TCF1+ CD8 T Cells are Functionally Diverse and Evolve During Tumorigenesis and Progression. <i>American Journal of Clinical Pathology</i> , 2020, 154, S5-S6.	0.4	0
119	Mitogenic and progenitor gene programmes in single pilocytic astrocytoma cells. <i>Nature Communications</i> , 2019, 10, 3731.	5.8	45
120	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. <i>Cell</i> , 2019, 178, 1115-1131.e15.	13.5	231
121	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	13.5	1,408
122	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	13.7	273
123	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. <i>Cell</i> , 2019, 178, 714-730.e22.	13.5	806
124	DNA Microscopy: Optics-free Spatio-genetic Imaging by a Stand-Alone Chemical Reaction. <i>Cell</i> , 2019, 178, 229-241.e16.	13.5	77
125	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019, 10, 2907.	5.8	117
126	Calcitonin Gene-Related Peptide Negatively Regulates Alarmin-Driven Type 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , 2019, 51, 709-723.e6.	6.6	144

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127	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide $\hat{\pm}$ -CGRP Modulates Group 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , 2019, 51, 696-708.e9.	6.6	154
128	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	13.7	392
129	Combinatorial prediction of marker panels from single-cell transcriptomic data. <i>Molecular Systems Biology</i> , 2019, 15, e9005.	3.2	73
130	Distinct Tissue-Specific Roles for the Disease-Associated Autophagy Genes ATG16L2 and ATG16L1. <i>Journal of Immunology</i> , 2019, 203, 1820-1829.	0.4	18
131	High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , 2019, 16, 987-990.	9.0	708
132	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. <i>Cell</i> , 2019, 176, 1222-1237.e22.	13.5	347
133	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. <i>Cell</i> , 2019, 176, 928-943.e22.	13.5	411
134	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019, 27, 3228-3240.e7.	2.9	122
135	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. <i>Circulation</i> , 2019, 140, 147-163.	1.6	231
136	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , 2019, 570, 523-527.	13.7	649
137	A Cellular Taxonomy of the Bone Marrow Stroma in Homeostasis and Leukemia. <i>Cell</i> , 2019, 177, 1915-1932.e16.	13.5	640
138	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
139	Streamlined Protocol for Deep Proteomic Profiling of FAC-sorted Cells and Its Application to Freshly Isolated Murine Immune Cells*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 995a-1009.	2.5	69
140	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	3.1	57
141	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	13.5	345
142	Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. <i>Nature Communications</i> , 2019, 10, 5462.	5.8	133
143	Integrative molecular and clinical modeling of clinical outcomes to PD1 blockade in patients with metastatic melanoma. <i>Nature Medicine</i> , 2019, 25, 1916-1927.	15.2	541
144	IL-33 Signaling Alters Regulatory T Cell Diversity in Support of Tumor Development. <i>Cell Reports</i> , 2019, 29, 2998-3008.e8.	2.9	53

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145	Single-Cell Profiles of Retinal Ganglion Cells Differing in Resilience to Injury Reveal Neuroprotective Genes. <i>Neuron</i> , 2019, 104, 1039-1055.e12.	3.8	396
146	Electrical and synaptic integration of glioma into neural circuits. <i>Nature</i> , 2019, 573, 539-545.	13.7	706
147	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	7.1	432
148	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019, 179, 1455-1467.	13.5	81
149	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019, 565, 234-239.	13.7	956
150	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1 ^{hi} CD8 ⁺ Tumor-Infiltrating T Cells. <i>Immunity</i> , 2019, 50, 181-194.e6.	6.6	424
151	A quantitative framework for characterizing the evolutionary history of mammalian gene expression. <i>Genome Research</i> , 2019, 29, 53-63.	2.4	78
152	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	6.0	461
153	Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis. <i>Science</i> , 2018, 360, .	6.0	624
154	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	13.5	296
155	Comprehensive Identification and Spatial Mapping of Habenular Neuronal Types Using Single-Cell RNA-Seq. <i>Current Biology</i> , 2018, 28, 1052-1065.e7.	1.8	139
156	Fas Promotes T Helper 17 Cell Differentiation and Inhibits T Helper 1 Cell Development by Binding and Sequestering Transcription Factor STAT1. <i>Immunity</i> , 2018, 48, 556-569.e7.	6.6	65
157	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of ERAP2 transcripts under balancing selection. <i>Genome Research</i> , 2018, 28, 1812-1825.	2.4	66
158	Heterogeneous Responses of Hematopoietic Stem Cells to Inflammatory Stimuli Are Altered with Age. <i>Cell Reports</i> , 2018, 25, 2992-3005.e5.	2.9	127
159	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	13.5	892
160	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. <i>Cell</i> , 2018, 175, 1307-1320.e22.	13.5	388
161	Molecular, spatial, and functional single-cell profiling of the hypothalamic preoptic region. <i>Science</i> , 2018, 362, .	6.0	812
162	Regulation of Cellular Heterogeneity and Rates of Symmetric and Asymmetric Divisions in Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2018, 24, 3237-3250.	2.9	31

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163	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. <i>Nature Neuroscience</i> , 2018, 21, 811-819.	7.1	422
164	Genome-scale identification of transcription factors that mediate an inflammatory network during breast cellular transformation. <i>Nature Communications</i> , 2018, 9, 2068.	5.8	24
165	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. <i>Nature</i> , 2018, 560, 319-324.	13.7	878
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