

# Aviv Regev

## List of Publications by Citations

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340  
papers

83,881  
citations

119  
h-index

289  
g-index

379  
ext. papers

114,980  
ext. citations

32.3  
avg. IF

7.85  
L-index

#	Paper	IF	Citations
340	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 644-52	44.5	11785
339	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. <i>Cell</i> , <b>2015</b> , 161, 1202-1214	56.2	3873
338	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , <b>2009</b> , 458, 223-7	50.4	3230
337	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. <i>Genes and Development</i> , <b>2011</b> , 25, 1915-27	12.6	2492
336	Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR-Cas system. <i>Cell</i> , <b>2015</b> , 163, 759-71	56.2	2414
335	Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. <i>Science</i> , <b>2014</b> , 344, 1396-401	33.3	2401
334	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> , <b>2009</b> , 106, 11667-72	11.5	2331
333	Spatial reconstruction of single-cell gene expression data. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 495-502	44.5	2009
332	Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq. <i>Science</i> , <b>2016</b> , 352, 189-96	33.3	1961
331	An embryonic stem cell-like gene expression signature in poorly differentiated aggressive human tumors. <i>Nature Genetics</i> , <b>2008</b> , 40, 499-507	36.3	1885
330	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> , <b>2020</b> , 181, 1016-1035.e19	56.2	1326
329	Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. <i>Nature Genetics</i> , <b>2003</b> , 34, 166-76	36.3	1275
328	Nucleic acid detection with CRISPR-Cas13a/C2c2. <i>Science</i> , <b>2017</b> , 356, 438-442	33.3	1240
327	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. <i>Science</i> , <b>2017</b> , 356,	33.3	1176
326	CRISPR-Cas9 knockin mice for genome editing and cancer modeling. <i>Cell</i> , <b>2014</b> , 159, 440-55	56.2	1089
325	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , <b>2016</b> , 353, aaf5573	33.3	1037
324	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 503-10	44.5	1030

323	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
322	RNA targeting with CRISPR-Cas13. <i>Nature</i> , <b>2017</b> , 550, 280-284	50.4	900
321	Single-Cell Transcriptomic Analysis of Primary and Metastatic Tumor Ecosystems in Head and Neck Cancer. <i>Cell</i> , <b>2017</b> , 171, 1611-1624.e24	56.2	883
320	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , <b>2013</b> , 498, 236-40	50.4	867
319	Induction and molecular signature of pathogenic TH17 cells. <i>Nature Immunology</i> , <b>2012</b> , 13, 991-9	19.1	757
318	Perturbation of m6A writers reveals two distinct classes of mRNA methylation at internal and 5' sites. <i>Cell Reports</i> , <b>2014</b> , 8, 284-96	10.6	700
317	A single-cell survey of the small intestinal epithelium. <i>Nature</i> , <b>2017</b> , 551, 333-339	50.4	676
316	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. <i>Cell</i> , <b>2016</b> , 166, 1308-1323.e30	56.2	675
315	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , <b>2016</b> , 167, 1853-1866.e17	56.2	675
314	Induction of pathogenic TH17 cells by inducible salt-sensing kinase SGK1. <i>Nature</i> , <b>2013</b> , 496, 513-7	50.4	662
313	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , <b>2014</b> , 510, 363-9	50.4	661
312	Densely interconnected transcriptional circuits control cell states in human hematopoiesis. <i>Cell</i> , <b>2011</b> , 144, 296-309	56.2	655
311	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , <b>2012</b> , 22, 577-91	9.7	590
310	CEL-Seq2: sensitive highly-multiplexed single-cell RNA-Seq. <i>Genome Biology</i> , <b>2016</b> , 17, 77	18.3	571
309	Neoantigen vaccine generates intratumoral T cell responses in phase Ib glioblastoma trial. <i>Nature</i> , <b>2019</b> , 565, 234-239	50.4	569
308	Comprehensive comparative analysis of strand-specific RNA sequencing methods. <i>Nature Methods</i> , <b>2010</b> , 7, 709-15	21.6	562
307	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , <b>2016</b> , 539, 309-313	50.4	561
306	Transcriptome-wide mapping reveals widespread dynamic-regulated pseudouridylation of ncRNA and mRNA. <i>Cell</i> , <b>2014</b> , 159, 148-162	56.2	559

305	An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. <i>Cell</i> , <b>2019</b> , 178, 835-849.e21	49.2	556
304	Reconstructing and reprogramming the tumor-propagating potential of glioblastoma stem-like cells. <i>Cell</i> , <b>2014</b> , 157, 580-94	56.2	549
303	A revised airway epithelial hierarchy includes CFTR-expressing ionocytes. <i>Nature</i> , <b>2018</b> , 560, 319-324	50.4	526
302	Massively parallel single-nucleus RNA-seq with DroNc-seq. <i>Nature Methods</i> , <b>2017</b> , 14, 955-958	21.6	525
301	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , <b>2016</b> , 167, 1867-1882.e21	56.2	518
300	Natural history and evolutionary principles of gene duplication in fungi. <i>Nature</i> , <b>2007</b> , 449, 54-61	50.4	517
299	Dynamic regulatory network controlling TH17 cell differentiation. <i>Nature</i> , <b>2013</b> , 496, 461-8	50.4	492
298	A Cancer Cell Program Promotes T Cell Exclusion and Resistance to Checkpoint Blockade. <i>Cell</i> , <b>2018</b> , 175, 984-997.e24	56.2	477
297	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , <b>2017</b> , 355,	33.3	455
296	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 479-84	44.5	434
295	Localization and abundance analysis of human lncRNAs at single-cell and single-molecule resolution. <i>Genome Biology</i> , <b>2015</b> , 16, 20	18.3	421
294	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , <b>2017</b> , 550, 244-248	50.4	417
293	Scaling single-cell genomics from phenomenology to mechanism. <i>Nature</i> , <b>2017</b> , 541, 331-338	50.4	414
292	Unbiased reconstruction of a mammalian transcriptional network mediating pathogen responses. <i>Science</i> , <b>2009</b> , 326, 257-63	33.3	411
291	Molecular, spatial, and functional single-cell profiling of the hypothalamic preoptic region. <i>Science</i> , <b>2018</b> , 362,	33.3	411
290	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 436-42	44.5	406
289	DNA methylation dynamics of the human preimplantation embryo. <i>Nature</i> , <b>2014</b> , 511, 611-5	50.4	390
288	Revealing the vectors of cellular identity with single-cell genomics. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 1145-1150	41.60	382

287	Polarization of the effects of autoimmune and neurodegenerative risk alleles in leukocytes. <i>Science</i> , <b>2014</b> , 344, 519-23	33.3	372
286	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. <i>Cell</i> , <b>2015</b> , 163, 1400-12	56.2	369
285	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. <i>Cell</i> , <b>2019</b> , 178, 714-730.e322	32.2	359
284	Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis. <i>Science</i> , <b>2018</b> , 360,	33.3	351
283	Individual brain organoids reproducibly form cell diversity of the human cerebral cortex. <i>Nature</i> , <b>2019</b> , 570, 523-527	50.4	349
282	Single-cell RNA-seq reveals changes in cell cycle and differentiation programs upon aging of hematopoietic stem cells. <i>Genome Research</i> , <b>2015</b> , 25, 1860-72	9.7	348
281	Generation of mouse models of myeloid malignancy with combinatorial genetic lesions using CRISPR-Cas9 genome editing. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 941-6	44.5	342
280	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. <i>Nature</i> , <b>2017</b> , 549, 351-356	50.4	330
279	Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons. <i>Science</i> , <b>2016</b> , 353, 925-8	33.3	328
278	High-definition spatial transcriptomics for in situ tissue profiling. <i>Nature Methods</i> , <b>2019</b> , 16, 987-990	21.6	322
277	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , <b>2013</b> , 10, 623-9	21.6	320
276	A Cellular Taxonomy of the Bone Marrow Stroma in Homeostasis and Leukemia. <i>Cell</i> , <b>2019</b> , 177, 1915-1932.e16314	32.1	314
275	Temporal Tracking of Microglia Activation in Neurodegeneration at Single-Cell Resolution. <i>Cell Reports</i> , <b>2017</b> , 21, 366-380	10.6	313
274	The Human Cell Atlas: from vision to reality. <i>Nature</i> , <b>2017</b> , 550, 451-453	50.4	310
273	Common genetic variants modulate pathogen-sensing responses in human dendritic cells. <i>Science</i> , <b>2014</b> , 343, 1246-980	33.3	309
272	Electrical and synaptic integration of glioma into neural circuits. <i>Nature</i> , <b>2019</b> , 573, 539-545	50.4	303
271	A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals. <i>Molecular Cell</i> , <b>2012</b> , 47, 810-22	17.6	299
270	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. <i>Cell</i> , <b>2015</b> , 162, 675-86	56.2	288

269	Immunogenetics. Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , <b>2015</b> , 347, 1259038	33.3	284
268	Many lncRNAs, 5'UTRs, and pseudogenes are translated and some are likely to express functional proteins. <i>ELife</i> , <b>2015</b> , 4, e08890	8.9	284
267	Single-cell transcriptomics to explore the immune system in health and disease. <i>Science</i> , <b>2017</b> , 358, 58-63	33.3	275
266	Deconstructing transcriptional heterogeneity in pluripotent stem cells. <i>Nature</i> , <b>2014</b> , 516, 56-61	50.4	262
265	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , <b>2018</b> , 360, 331-335	33.3	255
264	Checkpoint Blockade Immunotherapy Induces Dynamic Changes in PD-1/CD8 Tumor-Infiltrating T Cells. <i>Immunity</i> , <b>2019</b> , 50, 181-194.e6	32.3	240
263	Integrative molecular and clinical modeling of clinical outcomes to PD1 blockade in patients with metastatic melanoma. <i>Nature Medicine</i> , <b>2019</b> , 25, 1916-1927	50.5	227
262	CD5L/AIM Regulates Lipid Biosynthesis and Restrains Th17 Cell Pathogenicity. <i>Cell</i> , <b>2015</b> , 163, 1413-27	56.2	220
261	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. <i>Nature Neuroscience</i> , <b>2018</b> , 21, 811-819	25.5	220
260	Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 737-746	44.5	212
259	A Distinct Gene Module for Dysfunction Uncoupled from Activation in Tumor-Infiltrating T Cells. <i>Cell</i> , <b>2016</b> , 166, 1500-1511.e9	56.2	209
258	Small-molecule ROR $\gamma$ antagonists inhibit T helper 17 cell transcriptional network by divergent mechanisms. <i>Immunity</i> , <b>2014</b> , 40, 477-89	32.3	207
257	T Helper Cell Cytokines Modulate Intestinal Stem Cell Renewal and Differentiation. <i>Cell</i> , <b>2018</b> , 175, 1307-1320.e20	56.2	200
256	Induction and transcriptional regulation of the co-inhibitory gene module in T cells. <i>Nature</i> , <b>2018</b> , 558, 454-459	50.4	201
255	Decoding human fetal liver haematopoiesis. <i>Nature</i> , <b>2019</b> , 574, 365-371	50.4	200
254	Anatomically and Functionally Distinct Lung Mesenchymal Populations Marked by Lgr5 and Lgr6. <i>Cell</i> , <b>2017</b> , 170, 1149-1163.e12	56.2	200
253	The transcription factor BATF operates as an essential differentiation checkpoint in early effector CD8+ T cells. <i>Nature Immunology</i> , <b>2014</b> , 15, 373-83	19.1	197
252	High-resolution interrogation of functional elements in the noncoding genome. <i>Science</i> , <b>2016</b> , 353, 1545-1549	33.3	197

251	Ribosome profiling reveals resemblance between long non-coding RNAs and 5' leaders of coding RNAs. <i>Development (Cambridge)</i> , <b>2013</b> , 140, 2828-34	6.6	196
250	Pathogen Cell-to-Cell Variability Drives Heterogeneity in Host Immune Responses. <i>Cell</i> , <b>2015</b> , 162, 1309-34	36.2	188
249	Disease-associated astrocytes in Alzheimer's disease and aging. <i>Nature Neuroscience</i> , <b>2020</b> , 23, 701-706	25.5	188
248	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina. <i>Cell</i> , <b>2019</b> , 176, 1222-1237.e22	56.2	184
247	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. <i>Nature Genetics</i> , <b>2013</b> , 45, 299-303	36.3	183
246	Intersection of population variation and autoimmunity genetics in human T cell activation. <i>Science</i> , <b>2014</b> , 345, 1254665	33.3	175
245	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , <b>2018</b> , 173, 90-103.e19	56.2	174
244	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , <b>2019</b> , 176, 1325-1339.e22	56.2	174
243	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> , <b>2009</b> , 106, 3264-9	11.5	172
242	Impulse control: temporal dynamics in gene transcription. <i>Cell</i> , <b>2011</b> , 144, 886-96	56.2	171
241	The evolution of drug resistance in clinical isolates of <i>Candida albicans</i> . <i>ELife</i> , <b>2015</b> , 4, e00662	8.9	168
240	Single-Cell Profiles of Retinal Ganglion Cells Differing in Resilience to Injury Reveal Neuroprotective Genes. <i>Neuron</i> , <b>2019</b> , 104, 1039-1055.e12	13.9	168
239	Structure and function of a transcriptional network activated by the MAPK Hog1. <i>Nature Genetics</i> , <b>2008</b> , 40, 1300-6	36.3	165
238	Optimal-Transport Analysis of Single-Cell Gene Expression Identifies Developmental Trajectories in Reprogramming. <i>Cell</i> , <b>2019</b> , 176, 928-943.e22	56.2	163
237	Preparation of Single-Cell RNA-Seq Libraries for Next Generation Sequencing. <i>Current Protocols in Molecular Biology</i> , <b>2014</b> , 107, 4.22.1-17	2.9	162
236	The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. <i>Neuron</i> , <b>2017</b> , 96, 542-557	13.9	159
235	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. <i>Cell</i> , <b>2020</b> , 183, 1103-1116.e20	56.2	153
234	Single-cell transcriptomic profiling of the aging mouse brain. <i>Nature Neuroscience</i> , <b>2019</b> , 22, 1696-1708	25.5	152

233	Systematic discovery of TLR signaling components delineates viral-sensing circuits. <i>Cell</i> , <b>2011</b> , 147, 853-862	57.2	148
232	Transcriptional regulatory circuits: predicting numbers from alphabets. <i>Science</i> , <b>2009</b> , 325, 429-32	33.3	148
231	Benchmarking single-cell RNA-sequencing protocols for cell atlas projects. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 747-755	44.5	142
230	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , <b>2020</b> , 181, 236-249	56.2	140
229	A Generic and Cell-Type-Specific Wound Response Precedes Regeneration in Planarians. <i>Developmental Cell</i> , <b>2015</b> , 35, 632-645	10.2	139
228	High-resolution sequencing and modeling identifies distinct dynamic RNA regulatory strategies. <i>Cell</i> , <b>2014</b> , 159, 1698-710	56.2	136
227	Resolving medulloblastoma cellular architecture by single-cell genomics. <i>Nature</i> , <b>2019</b> , 572, 74-79	50.4	133
226	A Regression-Based Analysis of Ribosome-Profiling Data Reveals a Conserved Complexity to Mammalian Translation. <i>Molecular Cell</i> , <b>2015</b> , 60, 816-827	17.6	133
225	Activity motifs reveal principles of timing in transcriptional control of the yeast metabolic network. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 1251-9	44.5	131
224	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. <i>Nature Medicine</i> , <b>2020</b> , 26, 792-802	50.5	130
223	Core Circadian Clock Genes Regulate Leukemia Stem Cells in AML. <i>Cell</i> , <b>2016</b> , 165, 303-16	56.2	130
222	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , <b>2021</b> , 595, 107-113	50.4	124
221	Strand-specific RNA sequencing reveals extensive regulated long antisense transcripts that are conserved across yeast species. <i>Genome Biology</i> , <b>2010</b> , 11, R87	18.3	110
220	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. <i>Genome Biology</i> , <b>2016</b> , 17, 19	18.3	105
219	Single-Cell Analysis of the Normal Mouse Aorta Reveals Functionally Distinct Endothelial Cell Populations. <i>Circulation</i> , <b>2019</b> , 140, 147-163	16.7	104
218	IFN $\gamma$ -Dependent Tissue-Immune Homeostasis Is Co-opted in the Tumor Microenvironment. <i>Cell</i> , <b>2017</b> , 170, 127-141.e15	56.2	104
217	A single-cell landscape of high-grade serous ovarian cancer. <i>Nature Medicine</i> , <b>2020</b> , 26, 1271-1279	50.5	103
216	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer's disease. <i>Nature Communications</i> , <b>2020</b> , 11, 6129	17.4	102



215	Multiplexed, targeted profiling of single-cell proteomes and transcriptomes in a single reaction. <i>Genome Biology</i> , <b>2016</b> , 17, 188	18.3	102
214	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> , <b>2019</b> , 61, 31-41	5.7	98
213	The Human and Mouse Enteric Nervous System at Single-Cell Resolution. <i>Cell</i> , <b>2020</b> , 182, 1606-1622.e2356.2		96
212	Comprehensive Identification and Spatial Mapping of Habenular Neuronal Types Using Single-Cell RNA-Seq. <i>Current Biology</i> , <b>2018</b> , 28, 1052-1065.e7	6.3	95
211	snRNA-seq reveals a subpopulation of adipocytes that regulates thermogenesis. <i>Nature</i> , <b>2020</b> , 587, 98-102.4	10.4	92
210	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. <i>Cell</i> , <b>2019</b> , 178, 1115-1131.e15	56.2	91
209	STAR-Fusion: Fast and Accurate Fusion Transcript Detection from RNA-Seq		80
208	EPEN-21. IMPAIRED NEURONAL-GLIAL FATE SPECIFICATION IN PEDIATRIC EPENDYMOMA REVEALED BY SINGLE-CELL RNA-SEQ. <i>Neuro-Oncology</i> , <b>2020</b> , 22, iii311-iii312	1	78
207	Calcitonin Gene-Related Peptide Negatively Regulates Alarmin-Driven Type 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , <b>2019</b> , 51, 709-723.e6	32.3	76
206	Emergence of a High-Plasticity Cell State during Lung Cancer Evolution. <i>Cancer Cell</i> , <b>2020</b> , 38, 229-246.e11.3	11.3	76
205	Critical role of IRF1 and BATF in forming chromatin landscape during type 1 regulatory cell differentiation. <i>Nature Immunology</i> , <b>2017</b> , 18, 412-421	19.1	74
204	Regenerative potential of prostate luminal cells revealed by single-cell analysis. <i>Science</i> , <b>2020</b> , 368, 497-505	50.5	74
203	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , <b>2018</b> , 50, 1140-1150	36.3	74
202	Single cell census of human kidney organoids shows reproducibility and diminished off-target cells after transplantation. <i>Nature Communications</i> , <b>2019</b> , 10, 5462	17.4	71
201	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , <b>2019</b> , 27, 3228-3240.e7	10.6	70
200	The MicroRNA-132 and MicroRNA-212 Cluster Regulates Hematopoietic Stem Cell Maintenance and Survival with Age by Buffering FOXO3 Expression. <i>Immunity</i> , <b>2015</b> , 42, 1021-32	32.3	69
199	Transcriptional Atlas of Intestinal Immune Cells Reveals that Neuropeptide ECGRP Modulates Group 2 Innate Lymphoid Cell Responses. <i>Immunity</i> , <b>2019</b> , 51, 696-708.e9	32.3	69
198	RBPJ Controls Development of Pathogenic Th17 Cells by Regulating IL-23 Receptor Expression. <i>Cell Reports</i> , <b>2016</b> , 16, 392-404	10.6	65

197	Expansion sequencing: Spatially precise in situ transcriptomics in intact biological systems. <i>Science</i> , <b>2021</b> , 371,	33.3	64
196	Pan-cancer single-cell RNA-seq identifies recurring programs of cellular heterogeneity. <i>Nature Genetics</i> , <b>2020</b> , 52, 1208-1218	36.3	63
195	Heterogeneous Responses of Hematopoietic Stem Cells to Inflammatory Stimuli Are Altered with Age. <i>Cell Reports</i> , <b>2018</b> , 25, 2992-3005.e5	10.6	63
194	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , <b>2019</b> , 10, 2907	17.4	62
193	Deciphering eukaryotic gene-regulatory logic with 100 million random promoters. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 56-65	44.5	62
192	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 451-461	44.5	59
191	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. <i>Cell</i> , <b>2017</b> , 171, 1424-1436.e18	56.2	57
190	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. <i>Cancer Cell</i> , <b>2020</b> , 38, 212-228.e13	24.3	57
189	Inhibitory CD161 receptor identified in glioma-infiltrating T cells by single-cell analysis. <i>Cell</i> , <b>2021</b> , 184, 1281-1298.e26	56.2	55
188	Tumor and immune reprogramming during immunotherapy in advanced renal cell carcinoma. <i>Cancer Cell</i> , <b>2021</b> , 39, 649-661.e5	24.3	54
187	Cell Atlas of The Human Fovea and Peripheral Retina. <i>Scientific Reports</i> , <b>2020</b> , 10, 9802	4.9	52
186	Minreg: inferring an active regulator set. <i>Bioinformatics</i> , <b>2002</b> , 18 Suppl 1, S258-67	7.2	51
185	Strategies to discover regulatory circuits of the mammalian immune system. <i>Nature Reviews Immunology</i> , <b>2011</b> , 11, 873-80	36.5	50
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63	Cumulus: a cloud-based data analysis framework for large-scale single-cell and single-nucleus RNA-seq		7
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46	Single-cell transcriptomics of the aged mouse brain reveals convergent, divergent and unique aging signatures		4
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40	Mapping multicellular programs from single-cell profiles		3
39	Multi-modal pooled Perturb-CITE-Seq screens in patient models define novel mechanisms of cancer immune evasion		3
38	Massively parallel phenotyping of variant impact in cancer with Perturb-seq reveals a shift in the spectrum of cell states induced by somatic mutations		3
37	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics		3
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24	T helper cells modulate intestinal stem cell renewal and differentiation		2
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16	ECLIPSER: identifying causal cell types and genes for complex traits through single cell enrichment of e/sQTL-mapped genes in GWAS loci		1
15	Molecular Classification and Comparative Taxonomics of Foveal and Peripheral Cells in Primate Retina		1
14	Single-cell profiles of retinal neurons differing in resilience to injury reveal neuroprotective genes		1
13	MAUDE: Inferring expression changes in sorting-based CRISPR screens		1
12	GWAS of stool frequency reveals genes, pathways, and cell types relevant to human gastrointestinal motility and irritable bowel syndrome		1
11	BROCKMAN: Deciphering variance in epigenomic regulators byk-mer factorization		1
10	Combinatorial prediction of marker panels from single-cell transcriptomic data		1
9	Shuffle-Seq: En masse combinatorial encoding for n-way genetic interaction screens		1
8	Parental-fetal interplay of immune genes leads to intrauterine growth restriction		1
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