

Chun Jimmie Ye

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

10,867
citations

94381

37
h-index

82499

72
g-index

116
all docs

116
docs citations

116
times ranked

21203
citing authors

#	ARTICLE	IF	CITATIONS
1	Assessing computational tools for the discovery of transcription factor binding sites. <i>Nature Biotechnology</i> , 2005, 23, 137-144.	9.4	1,121
2	Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. <i>Nature Biotechnology</i> , 2018, 36, 89-94.	9.4	745
3	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 63.	3.8	608
4	Generation of knock-in primary human T cells using Cas9 ribonucleoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10437-10442.	3.3	600
5	CRISPR/Cas9-mediated PD-1 disruption enhances anti-tumor efficacy of human chimeric antigen receptor T cells. <i>Scientific Reports</i> , 2017, 7, 737.	1.6	543
6	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. <i>Science</i> , 2014, 344, 519-523.	6.0	480
7	Intratumoral CD4+ T Cells Mediate Anti-tumor Cytotoxicity in Human Bladder Cancer. <i>Cell</i> , 2020, 181, 1612-1625.e13.	13.5	436
8	Unleashing Type-2 Dendritic Cells to Drive Protective Antitumor CD4+ T Cell Immunity. <i>Cell</i> , 2019, 177, 556-571.e16.	13.5	405
9	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. <i>Science</i> , 2014, 343, 1246980.	6.0	391
10	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. <i>Cell</i> , 2015, 162, 675-686.	13.5	383
11	Single-Cell RNA Sequencing of Lymph Node Stromal Cells Reveals Niche-Associated Heterogeneity. <i>Immunity</i> , 2018, 48, 1014-1028.e6.	6.6	339
12	Transethnic Genetic-Correlation Estimates from Summary Statistics. <i>American Journal of Human Genetics</i> , 2016, 99, 76-88.	2.6	265
13	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. <i>Nature Biotechnology</i> , 2020, 38, 1174-1183.	9.4	251
14	Parsing the Interferon Transcriptional Network and Its Disease Associations. <i>Cell</i> , 2016, 164, 564-578.	13.5	250
15	Discovery of stimulation-responsive immune enhancers with CRISPR activation. <i>Nature</i> , 2017, 549, 111-115.	13.7	247
16	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
17	Intersection of population variation and autoimmunity genetics in human T cell activation. <i>Science</i> , 2014, 345, 1254665.	6.0	218
18	Global absence and targeting of protective immune states in severe COVID-19. <i>Nature</i> , 2021, 591, 124-130.	13.7	206

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19	A tissue checkpoint regulates type 2 immunity. <i>Nature Immunology</i> , 2016, 17, 1381-1387.	7.0	184
20	Single-cell eQTL mapping identifies cell type-specific genetic control of autoimmune disease. <i>Science</i> , 2022, 376, eabf3041.	6.0	171
21	Functional interpretation of single cell similarity maps. <i>Nature Communications</i> , 2019, 10, 4376.	5.8	169
22	Single-cell RNA-seq reveals cell type-specific molecular and genetic associations to lupus. <i>Science</i> , 2022, 376, eabf1970.	6.0	156
23	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. <i>Science Translational Medicine</i> , 2021, 13, eabh2624.	5.8	155
24	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	9.4	139
25	Lineage dynamics of murine pancreatic development at single-cell resolution. <i>Nature Communications</i> , 2018, 9, 3922.	5.8	137
26	Accurate Discovery of Expression Quantitative Trait Loci Under Confounding From Spurious and Genuine Regulatory Hotspots. <i>Genetics</i> , 2008, 180, 1909-1925.	1.2	136
27	Pooled Knockin Targeting for Genome Engineering of Cellular Immunotherapies. <i>Cell</i> , 2020, 181, 728-744.e21.	13.5	131
28	CRISPR activation and interference screens decode stimulation responses in primary human T cells. <i>Science</i> , 2022, 375, eabj4008.	6.0	119
29	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. <i>PLoS Genetics</i> , 2013, 9, e1003491.	1.5	109
30	Ultrarare variants drive substantial cis heritability of human gene expression. <i>Nature Genetics</i> , 2019, 51, 1349-1355.	9.4	98
31	Single-cell transcriptional profiling of human thymic stroma uncovers novel cellular heterogeneity in the thymic medulla. <i>Nature Communications</i> , 2021, 12, 1096.	5.8	96
32	Obesity alters pathology and treatment response in inflammatory disease. <i>Nature</i> , 2022, 604, 337-342.	13.7	93
33	The effect of low-dose IL-2 and Treg adoptive cell therapy in patients with type 1 diabetes. <i>JCI Insight</i> , 2021, 6, .	2.3	91
34	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of <i>ERAP2</i> transcripts under balancing selection. <i>Genome Research</i> , 2018, 28, 1812-1825.	2.4	66
35	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. <i>Nature Protocols</i> , 2020, 15, 2387-2412.	5.5	65
36	Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM. <i>Scientific Reports</i> , 2020, 10, 11019.	1.6	64

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37	XYZeq: Spatially resolved single-cell RNA sequencing reveals expression heterogeneity in the tumor microenvironment. <i>Science Advances</i> , 2021, 7, .	4.7	64
38	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. <i>Genome Research</i> , 2016, 26, 863-873.	2.4	63
39	The development and evolution of inhibitory neurons in primate cerebrum. <i>Nature</i> , 2022, 603, 871-877.	13.7	58
40	Functional CRISPR dissection of gene networks controlling human regulatory T cell identity. <i>Nature Immunology</i> , 2020, 21, 1456-1466.	7.0	57
41	On the cross-population generalizability of gene expression prediction models. <i>PLoS Genetics</i> , 2020, 16, e1008927.	1.5	41
42	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. <i>Nature Communications</i> , 2020, 11, 5504.	5.8	39
43	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. <i>Nature Communications</i> , 2022, 13, .	5.8	39
44	Orthologous repeats and mammalian phylogenetic inference. <i>Genome Research</i> , 2005, 15, 998-1006.	2.4	37
45	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. <i>Science Immunology</i> , 2023, 8, .	5.6	35
46	Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies. <i>Genome Biology</i> , 2014, 15, r61.	13.9	32
47	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. <i>PLoS Computational Biology</i> , 2009, 5, e1000311.	1.5	28
48	SCITO-seq: single-cell combinatorial indexed cytometry sequencing. <i>Nature Methods</i> , 2021, 18, 903-911.	9.0	28
49	Covariate selection for association screening in multiphenotype genetic studies. <i>Nature Genetics</i> , 2017, 49, 1789-1795.	9.4	27
50	Transcriptomic analysis of immune cells in a multi-ethnic cohort of systemic lupus erythematosus patients identifies ethnicity- and disease-specific expression signatures. <i>Communications Biology</i> , 2021, 4, 488.	2.0	25
51	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human Naive T Cells. <i>Cell Reports</i> , 2021, 34, 108573.	2.9	25
52	Monoclonal antibody-mediated neutralization of SARS-CoV-2 in an IRF9-deficient child. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
53	Single-cell transcriptome analysis defines heterogeneity of the murine pancreatic ductal tree. <i>ELife</i> , 2021, 10, .	2.8	23
54	CCR2 deficiency alters activation of microglia subsets in traumatic brain injury. <i>Cell Reports</i> , 2021, 36, 109727.	2.9	23

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55	Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. <i>Bioinformatics</i> , 2011, 27, i288-i294.	1.8	21
56	An ancestry-based approach for detecting interactions. <i>Genetic Epidemiology</i> , 2018, 42, 49-63.	0.6	17
57	Reverse gene-environment interaction approach to identify variants influencing body-mass index in humans. <i>Nature Metabolism</i> , 2019, 1, 630-642.	5.1	14
58	IL-27: An endogenous constitutive repressor of human monocytes. <i>Clinical Immunology</i> , 2020, 217, 108498.	1.4	13
59	Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. <i>Bioinformatics</i> , 2007, 23, e84-e90.	1.8	11
60	Combined Single Cell Transcriptome and Surface Epitope Profiling Identifies Potential Biomarkers of Psoriatic Arthritis and Facilitates Diagnosis via Machine Learning. <i>Frontiers in Immunology</i> , 2022, 13, 835760.	2.2	11
61	No detectable alloreactive transcriptional responses under standard sample preparation conditions during donor-multiplexed single-cell RNA sequencing of peripheral blood mononuclear cells. <i>BMC Biology</i> , 2021, 19, 10.	1.7	9
62	Mass cytometry reveals a conserved immune trajectory of recovery in hospitalized COVID-19 patients. <i>Immunity</i> , 2022, , .	6.6	9
63	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. <i>Journal of Computational Biology</i> , 2010, 17, 533-546.	0.8	8
64	Inhibition of MET Signaling with Ficlatusumab in Combination with Chemotherapy in Refractory AML: Clinical Outcomes and High-Dimensional Analysis. <i>Blood Cancer Discovery</i> , 2021, 2, 434-449.	2.6	7
65	Multiplexed droplet single-cell sequencing (Mux-Seq) of normal and transplant kidney. <i>American Journal of Transplantation</i> , 2022, 22, 876-885.	2.6	7
66	Integrated Computational and Experimental Analysis of the Neuroendocrine Transcriptome in Genetic Hypertension Identifies Novel Control Points for the Cardiometabolic Syndrome. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 430-440.	5.1	6
67	Multi-Modal Single-Cell Sequencing Identifies Cellular Immunophenotypes Associated With Juvenile Dermatomyositis Disease Activity. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	6
68	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. <i>SSRN Electronic Journal</i> , 2018, , .	0.4	4
69	CloudPred: Predicting Patient Phenotypes From Single-cell RNA-seq. , 2021, , .		3
70	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. <i>Lecture Notes in Computer Science</i> , 2009, , 466-481.	1.0	2
71	How mutations express themselves in blood-cell production. <i>Nature</i> , 2019, 571, 329-330.	13.7	1
72	Analysis of Multiplexed Single Cell RNA Sequencing Clinical Correlative Data in AML Reveals Biomarkers of Resistance. <i>Blood</i> , 2020, 136, 40-40.	0.6	1

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73	Reconstructing the Molecular Function of Genetic Variation in Regulatory Networks. <i>Genetics</i> , 2017, 207, 1699-1709.	1.2	0
74	Single cell Dissection of Resistance to anti-BCMA CAR-T cell Therapy. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e25-e26.	0.2	0
75	PhAT-QTL: A Phase-Aware Test for QTL Detection. <i>Lecture Notes in Computer Science</i> , 2017, , 150-161.	1.0	0
76	Abstract 5512: Identification of circulating myeloid cells induced in advanced biliary cancer patients responding to anti-PD1 through combined single cell RNA sequencing and protein expression analysis. , 2020, , .		0
77	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human Na ⁺ ve T Cells. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
78	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
79	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
80	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
81	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
82	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
83	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0