Aviv Regev

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8757241/publications.pdf Version: 2024-02-01

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

AVIN RECEN

#	Article	IF	CITATIONS
1	Full-length transcriptome assembly from RNA-Seq data without a reference genome. Nature Biotechnology, 2011, 29, 644-652.	17.5	17,264
2	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. Cell, 2015, 161, 1202-1214.	28.9	5,908
3	Spatial reconstruction of single-cell gene expression data. Nature Biotechnology, 2015, 33, 495-502.	17.5	4,254
4	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	27.8	3,801
5	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. Science, 2014, 344, 1396-1401.	12.6	3,648
6	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. Cell, 2015, 163, 759-771.	28.9	3,558
7	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. Science, 2016, 352, 189-196.	12.6	3,421
8	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. Genes and Development, 2011, 25, 1915-1927.	5.9	3,208
9	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11667-11672.	7.1	2,709
10	Nucleic acid detection with CRISPR-Cas13a/C2c2. Science, 2017, 356, 438-442.	12.6	2,275
11	An embryonic stem cell–like gene expression signature in poorly differentiated aggressive human tumors. Nature Genetics, 2008, 40, 499-507.	21.4	2,218
12	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
13	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. Science, 2017, 356, .	12.6	1,846
14	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
15	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science, 2016, 353, aaf5573.	12.6	1,647
16	CRISPR-Cas9 Knockin Mice for Genome Editing and Cancer Modeling. Cell, 2014, 159, 440-455.	28.9	1,566
17	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
18	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. Nature Genetics, 2003, 34, 166-176.	21.4	1,543

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19	RNA targeting with CRISPR–Cas13. Nature, 2017, 550, 280-284.	27.8	1,442
20	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. Cell, 2019, 178, 835-849.e21.	28.9	1,408
21	Ab initio reconstruction of cell type–specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. Nature Biotechnology, 2010, 28, 503-510.	17.5	1,251
22	A single-cell survey of the small intestinal epithelium. Nature, 2017, 551, 333-339.	27.8	1,197
23	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. Cell, 2016, 167, 1853-1866.e17.	28.9	1,144
24	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. Nature, 2013, 498, 236-240.	27.8	1,103
25	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. Cell, 2016, 166, 1308-1323.e30.	28.9	1,010
26	Induction and molecular signature of pathogenic TH17 cells. Nature Immunology, 2012, 13, 991-999.	14.5	980
27	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5′ Sites. Cell Reports, 2014, 8, 284-296.	6.4	972
28	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. Nature, 2019, 565, 234-239.	27.8	956
29	CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. Genome Biology, 2016, 17, 77.	8.8	900
30	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. Cell, 2018, 175, 984-997.e24.	28.9	892
31	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. Nature, 2018, 560, 319-324.	27.8	878
32	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	27.8	875
33	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. Nature, 2014, 510, 363-369.	27.8	872
34	Massively parallel single-nucleus RNA-seq with DroNc-seq. Nature Methods, 2017, 14, 955-958.	19.0	859
35	Induction of pathogenic TH17 cells by inducible salt-sensing kinase SGK1. Nature, 2013, 496, 513-517.	27.8	851
36	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. Cell, 2011, 144, 296-309.	28.9	843

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37	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. Cell, 2016, 167, 1867-1882.e21.	28.9	819
38	Molecular, spatial, and functional single-cell profiling of the hypothalamic preoptic region. Science, 2018, 362, .	12.6	812
39	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. Genome Research, 2012, 22, 577-591.	5.5	809
40	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. Cell, 2019, 178, 714-730.e22.	28.9	806
41	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. Cell, 2014, 159, 148-162.	28.9	770
42	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	27.8	764
43	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. Cell, 2014, 157, 580-594.	28.9	751
44	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
45	High-definition spatial transcriptomics for in situ tissue profiling. Nature Methods, 2019, 16, 987-990.	19.0	708
46	Electrical and synaptic integration of glioma into neural circuits. Nature, 2019, 573, 539-545.	27.8	706
47	Comprehensive comparative analysis of strand-specific RNA sequencing methods. Nature Methods, 2010, 7, 709-715.	19.0	662
48	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. Nature, 2019, 570, 523-527.	27.8	649
49	A Cellular Taxonomy of the Bone Marrow Stroma in Homeostasis and Leukemia. Cell, 2019, 177, 1915-1932.e16.	28.9	640
50	Scaling single-cell genomics from phenomenology to mechanism. Nature, 2017, 541, 331-338.	27.8	633
51	Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis. Science, 2018, 360, .	12.6	624
52	Single-cell RNA-seq reveals changes in cell cycle and differentiation programs upon aging of hematopoietic stem cells. Genome Research, 2015, 25, 1860-1872.	5.5	614
53	Natural history and evolutionary principles of gene duplication in fungi. Nature, 2007, 449, 54-61.	27.8	611
54	Dynamic regulatory network controlling TH17 cell differentiation. Nature, 2013, 496, 461-468.	27.8	608

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55	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. Cell, 2020, 183, 1103-1116.e20.	28.9	600
56	Localization and abundance analysis of human lncRNAs at single-cell and single-molecule resolution. Genome Biology, 2015, 16, 20.	8.8	565
57	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
58	Temporal Tracking of Microglia Activation in Neurodegeneration at Single-Cell Resolution. Cell Reports, 2017, 21, 366-380.	6.4	538
59	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
60	Revealing the vectors of cellular identity with single-cell genomics. Nature Biotechnology, 2016, 34, 1145-1160.	17.5	534
61	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. Nature Biotechnology, 2020, 38, 737-746.	17.5	527
62	Disease-associated astrocytes in Alzheimer's disease and aging. Nature Neuroscience, 2020, 23, 701-706.	14.8	525
63	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. Nature Biotechnology, 2011, 29, 436-442.	17.5	524
64	The Human Cell Atlas: from vision to reality. Nature, 2017, 550, 451-453.	27.8	511
65	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. Cell, 2015, 163, 1400-1412.	28.9	504
66	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	17.5	495
67	DNA methylation dynamics of the human preimplantation embryo. Nature, 2014, 511, 611-615.	27.8	488
68	Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons. Science, 2016, 353, 925-928.	12.6	482
69	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	12.6	480
70	Generation of mouse models of myeloid malignancy with combinatorial genetic lesions using CRISPR-Cas9 genome editing. Nature Biotechnology, 2014, 32, 941-946.	17.5	477
71	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. Science, 2009, 326, 257-263.	12.6	473
72	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	12.6	461

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73	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. Nature, 2017, 549, 351-356.	27.8	460
74	Single-cell transcriptomics to explore the immune system in health and disease. Science, 2017, 358, 58-63.	12.6	440
75	Many IncRNAs, 5'UTRs, and pseudogenes are translated and some are likely to express functional proteins. ELife, 2015, 4, e08890.	6.0	439
76	Single-cell transcriptomic profiling of the aging mouse brain. Nature Neuroscience, 2019, 22, 1696-1708.	14.8	432
77	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1â^CD8+ Tumor-Infiltrating T Cells. Immunity, 2019, 50, 181-194.e6.	14.3	424
78	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. Nature Neuroscience, 2018, 21, 811-819.	14.8	422
79	Comparative analysis of RNA sequencing methods for degraded or low-input samples. Nature Methods, 2013, 10, 623-629.	19.0	419
80	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. Cell, 2019, 176, 928-943.e22.	28.9	411
81	Dynamic profiling of the protein life cycle in response to pathogens. Science, 2015, 347, 1259038.	12.6	408
82	Single-Cell Profiles of Retinal Ganglion Cells Differing in Resilience to Injury Reveal Neuroprotective Genes. Neuron, 2019, 104, 1039-1055.e12.	8.1	396
83	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	27.8	392
84	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	12.6	391
85	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. Cell, 2018, 175, 1307-1320.e22.	28.9	388
86	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686.	28.9	383
87	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	30.7	381
88	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. Molecular Cell, 2012, 47, 810-822.	9.7	375
89	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer's disease. Nature Communications, 2020, 11, 6129.	12.8	371
90	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361

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91	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. Cell, 2019, 176, 1222-1237.e22.	28.9	347
92	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	28.9	345
93	Deconstructing transcriptional heterogeneity in pluripotent stem cells. Nature, 2014, 516, 56-61.	27.8	343
94	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. Nature, 2018, 558, 454-459.	27.8	336
95	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
96	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
97	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. Cell, 2016, 166, 1500-1511.e9.	28.9	315
98	CD5L/AIM Regulates Lipid Biosynthesis and Restrains Th17 Cell Pathogenicity. Cell, 2015, 163, 1413-1427.	28.9	313
99	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. Nature Biotechnology, 2020, 38, 747-755.	17.5	313
100	Anatomically and Functionally Distinct Lung Mesenchymal Populations Marked by Lgr5 and Lgr6. Cell, 2017, 170, 1149-1163.e12.	28.9	304
101	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell, 2018, 173, 90-103.e19.	28.9	296
102	The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. Nature Immunology, 2014, 15, 373-383.	14.5	289
103	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. Cell, 2020, 182, 1606-1622.e23.	28.9	287
104	A single-cell atlas of human and mouse white adipose tissue. Nature, 2022, 603, 926-933.	27.8	277
105	Deep learning and alignment of spatially resolved single-cell transcriptomes with Tangram. Nature Methods, 2021, 18, 1352-1362.	19.0	276
106	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	27.8	273
107	The evolution of drug resistance in clinical isolates of Candida albicans. ELife, 2015, 4, e00662.	6.0	268
108	A single-cell landscape of high-grade serous ovarian cancer. Nature Medicine, 2020, 26, 1271-1279.	30.7	267

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109	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. Cancer Cell, 2021, 39, 649-661.e5.	16.8	263
110	Spatially organized multicellular immune hubs in human colorectal cancer. Cell, 2021, 184, 4734-4752.e20.	28.9	256
111	Pathogen Cell-to-Cell Variability Drives Heterogeneity in Host Immune Responses. Cell, 2015, 162, 1309-1321.	28.9	255
112	Small-Molecule RORÎ ³ t Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms. Immunity, 2014, 40, 477-489.	14.3	253
113	High-resolution interrogation of functional elements in the noncoding genome. Science, 2016, 353, 1545-1549.	12.6	251
114	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
115	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. Nature Biotechnology, 2021, 39, 1246-1258.	17.5	244
116	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. Nature Genetics, 2013, 45, 299-303.	21.4	237
117	Ribosome profiling reveals resemblance between long non-coding RNAs and 5′ leaders of coding RNAs. Development (Cambridge), 2013, 140, 2828-2834.	2.5	237
118	Cycling cancer persister cells arise from lineages with distinct programs. Nature, 2021, 596, 576-582.	27.8	236
119	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. Neuron, 2017, 96, 542-557.	8.1	235
120	Preparation of Singleâ€Cell RNAâ€Seq Libraries for Next Generation Sequencing. Current Protocols in Molecular Biology, 2014, 107, 4.22.1-17.	2.9	232
121	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. Cell, 2019, 178, 1115-1131.e15.	28.9	231
122	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. Circulation, 2019, 140, 147-163.	1.6	231
123	Impulse Control: Temporal Dynamics in Gene Transcription. Cell, 2011, 144, 886-896.	28.9	227
124	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. Nature Genetics, 2020, 52, 1208-1218.	21.4	226
125	snRNA-seq reveals a subpopulation of adipocytes that regulates thermogenesis. Nature, 2020, 587, 98-102.	27.8	221
126	Intersection of population variation and autoimmunity genetics in human T cell activation. Science, 2014. 345. 1254665.	12.6	218

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127	Molecular logic of cellular diversification in the mouse cerebral cortex. Nature, 2021, 595, 554-559.	27.8	212
128	Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. Cancer Cell, 2020, 38, 229-246.e13.	16.8	210
129	Inhibitory CD161 receptor identified in glioma-infiltrating TÂcells by single-cell analysis. Cell, 2021, 184, 1281-1298.e26.	28.9	210
130	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. Cell, 2021, 184, 4168-4185.e21.	28.9	203
131	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3264-3269.	7.1	201
132	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. Molecular Cell, 2015, 60, 816-827.	9.7	200
133	Core Circadian Clock Genes Regulate Leukemia Stem Cells in AML. Cell, 2016, 165, 303-316.	28.9	200
134	Structure and function of a transcriptional network activated by the MAPK Hog1. Nature Genetics, 2008, 40, 1300-1306.	21.4	197
135	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. Science, 2021, 371, .	12.6	197
136	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. Cell, 2014, 159, 1698-1710.	28.9	196
137	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. Nature Biotechnology, 2020, 38, 56-65.	17.5	188
138	A Generic and Cell-Type-Specific Wound Response Precedes Regeneration in Planarians. Developmental Cell, 2015, 35, 632-645.	7.0	184
139	Autism genes converge on asynchronous development of shared neuron classes. Nature, 2022, 602, 268-273.	27.8	180
140	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. Science, 2022, 376, eabl4290.	12.6	180
141	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
142	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. Cell, 2011, 147, 853-867.	28.9	177
143	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. Nature, 2021, 595, 101-106.	27.8	169
144	Transcriptional Regulatory Circuits: Predicting Numbers from Alphabets. Science, 2009, 325, 429-432.	12.6	168

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145	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 2021, 598, 103-110.	27.8	166
146	Regenerative potential of prostate luminal cells revealed by single-cell analysis. Science, 2020, 368, 497-505.	12.6	165
147	Activity motifs reveal principles of timing in transcriptional control of the yeast metabolic network. Nature Biotechnology, 2008, 26, 1251-1259.	17.5	160
148	Single-cell RNA-seq reveals cell type–specific molecular and genetic associations to lupus. Science, 2022, 376, eabf1970.	12.6	156
149	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. Science, 2020, 370, .	12.6	155
150	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
151	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	17.5	150
152	A cellular and spatial map of the choroid plexus across brain ventricles and ages. Cell, 2021, 184, 3056-3074.e21.	28.9	150
153	CAR T cell killing requires the IFNÎ ³ R pathway in solid but not liquid tumours. Nature, 2022, 604, 563-570.	27.8	150
154	Spatial components of molecular tissue biology. Nature Biotechnology, 2022, 40, 308-318.	17.5	148
155	A transcriptomic atlas of mouse cerebellar cortex comprehensivelyÂdefines cell types. Nature, 2021, 598, 214-219.	27.8	147
156	Cell Atlas of The Human Fovea and Peripheral Retina. Scientific Reports, 2020, 10, 9802.	3.3	145
157	Calcitonin Gene-Related Peptide Negatively Regulates Alarmin-Driven Type 2 Innate Lymphoid Cell Responses. Immunity, 2019, 51, 709-723.e6.	14.3	144
158	Multiplexed, targeted profiling of single-cell proteomes and transcriptomes in a single reaction. Genome Biology, 2016, 17, 188.	8.8	143
159	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. Genome Biology, 2016, 17, 19.	8.8	141
160	IFNγ-Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. Cell, 2017, 170, 127-141.e15.	28.9	140
161	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. Cancer Cell, 2020, 38, 212-228.e13.	16.8	140
162	Comprehensive Identification and Spatial Mapping of Habenular Neuronal Types Using Single-Cell RNA-Seq. Current Biology, 2018, 28, 1052-1065.e7.	3.9	139

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163	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	21.4	139
164	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
165	Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. Nature Communications, 2019, 10, 5462.	12.8	133
166	Heterogeneous Responses of Hematopoietic Stem Cells to Inflammatory Stimuli Are Altered with Age. Cell Reports, 2018, 25, 2992-3005.e5.	6.4	127
167	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	17.5	127
168	The evolution, evolvability and engineering of gene regulatory DNA. Nature, 2022, 603, 455-463.	27.8	126
169	Differential pre-malignant programs and microenvironment chart distinct paths to malignancy in human colorectal polyps. Cell, 2021, 184, 6262-6280.e26.	28.9	125
170	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. Genome Biology, 2010, 11, R87.	9.6	122
171	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	6.4	122
172	Skin-resident innate lymphoid cells converge on a pathogenic effector state. Nature, 2021, 592, 128-132.	27.8	119
173	The CD155/TIGIT axis promotes and maintains immune evasion in neoantigen-expressing pancreatic cancer. Cancer Cell, 2021, 39, 1342-1360.e14.	16.8	119
174	L1CAM is not associated with extracellular vesicles in human cerebrospinal fluid or plasma. Nature Methods, 2021, 18, 631-634.	19.0	118
175	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. Nature Communications, 2019, 10, 2907.	12.8	117
176	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. Nature Immunology, 2021, 22, 216-228.	14.5	116
177	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	27.8	114
178	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
179	Tissue-resident memory and circulating T cells are early responders to pre-surgical cancer immunotherapy. Cell, 2022, 185, 2918-2935.e29.	28.9	113
180	Multimodal pooled Perturb-CITE-seq screens in patient models define mechanisms of cancer immune evasion. Nature Genetics, 2021, 53, 332-341.	21.4	112

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181	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
182	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
183	MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. Nature Methods, 2022, 19, 311-315.	19.0	102
184	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	27.8	101
185	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. Nature Genetics, 2021, 53, 1469-1479.	21.4	100
186	Stem-like intestinal Th17 cells give rise to pathogenic effector TÂcells during autoimmunity. Cell, 2021, 184, 6281-6298.e23.	28.9	99
187	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. Nature Communications, 2020, 11, 4296.	12.8	98
188	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
189	Singleâ€Cell, Singleâ€Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity. Hepatology Communications, 2022, 6, 821-840.	4.3	98
190	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	17.5	96
191	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. Cell, 2017, 171, 1424-1436.e18.	28.9	95
192	Single-Cell RNA-Seq Reveals Cellular Hierarchies and Impaired Developmental Trajectories in Pediatric Ependymoma. Cancer Cell, 2020, 38, 44-59.e9.	16.8	94
193	Transcriptional mediators of treatment resistance in lethal prostate cancer. Nature Medicine, 2021, 27, 426-433.	30.7	90
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195	The MicroRNA-132 and MicroRNA-212 Cluster Regulates Hematopoietic Stem Cell Maintenance and Survival with Age by Buffering FOXO3 Expression. Immunity, 2015, 42, 1021-1032.	14.3	84
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