

Kai Tan

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

5,775
citations

109321

35
h-index

88630

70
g-index

92
all docs

92
docs citations

92
times ranked

11418
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome and unique cytokine microenvironment of Castleman disease. <i>Modern Pathology</i> , 2022, 35, 451-461.	5.5	10
2	Decade-long leukaemia remissions with persistence of CD4+ CAR T cells. <i>Nature</i> , 2022, 602, 503-509.	27.8	369
3	Epigenetic state determines inflammatory sensing in neuroblastoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	21
4	Endothelial MEKK3-KLF2/4 signaling integrates inflammatory and hemodynamic signals during definitive hematopoiesis. <i>Blood</i> , 2022, 139, 2942-2957.	1.4	9
5	Single-cell multiomics reveals increased plasticity, resistant populations, and stem-cell-like blasts in <i>KMT2A</i> -rearranged leukemia. <i>Blood</i> , 2022, 139, 2198-2211.	1.4	37
6	Kikuchi-Fujimoto disease is mediated by an aberrant type I interferon response. <i>Modern Pathology</i> , 2022, 35, 462-469.	5.5	4
7	B cell targeting in CAR T cell therapy: Side effect or driver of CAR T cell function?. <i>Science Translational Medicine</i> , 2022, 14, .	12.4	4
8	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. <i>Genome Research</i> , 2021, 31, 101-109.	5.5	12
9	Integrative Bulk and Single-Cell Profiling of Premanufacture T-cell Populations Reveals Factors Mediating Long-Term Persistence of CAR T-cell Therapy. <i>Cancer Discovery</i> , 2021, 11, 2186-2199.	9.4	85
10	CytoTalk: De novo construction of signal transduction networks using single-cell transcriptomic data. <i>Science Advances</i> , 2021, 7, .	10.3	51
11	RUNX-1 haploinsufficiency causes a marked deficiency of megakaryocyte-biased hematopoietic progenitor cells. <i>Blood</i> , 2021, 137, 2662-2675.	1.4	16
12	Network Analysis Reveals Synergistic Genetic Dependencies for Rational Combination Therapy in Philadelphia Chromosome-Like Acute Lymphoblastic Leukemia. <i>Clinical Cancer Research</i> , 2021, 27, 5109-5122.	7.0	8
13	Dynamic Transcriptional and Epigenetic Changes Drive Cellular Plasticity in the Liver. <i>Hepatology</i> , 2021, 74, 444-457.	7.3	20
14	Efficient hemogenic endothelial cell specification by RUNX1 is dependent on baseline chromatin accessibility of RUNX1-regulated <i>TGFβ2</i> target genes. <i>Genes and Development</i> , 2021, 35, 1475-1489.	5.9	11
15	Analysis of multiple gene co-expression networks to discover interactions favoring CFTR biogenesis and β 508-CFTR rescue. <i>BMC Medical Genomics</i> , 2021, 14, 258.	1.5	2
16	Decade-Long Remissions of Leukemia Sustained By the Persistence of Activated CD4+ CAR T-Cells. <i>Blood</i> , 2021, 138, 166-166.	1.4	2
17	Diverse noncoding mutations contribute to deregulation of cis-regulatory landscape in pediatric cancers. <i>Science Advances</i> , 2020, 6, eaba3064.	10.3	14
18	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23626-23635.	7.1	18

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19	Developmental trajectory of prehematopoietic stem cell formation from endothelium. <i>Blood</i> , 2020, 136, 845-856.	1.4	117
20	Transcriptional regulatory network controlling the ontogeny of hematopoietic stem cells. <i>Genes and Development</i> , 2020, 34, 950-964.	5.9	33
21	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
22	Dissecting the Tumor Immune Landscape in Chimeric Antigen Receptor T-cell Therapy: Key Challenges and Opportunities for a Systems Immunology Approach. <i>Clinical Cancer Research</i> , 2020, 26, 3505-3513.	7.0	18
23	Mechanisms of Entrectinib Resistance in a Neuroblastoma Xenograft Model. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 920-926.	4.1	15
24	scATAC-pro: a comprehensive workbench for single-cell chromatin accessibility sequencing data. <i>Genome Biology</i> , 2020, 21, 94.	8.8	28
25	Runx1 negatively regulates inflammatory cytokine production by neutrophils in response to Toll-like receptor signaling. <i>Blood Advances</i> , 2020, 4, 1145-1158.	5.2	39
26	A lineage-resolved molecular atlas of <i>C. elegans</i> embryogenesis at single-cell resolution. <i>Science</i> , 2019, 365, .	12.6	354
27	SCRABBLE: single-cell RNA-seq imputation constrained by bulk RNA-seq data. <i>Genome Biology</i> , 2019, 20, 88.	8.8	88
28	Optimal control nodes in disease-perturbed networks as targets for combination therapy. <i>Nature Communications</i> , 2019, 10, 2180.	12.8	37
29	Risk variants disrupting enhancers of T _H 1 and T _{REG} cells in type 1 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7581-7590.	7.1	33
30	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019, 49, 10-29.	7.0	57
31	Spatial Genome Re-organization between Fetal and Adult Hematopoietic Stem Cells. <i>Cell Reports</i> , 2019, 29, 4200-4211.e7.	6.4	46
32	H3K9me3-heterochromatin loss at protein-coding genes enables developmental lineage specification. <i>Science</i> , 2019, 363, 294-297.	12.6	161
33	The Inherited Platelet Disorder of RUNX1 Haploinsufficiency (Familial Platelet Disorder with) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS Hematopoietic Progenitor Cells: Mechanistic Studies and Drug Correction. <i>Blood</i> , 2019, 134, 220-220.	1.4	0
34	Developmental Biology of the Blood System. <i>Blood</i> , 2019, 134, SCI-29-SCI-29.	1.4	0
35	Identifying noncoding risk variants using disease-relevant gene regulatory networks. <i>Nature Communications</i> , 2018, 9, 702.	12.8	35
36	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. <i>Nature Communications</i> , 2018, 9, 782.	12.8	36

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37	Maturation of hematopoietic stem cells from prehematopoietic stem cells is accompanied by up-regulation of PD-L1. <i>Journal of Experimental Medicine</i> , 2018, 215, 645-659.	8.5	19
38	RUNX1 and the endothelial origin of blood. <i>Experimental Hematology</i> , 2018, 68, 2-9.	0.4	68
39	CD27 marks murine embryonic hematopoietic stem cells and type II prehematopoietic stem cells. <i>Blood</i> , 2017, 130, 372-376.	1.4	18
40	Prostaglandin E1 and Its Analog Misoprostol Inhibit Human CML Stem Cell Self-Renewal via EP4 Receptor Activation and Repression of AP-1. <i>Cell Stem Cell</i> , 2017, 21, 359-373.e5.	11.1	40
41	Identifying topologically associating domains and subdomains by Gaussian Mixture model And Proportion test. <i>Nature Communications</i> , 2017, 8, 535.	12.8	58
42	CD8 + T Cells Utilize Highly Dynamic Enhancer Repertoires and Regulatory Circuitry in Response to Infections. <i>Immunity</i> , 2016, 45, 1341-1354.	14.3	79
43	EnhancerAtlas: a resource for enhancer annotation and analysis in 105 human cell/tissue types. <i>Bioinformatics</i> , 2016, 32, 3543-3551.	4.1	148
44	FLAGS: A Flexible and Adaptive Association Test for Gene Sets Using Summary Statistics. <i>Genetics</i> , 2016, 202, 919-929.	2.9	11
45	Understanding transcriptional regulatory networks using computational models. <i>Current Opinion in Genetics and Development</i> , 2016, 37, 101-108.	3.3	34
46	Functional screen identifies regulators of murine hematopoietic stem cell repopulation. <i>Journal of Experimental Medicine</i> , 2016, 213, 433-449.	8.5	78
47	Revealing Pathway Dynamics in Heart Diseases by Analyzing Multiple Differential Networks. <i>PLoS Computational Biology</i> , 2015, 11, e1004332.	3.2	43
48	A microfluidic device for epigenomic profiling using 100 cells. <i>Nature Methods</i> , 2015, 12, 959-962.	19.0	111
49	Runx1 Deficiency Decreases Ribosome Biogenesis and Confers Stress Resistance to Hematopoietic Stem and Progenitor Cells. <i>Cell Stem Cell</i> , 2015, 17, 165-177.	11.1	195
50	4DGenome: a comprehensive database of chromatin interactions. <i>Bioinformatics</i> , 2015, 31, 2560-2564.	4.1	112
51	Discover context-specific combinatorial transcription factor interactions by integrating diverse CHIP-Seq data sets. <i>Nucleic Acids Research</i> , 2014, 42, e24-e24.	14.5	18
52	The effect of smoking on DNA methylation of peripheral blood mononuclear cells from African American women. <i>BMC Genomics</i> , 2014, 15, 151.	2.8	193
53	Modeling disease progression using dynamics of pathway connectivity. <i>Bioinformatics</i> , 2014, 30, 2343-2350.	4.1	56
54	Inflammatory signaling regulates embryonic hematopoietic stem and progenitor cell production. <i>Genes and Development</i> , 2014, 28, 2597-2612.	5.9	214

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55	Global view of enhancer-promoter interactome in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2191-9.	7.1	226
56	TCF-1 and LEF-1 act upstream of Th-POK to promote the CD4+ T cell fate and interact with Runx3 to silence Cd4 in CD8+ T cells. Nature Immunology, 2014, 15, 646-656.	14.5	158
57	The insulator protein Suppressor of Hairy-wing is an essential transcriptional repressor in the <i>Drosophila</i> ovary. Development (Cambridge), 2013, 140, 3613-3623.	2.5	47
58	Genome-wide studies of the multi-zinc finger <i>Drosophila</i> Suppressor of Hairy-wing protein in the ovary. Nucleic Acids Research, 2012, 40, 5415-5431.	14.5	47
59	Discovering distal regulatory elements by integrating multiple types of chromatin state maps. , 2012, , .		1
60	Dynamic HoxB4-regulatory network during embryonic stem cell differentiation to hematopoietic cells. Blood, 2012, 119, e139-e147.	1.4	45
61	Finding combinatorial histone code by semi-supervised biclustering. BMC Genomics, 2012, 13, 301.	2.8	12
62	Multi-Analyte Network Markers for Tumor Prognosis. PLoS ONE, 2012, 7, e52973.	2.5	22
63	Enhancers in embryonic stem cells are enriched for transposable elements and genetic variations associated with cancers. Nucleic Acids Research, 2011, 39, 7371-7379.	14.5	21
64	Combinatorial chromatin modification patterns in the human genome revealed by subspace clustering. Nucleic Acids Research, 2011, 39, 4063-4075.	14.5	49
65	Discover Protein Complexes in Protein-Protein Interaction Networks Using Parametric Local Modularity. BMC Bioinformatics, 2010, 11, 521.	2.6	13
66	Discover regulatory DNA elements using chromatin signatures and artificial neural network. Bioinformatics, 2010, 26, 1579-1586.	4.1	157
67	Coevolution within a transcriptional network by compensatory <i>trans</i> and <i>cis</i> mutations. Genome Research, 2010, 20, 1672-1678.	5.5	62
68	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
69	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	28.9	4
70	Evolutionary divergence in the fungal response to fluconazole revealed by soft clustering. Genome Biology, 2010, 11, R77.	9.6	38
71	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
72	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. Genomics, 2008, 91, 219-231.	2.9	38

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73	A systems approach to delineate functions of paralogous transcription factors: Role of the Yap family in the DNA damage response. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2934-2939.	7.1	55
74	Transcriptional regulation of protein complexes within and across species. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1283-1288.	7.1	52
75	Single-Cell Multi-Omics Reveals Elevated Plasticity and Stem-Cell-Like Blasts Relevant to the Poor Prognosis of <i>KMT2A</i>-Rearranged Leukemia. SSRN Electronic Journal, 0, , .	0.4	0