Chun Jimmie Ye

List of Publications by Year
in descending order

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	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. Science Immunology, 2023, 8, .	5.6	35
2	Multiplexed droplet single-cell sequencing (Mux-Seq) of normal and transplant kidney. American Journal of Transplantation, 2022, 22, 876-885.	2.6	7
3	CRISPR activation and interference screens decode stimulation responses in primary human T cells. Science, 2022, 375, eabj4008.	6.0	119
4	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.	2.2	11
5	The development and evolution of inhibitory neurons in primate cerebrum. Nature, 2022, 603, 871-877.	13.7	58
6	Obesity alters pathology and treatment response in inflammatory disease. Nature, 2022, 604, 337-342.	13.7	93
7	Single-cell eQTL mapping identifies cell typeâ€"specific genetic control of autoimmune disease. Science, 2022, 376, eabf3041.	6.0	171
8	Single-cell RNA-seq reveals cell typeâ€"specific molecular and genetic associations to lupus. Science, 2022, 376, eabf1970.	6.0	156
9	Mass cytometry reveals a conserved immune trajectory of recovery in hospitalized COVID-19 patients. Immunity, 2022, , .	6.6	9
10	Single-cell RNA-sequencing of peripheral blood mononuclear cells reveals widespread, context-specific gene expression regulation upon pathogenic exposure. Nature Communications, 2022, 13, .	5.8	39
11	Global absence and targeting of protective immune states in severe COVID-19. Nature, 2021, 591, 124-130.	13.7	206
12	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.	1.7	9
13	Single-cell transcriptional profiling of human thymic stroma uncovers novel cellular heterogeneity in the thymic medulla. Nature Communications, 2021, 12, 1096.	5.8	96
14	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.	2.0	25
15	XYZeq: Spatially resolved single-cell RNA sequencing reveals expression heterogeneity in the tumor microenvironment. Science Advances, 2021, 7, .	4.7	64
16	Single-cell transcriptome analysis defines heterogeneity of the murine pancreatic ductal tree. ELife, 2021, 10, .	2.8	23
17	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.	2.6	7
18	SCITO-seq: single-cell combinatorial indexed cytometry sequencing. Nature Methods, 2021, 18, 903-911.	9.0	28

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19	Type I interferon autoantibodies are associated with systemic immune alterations in patients with COVID-19. Science Translational Medicine, 2021, 13, eabh2624.	5.8	155
20	The effect of low-dose IL-2 and Treg adoptive cell therapy in patients with type 1 diabetes. JCI Insight, 2021, 6, .	2.3	91
21	CCR2 deficiency alters activation of microglia subsets in traumatic brain injury. Cell Reports, 2021, 36, 109727.	2.9	23
22	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human Naive T Cells. Cell Reports, 2021, 34, 108573.	2.9	25
23	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, .	3.3	24
24	CloudPred: Predicting Patient Phenotypes From Single-cell RNA-seq. , 2021, , .		3
25	Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis. Nature Communications, 2020, 11, 5504.	5.8	39
26	Evaluation of SARS-CoV-2 serology assays reveals a range of test performance. Nature Biotechnology, 2020, 38, 1174-1183.	9.4	251
27	On the cross-population generalizability of gene expression prediction models. PLoS Genetics, 2020, 16, e1008927.	1.5	41
28	Intratumoral CD4+ T Cells Mediate Anti-tumor Cytotoxicity in Human Bladder Cancer. Cell, 2020, 181, 1612-1625.e13.	13.5	436
29	IL-27: An endogenous constitutive repressor of human monocytes. Clinical Immunology, 2020, 217, 108498.	1.4	13
30	Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM. Scientific Reports, 2020, 10, 11019.	1.6	64
31	lentiMPRA and MPRAflow for high-throughput functional characterization of gene regulatory elements. Nature Protocols, 2020, 15, 2387-2412.	5.5	65
32	Pooled Knockin Targeting for Genome Engineering of Cellular Immunotherapies. Cell, 2020, 181, 728-744.e21.	13.5	131
33	Functional CRISPR dissection of gene networks controlling human regulatory T cell identity. Nature Immunology, 2020, 21, 1456-1466.	7.0	57
34	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
35	Analysis of Multiplexed Single Cell RNA Sequencing Clinical Correlative Data in AML Reveals Biomarkers of Resistance. Blood, 2020, 136, 40-40.	0.6	1
36	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0

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37	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
38	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
39	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
40	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
41	On the cross-population generalizability of gene expression prediction models. , 2020, 16, e1008927.		0
42	Ultrarare variants drive substantial cis heritability of human gene expression. Nature Genetics, 2019, 51, 1349-1355.	9.4	98
43	How mutations express themselves in blood-cell production. Nature, 2019, 571, 329-330.	13.7	1
44	Functional interpretation of single cell similarity maps. Nature Communications, 2019, 10, 4376.	5.8	169
45	Reverse geneâ€"environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	5.1	14
46	EmptyDrops: distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data. Genome Biology, 2019, 20, 63.	3.8	608
47	Unleashing Type-2 Dendritic Cells to Drive Protective Antitumor CD4+ T Cell Immunity. Cell, 2019, 177, 556-571.e16.	13.5	405
48	Single cell Dissection of Resistance to anti-BCMA CAR-T cell Therapy. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e25-e26.	0.2	0
49	Multiplexed droplet single-cell RNA-sequencing using natural genetic variation. Nature Biotechnology, 2018, 36, 89-94.	9.4	745
50	An ancestryâ€based approach for detecting interactions. Genetic Epidemiology, 2018, 42, 49-63.	0.6	17
51	Genetic analysis of isoform usage in the human anti-viral response reveals influenza-specific regulation of <i>ERAP2</i> transcripts under balancing selection. Genome Research, 2018, 28, 1812-1825.	2.4	66
52	Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. SSRN Electronic Journal, 2018, , .	0.4	4
53	Lineage dynamics of murine pancreatic development at single-cell resolution. Nature Communications, 2018, 9, 3922.	5.8	137
54	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. Nature Genetics, 2018, 50, 1140-1150.	9.4	139

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55	Single-Cell RNA Sequencing of Lymph Node Stromal Cells Reveals Niche-Associated Heterogeneity. Immunity, 2018, 48, 1014-1028.e6.	6.6	339
56	CRISPR/Cas9-mediated PD-1 disruption enhances anti-tumor efficacy of human chimeric antigen receptor T cells. Scientific Reports, 2017, 7, 737.	1.6	543
57	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	9.4	27
58	Reconstructing the Molecular Function of Genetic Variation in Regulatory Networks. Genetics, 2017, 207, 1699-1709.	1.2	0
59	Discovery of stimulation-responsive immune enhancers with CRISPR activation. Nature, 2017, 549, 111-115.	13.7	247
60	PhAT-QTL: A Phase-Aware Test for QTL Detection. Lecture Notes in Computer Science, 2017, , 150-161.	1.0	0
61	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. Genome Research, 2016, 26, 863-873.	2.4	63
62	A tissue checkpoint regulates type 2 immunity. Nature Immunology, 2016, 17, 1381-1387.	7.0	184
63	Transethnic Genetic-Correlation Estimates from Summary Statistics. American Journal of Human Genetics, 2016, 99, 76-88.	2.6	265
64	Parsing the Interferon Transcriptional Network and Its Disease Associations. Cell, 2016, 164, 564-578.	13.5	250
65	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.	3.3	600
66	A Genome-wide CRISPR Screen in Primary Immune Cells to Dissect Regulatory Networks. Cell, 2015, 162, 675-686.	13.5	383
67	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	6.0	391
68	Intersection of population variation and autoimmunity genetics in human T cell activation. Science, 2014, 345, 1254665.	6.0	218
69	Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies. Genome Biology, 2014, 15, r61.	13.9	32
70	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. Science, 2014, 344, 519-523.	6.0	480
71	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.	9.4	237
72	Effectively Identifying eQTLs from Multiple Tissues by Combining Mixed Model and Meta-analytic Approaches. PLoS Genetics, 2013, 9, e1003491.	1.5	109

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73	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
74	Mixed-model coexpression: calculating gene coexpression while accounting for expression heterogeneity. Bioinformatics, 2011, 27, i288-i294.	1.8	21
75	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.	0.8	8
76	Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast. PLoS Computational Biology, 2009, 5, e1000311.	1.5	28
77	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.	1.0	2
78	Accurate Discovery of Expression Quantitative Trait Loci Under Confounding From Spurious and Genuine Regulatory Hotspots. Genetics, 2008, 180, 1909-1925.	1.2	136
79	Discovering tightly regulated and differentially expressed gene sets in whole genome expression data. Bioinformatics, 2007, 23, e84-e90.	1.8	11
80	Assessing computational tools for the discovery of transcription factor binding sites. Nature Biotechnology, 2005, 23, 137-144.	9.4	1,121
81	Orthologous repeats and mammalian phylogenetic inference. Genome Research, 2005, 15, 998-1006.	2.4	37
82	Single-Cell Mapping of Progressive Fetal-to-Adult Transition in Human NaÃ¯ve T Cells. SSRN Electronic Journal, 0, , .	0.4	0
83	Multi-Modal Single-Cell Sequencing Identifies Cellular Immunophenotypes Associated With Juvenile Dermatomyositis Disease Activity. Frontiers in Immunology, 0, 13, .	2.2	6