

Aviv Regev

List of Publications by Year in descending order

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Version: 2024-02-01

277
papers

136,430
citations

317

138
h-index

373

281
g-index

379
all docs

379
docs citations

379
times ranked

137791
citing authors

#	ARTICLE	IF	CITATIONS
1	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011, 29, 644-652.	9.4	17,264
2	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. <i>Cell</i> , 2015, 161, 1202-1214.	13.5	5,908
3	Spatial reconstruction of single-cell gene expression data. <i>Nature Biotechnology</i> , 2015, 33, 495-502.	9.4	4,254
4	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	13.7	3,801
5	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , 2014, 344, 1396-1401.	6.0	3,648
6	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. <i>Cell</i> , 2015, 163, 759-771.	13.5	3,558
7	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. <i>Science</i> , 2016, 352, 189-196.	6.0	3,421
8	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. <i>Genes and Development</i> , 2011, 25, 1915-1927.	2.7	3,208
9	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11667-11672.	3.3	2,709
10	Nucleic acid detection with CRISPR-Cas13a/C2c2. <i>Science</i> , 2017, 356, 438-442.	6.0	2,275
11	An embryonic stem cell-like gene expression signature in poorly differentiated aggressive human tumors. <i>Nature Genetics</i> , 2008, 40, 499-507.	9.4	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. <i>Cell</i> , 2020, 181, 1016-1035.e19.	13.5	1,956
13	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. <i>Science</i> , 2017, 356, .	6.0	1,846
14	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , 2017, 171, 1611-1624.e24.	13.5	1,656
15	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016, 353, aaf5573.	6.0	1,647
16	CRISPR-Cas9 Knockin Mice for Genome Editing and Cancer Modeling. <i>Cell</i> , 2014, 159, 440-455.	13.5	1,566
17	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
18	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , 2003, 34, 166-176.	9.4	1,543

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19	RNA targeting with CRISPR-Cas13. <i>Nature</i> , 2017, 550, 280-284.	13.7	1,442
20	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , 2019, 178, 835-849.e21.	13.5	1,408
21	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010, 28, 503-510.	9.4	1,251
22	A single-cell survey of the small intestinal epithelium. <i>Nature</i> , 2017, 551, 333-339.	13.7	1,197
23	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016, 167, 1853-1866.e17.	13.5	1,144
24	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , 2013, 498, 236-240.	13.7	1,103
25	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. <i>Cell</i> , 2016, 166, 1308-1323.e30.	13.5	1,010
26	Induction and molecular signature of pathogenic TH17 cells. <i>Nature Immunology</i> , 2012, 13, 991-999.	7.0	980
27	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5' Sites. <i>Cell Reports</i> , 2014, 8, 284-296.	2.9	972
28	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , 2019, 565, 234-239.	13.7	956
29	CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. <i>Genome Biology</i> , 2016, 17, 77.	3.8	900
30	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , 2018, 175, 984-997.e24.	13.5	892
31	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. <i>Nature</i> , 2018, 560, 319-324.	13.7	878
32	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016, 539, 309-313.	13.7	875
33	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , 2014, 510, 363-369.	13.7	872
34	Massively parallel single-nucleus RNA-seq with DroNc-seq. <i>Nature Methods</i> , 2017, 14, 955-958.	9.0	859
35	Induction of pathogenic TH17 cells by inducible salt-sensing kinase SGK1. <i>Nature</i> , 2013, 496, 513-517.	13.7	851
36	Densely Interconnected Transcriptional Circuits Control Cell States in Human Hematopoiesis. <i>Cell</i> , 2011, 144, 296-309.	13.5	843

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37	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , 2016, 167, 1867-1882.e21.	13.5	819
38	Molecular, spatial, and functional single-cell profiling of the hypothalamic preoptic region. <i>Science</i> , 2018, 362, .	6.0	812
39	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012, 22, 577-591.	2.4	809
40	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. <i>Cell</i> , 2019, 178, 714-730.e22.	13.5	806
41	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. <i>Cell</i> , 2014, 159, 148-162.	13.5	770
42	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
43	Reconstructing and Reprogramming the Tumor-Propagating Potential of Glioblastoma Stem-like Cells. <i>Cell</i> , 2014, 157, 580-594.	13.5	751
44	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	6.0	743
45	High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , 2019, 16, 987-990.	9.0	708
46	Electrical and synaptic integration of glioma into neural circuits. <i>Nature</i> , 2019, 573, 539-545.	13.7	706
47	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , 2010, 7, 709-715.	9.0	662
48	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , 2019, 570, 523-527.	13.7	649
49	A Cellular Taxonomy of the Bone Marrow Stroma in Homeostasis and Leukemia. <i>Cell</i> , 2019, 177, 1915-1932.e16.	13.5	640
50	Scaling single-cell genomics from phenomenology to mechanism. <i>Nature</i> , 2017, 541, 331-338.	13.7	633
51	Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis. <i>Science</i> , 2018, 360, .	6.0	624
52	Single-cell RNA-seq reveals changes in cell cycle and differentiation programs upon aging of hematopoietic stem cells. <i>Genome Research</i> , 2015, 25, 1860-1872.	2.4	614
53	Natural history and evolutionary principles of gene duplication in fungi. <i>Nature</i> , 2007, 449, 54-61.	13.7	611
54	Dynamic regulatory network controlling TH17 cell differentiation. <i>Nature</i> , 2013, 496, 461-468.	13.7	608

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55	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. <i>Cell</i> , 2020, 183, 1103-1116.e20.	13.5	600
56	Localization and abundance analysis of human lncRNAs at single-cell and single-molecule resolution. <i>Genome Biology</i> , 2015, 16, 20.	3.8	565
57	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
58	Temporal Tracking of Microglia Activation in Neurodegeneration at Single-Cell Resolution. <i>Cell Reports</i> , 2017, 21, 366-380.	2.9	538
59	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	13.7	537
60	Revealing the vectors of cellular identity with single-cell genomics. <i>Nature Biotechnology</i> , 2016, 34, 1145-1160.	9.4	534
61	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , 2020, 38, 737-746.	9.4	527
62	Disease-associated astrocytes in Alzheimer's disease and aging. <i>Nature Neuroscience</i> , 2020, 23, 701-706.	7.1	525
63	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , 2011, 29, 436-442.	9.4	524
64	The Human Cell Atlas: from vision to reality. <i>Nature</i> , 2017, 550, 451-453.	13.7	511
65	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. <i>Cell</i> , 2015, 163, 1400-1412.	13.5	504
66	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484.	9.4	495
67	DNA methylation dynamics of the human preimplantation embryo. <i>Nature</i> , 2014, 511, 611-615.	13.7	488
68	Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons. <i>Science</i> , 2016, 353, 925-928.	6.0	482
69	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. <i>Science</i> , 2014, 344, 519-523.	6.0	480
70	Generation of mouse models of myeloid malignancy with combinatorial genetic lesions using CRISPR-Cas9 genome editing. <i>Nature Biotechnology</i> , 2014, 32, 941-946.	9.4	477
71	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	6.0	473
72	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	6.0	461

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73	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. <i>Nature</i> , 2017, 549, 351-356.	13.7	460
74	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , 2017, 358, 58-63.	6.0	440
75	Many lncRNAs, 5'UTRs, and pseudogenes are translated and some are likely to express functional proteins. <i>ELife</i> , 2015, 4, e08890.	2.8	439
76	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , 2019, 22, 1696-1708.	7.1	432
77	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
78	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
79	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , 2013, 10, 623-629.	9.0	419
80	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. <i>Cell</i> , 2019, 176, 928-943.e22.	13.5	411
81	Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015, 347, 1259038.	6.0	408
82	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
83	Decoding human fetal liver haematopoiesis. <i>Nature</i> , 2019, 574, 365-371.	13.7	392
84	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. <i>Science</i> , 2014, 343, 1246980.	6.0	391
85	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. <i>Cell</i> , 2018, 175, 1307-1320.e22.	13.5	388
86	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. <i>Cell</i> , 2015, 162, 675-686.	13.5	383
87	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
88	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	4.5	375
89	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
90	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361

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91	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. <i>Cell</i> , 2019, 176, 1222-1237.e22.	13.5	347
92	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	13.5	345
93	Deconstructing transcriptional heterogeneity in pluripotent stem cells. <i>Nature</i> , 2014, 516, 56-61.	13.7	343
94	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. <i>Nature</i> , 2018, 558, 454-459.	13.7	336
95	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
96	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
97	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. <i>Cell</i> , 2016, 166, 1500-1511.e9.	13.5	315
98	CD5L/AIM Regulates Lipid Biosynthesis and Restrains Th17 Cell Pathogenicity. <i>Cell</i> , 2015, 163, 1413-1427.	13.5	313
99	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , 2020, 38, 747-755.	9.4	313
100	Anatomically and Functionally Distinct Lung Mesenchymal Populations Marked by Lgr5 and Lgr6. <i>Cell</i> , 2017, 170, 1149-1163.e12.	13.5	304
101	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	13.5	296
102	The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. <i>Nature Immunology</i> , 2014, 15, 373-383.	7.0	289
103	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. <i>Cell</i> , 2020, 182, 1606-1622.e23.	13.5	287
104	A single-cell atlas of human and mouse white adipose tissue. <i>Nature</i> , 2022, 603, 926-933.	13.7	277
105	Deep learning and alignment of spatially resolved single-cell transcriptomes with Tangram. <i>Nature Methods</i> , 2021, 18, 1352-1362.	9.0	276
106	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , 2019, 572, 74-79.	13.7	273
107	The evolution of drug resistance in clinical isolates of <i>Candida albicans</i> . <i>ELife</i> , 2015, 4, e00662.	2.8	268
108	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , 2020, 26, 1271-1279.	15.2	267

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109	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 649-661.e5.	7.7	263
110	Spatially organized multicellular immune hubs in human colorectal cancer. <i>Cell</i> , 2021, 184, 4734-4752.e20.	13.5	256
111	Pathogen Cell-to-Cell Variability Drives Heterogeneity in Host Immune Responses. <i>Cell</i> , 2015, 162, 1309-1321.	13.5	255
112	Small-Molecule ROR γ t Antagonists Inhibit T Helper 17 Cell Transcriptional Network by Divergent Mechanisms. <i>Immunity</i> , 2014, 40, 477-489.	6.6	253
113	High-resolution interrogation of functional elements in the noncoding genome. <i>Science</i> , 2016, 353, 1545-1549.	6.0	251
114	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
115	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
116	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. <i>Nature Genetics</i> , 2013, 45, 299-303.	9.4	237
117	Ribosome profiling reveals resemblance between long non-coding RNAs and 5' leaders of coding RNAs. <i>Development (Cambridge)</i> , 2013, 140, 2828-2834.	1.2	237
118	Cycling cancer persister cells arise from lineages with distinct programs. <i>Nature</i> , 2021, 596, 576-582.	13.7	236
119	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
120	Preparation of Single-Cell RNA-seq Libraries for Next Generation Sequencing. <i>Current Protocols in Molecular Biology</i> , 2014, 107, 4.22.1-17.	2.9	232
121	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. <i>Cell</i> , 2019, 178, 1115-1131.e15.	13.5	231
122	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. <i>Circulation</i> , 2019, 140, 147-163.	1.6	231
123	Impulse Control: Temporal Dynamics in Gene Transcription. <i>Cell</i> , 2011, 144, 886-896.	13.5	227
124	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. <i>Nature Genetics</i> , 2020, 52, 1208-1218.	9.4	226
125	snRNA-seq reveals a subpopulation of adipocytes that regulates thermogenesis. <i>Nature</i> , 2020, 587, 98-102.	13.7	221
126	Intersection of population variation and autoimmunity genetics in human T cell activation. <i>Science</i> , 2014, 345, 1254665.	6.0	218

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127	Molecular logic of cellular diversification in the mouse cerebral cortex. <i>Nature</i> , 2021, 595, 554-559.	13.7	212
128	Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. <i>Cancer Cell</i> , 2020, 38, 229-246.e13.	7.7	210
129	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , 2021, 184, 1281-1298.e26.	13.5	210
130	Metabolic modeling of single Th17 cells reveals regulators of autoimmunity. <i>Cell</i> , 2021, 184, 4168-4185.e21.	13.5	203
131	Ab initio construction of a eukaryotic transcriptome by massively parallel mRNA sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3264-3269.	3.3	201
132	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , 2015, 60, 816-827.	4.5	200
133	Core Circadian Clock Genes Regulate Leukemia Stem Cells in AML. <i>Cell</i> , 2016, 165, 303-316.	13.5	200
134	Structure and function of a transcriptional network activated by the MAPK Hog1. <i>Nature Genetics</i> , 2008, 40, 1300-1306.	9.4	197
135	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , 2021, 371, .	6.0	197
136	High-Resolution Sequencing and Modeling Identifies Distinct Dynamic RNA Regulatory Strategies. <i>Cell</i> , 2014, 159, 1698-1710.	13.5	196
137	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. <i>Nature Biotechnology</i> , 2020, 38, 56-65.	9.4	188
138	A Generic and Cell-Type-Specific Wound Response Precedes Regeneration in Planarians. <i>Developmental Cell</i> , 2015, 35, 632-645.	3.1	184
139	Autism genes converge on asynchronous development of shared neuron classes. <i>Nature</i> , 2022, 602, 268-273.	13.7	180
140	Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. <i>Science</i> , 2022, 376, eabl4290.	6.0	180
141	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
142	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. <i>Cell</i> , 2011, 147, 853-867.	13.5	177
143	TIM-3 restrains anti-tumour immunity by regulating inflammasome activation. <i>Nature</i> , 2021, 595, 101-106.	13.7	169
144	Transcriptional Regulatory Circuits: Predicting Numbers from Alphabets. <i>Science</i> , 2009, 325, 429-432.	6.0	168

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145	A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , 2021, 598, 103-110.	13.7	166
146	Regenerative potential of prostate luminal cells revealed by single-cell analysis. <i>Science</i> , 2020, 368, 497-505.	6.0	165
147	Activity motifs reveal principles of timing in transcriptional control of the yeast metabolic network. <i>Nature Biotechnology</i> , 2008, 26, 1251-1259.	9.4	160
148	Single-cell RNA-seq reveals cell type-specific molecular and genetic associations to lupus. <i>Science</i> , 2022, 376, eabf1970.	6.0	156
149	In vivo Perturb-Seq reveals neuronal and glial abnormalities associated with autism risk genes. <i>Science</i> , 2020, 370, .	6.0	155
150	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide \pm -CGRP Modulates Group 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , 2019, 51, 696-708.e9.	6.6	154
151	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021, 39, 451-461.	9.4	150
152	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
153	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
154	Spatial components of molecular tissue biology. <i>Nature Biotechnology</i> , 2022, 40, 308-318.	9.4	148
155	A transcriptomic atlas of mouse cerebellar cortex comprehensively defines cell types. <i>Nature</i> , 2021, 598, 214-219.	13.7	147
156	Cell Atlas of The Human Fovea and Peripheral Retina. <i>Scientific Reports</i> , 2020, 10, 9802.	1.6	145
157	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
158	Multiplexed, targeted profiling of single-cell proteomes and transcriptomes in a single reaction. <i>Genome Biology</i> , 2016, 17, 188.	3.8	143
159	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. <i>Genome Biology</i> , 2016, 17, 19.	3.8	141
160	IFN γ -Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. <i>Cell</i> , 2017, 170, 127-141.e15.	13.5	140
161	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. <i>Cancer Cell</i> , 2020, 38, 212-228.e13.	7.7	140
162	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

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163	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	9.4	139
164	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
165	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
166	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
167	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217.	9.4	127
168	The evolution, evolvability and engineering of gene regulatory DNA. <i>Nature</i> , 2022, 603, 455-463.	13.7	126
169	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
170	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , 2010, 11, R87.	13.9	122
171	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019, 27, 3228-3240.e7.	2.9	122
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