Chun Jimmie Ye

List of Publications by Year
in descending order

84 papers	10,867 citations	94433 37 h-index	82547 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. Nature Biotechnology, 2005, 23, 137-144.	17.5	1,121
2	Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nature Biotechnology, 2018, 36, 89-94.	17.5	745
3	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. Genome Biology, 2019, 20, 63.	8.8	608
4	Generation of knock-in primary human T cells using Cas9 ribonucleoproteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10437-10442.	7.1	600
5	CRISPR/Cas9-mediated PD-1 disruption enhances anti-tumor efficacy of human chimeric antigen receptor T cells. Scientific Reports, 2017, 7, 737.	3.3	543
6	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	12.6	480
7	Intratumoral CD4+ T Cells Mediate Anti-tumor Cytotoxicity in Human Bladder Cancer. Cell, 2020, 181, 1612-1625.e13.	28.9	436
8	Unleashing Type-2 Dendritic Cells to Drive Protective Antitumor CD4+ T Cell Immunity. Cell, 2019, 177, 556-571.e16.	28.9	405
9	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	12.6	391
10	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686.	28.9	383
11	Single-Cell RNA Sequencing of Lymph Node Stromal Cells Reveals Niche-Associated Heterogeneity. Immunity, 2018, 48, 1014-1028.e6.	14.3	339
12	Transethnic Genetic-Correlation Estimates from Summary Statistics. American Journal of Human Genetics, 2016, 99, 76-88.	6.2	265
13	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. Nature Biotechnology, 2020, 38, 1174-1183.	17.5	251
14	Parsing the Interferon Transcriptional Network and Its Disease Associations. Cell, 2016, 164, 564-578.	28.9	250
15	Discovery of stimulation-responsive immune enhancers with CRISPR activation. Nature, 2017, 549, 111-115.	27.8	247
16	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
17	Intersection of population variation and autoimmunity genetics in human T cell activation. Science, 2014, 345, 1254665.	12.6	218
18	Global absence and targeting of protective immune states in severe COVID-19. Nature, 2021, 591, 124-130.	27.8	206

#	Article	IF	Citations
19	A tissue checkpoint regulates type 2 immunity. Nature Immunology, 2016, 17, 1381-1387.	14.5	184
20	Single-cell eQTL mapping identifies cell type–specific genetic control of autoimmune disease. Science, 2022, 376, eabf3041.	12.6	171
21	Functional interpretation of single cell similarity maps. Nature Communications, 2019, 10, 4376.	12.8	169
22	Single-cell RNA-seq reveals cell type–specific molecular and genetic associations to lupus. Science, 2022, 376, eabf1970.	12.6	156
23	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. Science Translational Medicine, 2021, 13, eabh2624.	12.4	155
24	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	21.4	139
25	Lineage dynamics of murine pancreatic development at single-cell resolution. Nature Communications, 2018, 9, 3922.	12.8	137
26	Accurate Discovery of Expression Quantitative Trait Loci Under Confounding From Spurious and Genuine Regulatory Hotspots. Genetics, 2008, 180, 1909-1925.	2.9	136
27	Pooled Knockin Targeting for Genome Engineering of Cellular Immunotherapies. Cell, 2020, 181, 728-744.e21.	28.9	131
28	CRISPR activation and interference screens decode stimulation responses in primary human T cells. Science, 2022, 375, eabj4008.	12.6	119
29	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. PLoS Genetics, 2013, 9, e1003491.	3.5	109
30	Ultrarare variants drive substantial cis heritability of human gene expression. Nature Genetics, 2019, 51, 1349-1355.	21.4	98
31	Single-cell transcriptional profiling of human thymic stroma uncovers novel cellular heterogeneity in the thymic medulla. Nature Communications, 2021, 12, 1096.	12.8	96
32	Obesity alters pathology and treatment response in inflammatory disease. Nature, 2022, 604, 337-342.	27.8	93
33	The effect of low-dose IL-2 and Treg adoptive cell therapy in patients with type 1 diabetes. JCI Insight, 2021, 6, .	5.0	91
34	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of *ERAP2* transcripts under balancing selection. Genome Research, 2018, 28, 1812-1825.	5.5	66
35	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. Nature Protocols, 2020, 15, 2387-2412.	12.0	65
36	Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM. Scientific Reports, 2020, 10, 11019.	3.3	64

#	Article	IF	Citations
37	XYZeq: Spatially resolved single-cell RNA sequencing reveals expression heterogeneity in the tumor microenvironment. Science Advances, 2021, 7, .	10.3	64
38	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. Genome Research, 2016, 26, 863-873.	5.5	63
39	The development and evolution of inhibitory neurons in primate cerebrum. Nature, 2022, 603, 871-877.	27.8	58
40	Functional CRISPR dissection of gene networks controlling human regulatory T cell identity. Nature Immunology, 2020, 21, 1456-1466.	14.5	57
41	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	3.5	41
42	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. Nature Communications, 2020, 11, 5504.	12.8	39
43	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. Nature Communications, 2022, 13, .	12.8	39
44	Orthologous repeats and mammalian phylogenetic inference. Genome Research, 2005, 15, 998-1006.	5.5	37
45	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. Science Immunology, 2023, 8, .	11.9	35
46	Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies. Genome Biology, 2014, 15, r61.	9.6	32
47	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. PLoS Computational Biology, 2009, 5, e1000311.	3.2	28
48	SCITO-seq: single-cell combinatorial indexed cytometry sequencing. Nature Methods, 2021, 18, 903-911.	19.0	28
49	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	21.4	27
50	Transcriptomic analysis of immune cells in a multi-ethnic cohort of systemic lupus erythematosus patients identifies ethnicity- and disease-specific expression signatures. Communications Biology, 2021, 4, 488.	4.4	25
51	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human Naive T Cells. Cell Reports, 2021, 34, 108573.	6.4	25
52	Monoclonal antibody-mediated neutralization of SARS-CoV-2 in an IRF9-deficient child. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	24
53	Single-cell transcriptome analysis defines heterogeneity of the murine pancreatic ductal tree. ELife, 2021, 10, .	6.0	23
54	CCR2 deficiency alters activation of microglia subsets in traumatic brain injury. Cell Reports, 2021, 36, 109727.	6.4	23

#	ARTICLE	IF	CITATIONS
55	Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. Bioinformatics, 2011, 27, i288-i294.	4.1	21
56	An ancestry‐based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	1.3	17
57	Reverse gene–environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	11.9	14
58	IL-27: An endogenous constitutive repressor of human monocytes. Clinical Immunology, 2020, 217, 108498.	3.2	13
59	Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. Bioinformatics, 2007, 23, e84-e90.	4.1	11
60	Combined Single Cell Transcriptome and Surface Epitope Profiling Identifies Potential Biomarkers of Psoriatic Arthritis and Facilitates Diagnosis via Machine Learning. Frontiers in Immunology, 2022, 13, 835760.	4.8	11
61	No detectable alloreactive transcriptional responses under standard sample preparation conditions during donor-multiplexed single-cell RNA sequencing of peripheral blood mononuclear cells. BMC Biology, 2021, 19, 10.	3.8	9
62	Mass cytometry reveals a conserved immune trajectory of recovery in hospitalized COVID-19 patients. Immunity, 2022, , .	14.3	9
63	Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples. Journal of Computational Biology, 2010, 17, 533-546.	1.6	8
64	Inhibition of MET Signaling with Ficlatuzumab in Combination with Chemotherapy in Refractory AML: Clinical Outcomes and High-Dimensional Analysis. Blood Cancer Discovery, 2021, 2, 434-449.	5.0	7
65	Multiplexed droplet single-cell sequencing (Mux-Seq) of normal and transplant kidney. American Journal of Transplantation, 2022, 22, 876-885.	4.7	7
66	Integrated Computational and Experimental Analysis of the Neuroendocrine Transcriptome in Genetic Hypertension Identifies Novel Control Points for the Cardiometabolic Syndrome. Circulation: Cardiovascular Genetics, 2012, 5, 430-440.	5.1	6
67	Multi-Modal Single-Cell Sequencing Identifies Cellular Immunophenotypes Associated With Juvenile Dermatomyositis Disease Activity. Frontiers in Immunology, 0, 13, .	4.8	6
68	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. SSRN Electronic Journal, 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. Lecture Notes in Computer Science, 2009, , 466-481.	1.3	2
71	How mutations express themselves in blood-cell production. Nature, 2019, 571, 329-330.	27.8	1
72	Analysis of Multiplexed Single Cell RNA Sequencing Clinical Correlative Data in AML Reveals Biomarkers of Resistance. Blood, 2020, 136, 40-40.	1.4	1

#	Article	IF	Citations
73	Reconstructing the Molecular Function of Genetic Variation in Regulatory Networks. Genetics, 2017, 207, 1699-1709.	2.9	0
74	Principles of Systems Biology, No. 27. Cell Systems, 2018, 6, 260-262.	6.2	0
75	Single cell Dissection of Resistance to anti-BCMA CAR-T cell Therapy. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e25-e26.	0.4	0
76	PhAT-QTL: A Phase-Aware Test for QTL Detection. Lecture Notes in Computer Science, 2017, , 150-161.	1.3	0
77	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
78	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human NaÃ¯ve T Cells. SSRN Electronic Journal, 0, , .	0.4	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
84	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0