

Rahul Satija

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

60,887
citations

44042

48
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114418

63
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86
all docs

86
docs citations

86
times ranked

64143
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary systems biology reveals patterns of rice adaptation to drought-prone agro-ecosystems. <i>Plant Cell</i> , 2022, 34, 759-783.	3.1	19
2	Comparison and evaluation of statistical error models for scRNA-seq. <i>Genome Biology</i> , 2022, 23, 27.	3.8	140
3	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro. <i>Nature Biotechnology</i> , 2022, 40, 1220-1230.	9.4	46
4	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
5	Characterizing the molecular regulation of inhibitory immune checkpoints with multimodal single-cell screens. <i>Nature Genetics</i> , 2021, 53, 322-331.	9.4	96
6	A latent subset of human hematopoietic stem cells resists regenerative stress to preserve stemness. <i>Nature Immunology</i> , 2021, 22, 723-734.	7.0	26
7	Integrated analysis of multimodal single-cell data. <i>Cell</i> , 2021, 184, 3573-3587.e29.	13.5	5,912
8	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
9	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , 2021, 597, 196-205.	13.7	114
10	Single-cell chromatin state analysis with Signac. <i>Nature Methods</i> , 2021, 18, 1333-1341.	9.0	595
11	geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq. <i>Genome Biology</i> , 2021, 22, 333.	3.8	15
12	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. <i>Nature Communications</i> , 2020, 11, 5504.	5.8	39
13	Niche-Selective Inhibition of Pathogenic Th17 Cells by Targeting Metabolic Redundancy. <i>Cell</i> , 2020, 182, 641-654.e20.	13.5	77
14	The strength and pattern of natural selection on gene expression in rice. <i>Nature</i> , 2020, 578, 572-576.	13.7	92
15	3017 "A DISTINCT SUBSET OF LATENT LONG-TERM HUMAN HEMATOPOIETIC STEM CELLS RESISTS REGENERATIVE STRESS TO PRESERVES STEMNESS. <i>Experimental Hematology</i> , 2020, 88, S43.	0.2	0
16	Divergent Levels of CD112 and INKA1 Define a Subset of Human Hematopoietic Stem Cells That Resists Regenerative Stress to Preserve Stemness. <i>Blood</i> , 2020, 136, 5-5.	0.6	0
17	Integrative single-cell analysis. <i>Nature Reviews Genetics</i> , 2019, 20, 257-272.	7.7	932
18	Comprehensive Integration of Single-Cell Data. <i>Cell</i> , 2019, 177, 1888-1902.e21.	13.5	9,755

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19	A single-cell transcriptional roadmap for cardiopharyngeal fate diversification. <i>Nature Cell Biology</i> , 2019, 21, 674-686.	4.6	78
20	Multiplexed detection of proteins, transcriptomes, clonotypes and CRISPR perturbations in single cells. <i>Nature Methods</i> , 2019, 16, 409-412.	9.0	364
21	The bone marrow microenvironment at single-cell resolution. <i>Nature</i> , 2019, 569, 222-228.	13.7	624
22	Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression. <i>Genome Biology</i> , 2019, 20, 296.	3.8	2,460
23	Toward a Common Coordinate Framework for the Human Body. <i>Cell</i> , 2019, 179, 1455-1467.	13.5	81
24	Single-cell RNA-seq of rheumatoid arthritis synovial tissue using low-cost microfluidic instrumentation. <i>Nature Communications</i> , 2018, 9, 791.	5.8	284
25	Developmental diversification of cortical inhibitory interneurons. <i>Nature</i> , 2018, 555, 457-462.	13.7	393
26	Strength in numbers from integrated single-cell neuroscience. <i>Nature Biotechnology</i> , 2018, 36, 41-42.	9.4	1
27	Integrating single-cell transcriptomic data across different conditions, technologies, and species. <i>Nature Biotechnology</i> , 2018, 36, 411-420.	9.4	8,878
28	Molecular transitions in early progenitors during human cord blood hematopoiesis. <i>Molecular Systems Biology</i> , 2018, 14, e8041.	3.2	125
29	Single-cell RNA sequencing to explore immune cell heterogeneity. <i>Nature Reviews Immunology</i> , 2018, 18, 35-45.	10.6	1,085
30	Cell Hashing with barcoded antibodies enables multiplexing and doublet detection for single cell genomics. <i>Genome Biology</i> , 2018, 19, 224.	3.8	674
31	Kinetics of adult hematopoietic stem cell differentiation in vivo. <i>Journal of Experimental Medicine</i> , 2018, 215, 2815-2832.	4.2	61
32	Phenotypic Convergence: Distinct Transcription Factors Regulate Common Terminal Features. <i>Cell</i> , 2018, 174, 622-635.e13.	13.5	180
33	Seq-Well: portable, low-cost RNA sequencing of single cells at high throughput. <i>Nature Methods</i> , 2017, 14, 395-398.	9.0	706
34	Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. <i>Science</i> , 2017, 356, .	6.0	1,846
35	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
36	Simultaneous epitope and transcriptome measurement in single cells. <i>Nature Methods</i> , 2017, 14, 865-868.	9.0	2,124

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37	The Human Cell Atlas. <i>ELife</i> , 2017, 6, .	2.8	1,547
38	Root Regeneration Triggers an Embryo-like Sequence Guided by Hormonal Interactions. <i>Cell</i> , 2016, 165, 1721-1733.	13.5	215
39	Human dendritic cells (DCs) are derived from distinct circulating precursors that are precommitted to become CD1c+ or CD141+ DCs. <i>Journal of Experimental Medicine</i> , 2016, 213, 2861-2870.	4.2	124
40	Single-cell RNA-seq supports a developmental hierarchy in human oligodendrogloma. <i>Nature</i> , 2016, 539, 309-313.	13.7	875
41	Single-cell analysis reveals key roles for Bcl11a in regulating stem cell fate decisions. <i>Genome Biology</i> , 2015, 16, 199.	3.8	11
42	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. <i>Cell</i> , 2015, 161, 1202-1214.	13.5	5,908
43	MERFISHing for spatial context. <i>Trends in Immunology</i> , 2015, 36, 390-391.	2.9	6
44	A Generic and Cell-Type-Specific Wound Response Precedes Regeneration in Planarians. <i>Developmental Cell</i> , 2015, 35, 632-645.	3.1	184
45	Dynamic profiling of the protein life cycle in response to pathogens. <i>Science</i> , 2015, 347, 1259038.	6.0	408
46	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. <i>Cell</i> , 2015, 162, 675-686.	13.5	383
47	Spatial reconstruction of single-cell gene expression data. <i>Nature Biotechnology</i> , 2015, 33, 495-502.	9.4	4,254
48	Pathogen Cell-to-Cell Variability Drives Heterogeneity in Host Immune Responses. <i>Cell</i> , 2015, 162, 1309-1321.	13.5	255
49	The Regulatory Factor ZFH3 Modifies Circadian Function in SCN via an AT Motif-Driven Axis. <i>Cell</i> , 2015, 162, 607-621.	13.5	74
50	Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity. <i>Cell</i> , 2015, 163, 1400-1412.	13.5	504
51	Deconstructing transcriptional heterogeneity in pluripotent stem cells. <i>Nature</i> , 2014, 516, 56-61.	13.7	343
52	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
53	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. <i>Cell</i> , 2014, 159, 148-162.	13.5	770
54	Heterogeneity in immune responses: from populations to single cells. <i>Trends in Immunology</i> , 2014, 35, 219-229.	2.9	166

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55	Single-cell RNA-seq reveals dynamic paracrine control of cellular variation. <i>Nature</i> , 2014, 510, 363-369.	13.7	872
56	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. <i>Cell</i> , 2013, 155, 1409-1421.	13.5	554
57	Dynamic regulatory network controlling TH17 cell differentiation. <i>Nature</i> , 2013, 496, 461-468.	13.7	608
58	Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. <i>Nature</i> , 2013, 498, 236-240.	13.7	1,103
59	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , 2013, 10, 623-629.	9.0	419
60	The Atypical Calpains: Evolutionary Analyses and Roles in <i>Caenorhabditis elegans</i> Cellular Degeneration. <i>PLoS Genetics</i> , 2012, 8, e1002602.	1.5	23
61	The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the <i>Drosophila</i> embryo. <i>Genome Research</i> , 2012, 22, 656-665.	2.4	44
62	Stochastic models of sequence evolution including insertion-deletion events. <i>Statistical Methods in Medical Research</i> , 2009, 18, 453-485.	0.7	22
63	The Genome of the Sea Urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006, 314, 941-952.	6.0	1,018