Kai Tan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6752151/publications.pdf

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	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
2	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
3	Decade-long leukaemia remissions with persistence of CD4+ CAR T cells. Nature, 2022, 602, 503-509.	27.8	369
4	A lineage-resolved molecular atlas of <i>C. elegans</i> embryogenesis at single-cell resolution. Science, 2019, 365, .	12.6	354
5	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
6	Global view of enhancerâ€“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
7	Inflammatory signaling regulates embryonic hematopoietic stem and progenitor cell production. Genes and Development, 2014, 28, 2597-2612.	5.9	214
8	Runx1 Deficiency Decreases Ribosome Biogenesis and Confers Stress Resistance to Hematopoietic Stem and Progenitor Cells. Cell Stem Cell, 2015, 17, 165-177.	11.1	195
9	The effect of smoking on DNA methylation of peripheral blood mononuclear cells from African American women. BMC Genomics, 2014, 15, 151.	2.8	193
10	H3K9me3-heterochromatin loss at protein-coding genes enables developmental lineage specification. Science, 2019, 363, 294-297.	12.6	161
11	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
12	Discover regulatory DNA elements using chromatin signatures and artificial neural network. Bioinformatics, 2010, 26, 1579-1586.	4.1	157
13	EnhancerAtlas: a resource for enhancer annotation and analysis in 105 human cell/tissue types. Bioinformatics, 2016, 32, 3543-3551.	4.1	148
14	Developmental trajectory of prehematopoietic stem cell formation from endothelium. Blood, 2020, 136, 845-856.	1.4	117
15	4DGenome: a comprehensive database of chromatin interactions. Bioinformatics, 2015, 31, 2560-2564.	4.1	112
16	A microfluidic device for epigenomic profiling using 100 cells. Nature Methods, 2015, 12, 959-962.	19.0	111
17	SCRABBLE: single-cell RNA-seq imputation constrained by bulk RNA-seq data. Genome Biology, 2019, 20, 88.	8.8	88
18	Integrative Bulk and Single-Cell Profiling of Premanufacture T-cell Populations Reveals Factors Mediating Long-Term Persistence of CAR T-cell Therapy. Cancer Discovery, 2021, 11, 2186-2199.	9.4	85

#	ARTICLE	IF	CITATIONS
19	CD8 + T Cells Utilize Highly Dynamic Enhancer Repertoires and Regulatory Circuitry in Response to Infections. Immunity, 2016, 45, 1341-1354.	14.3	79
20	Functional screen identifies regulators of murine hematopoietic stem cell repopulation. Journal of Experimental Medicine, 2016, 213, 433-449.	8.5	78
21	RUNX1 and the endothelial origin of blood. Experimental Hematology, 2018, 68, 2-9.	0.4	68
22	Coevolution within a transcriptional network by compensatory <i>trans</i> and <i>cis</i> mutations. Genome Research, 2010, 20, 1672-1678.	5.5	62
23	Identifying topologically associating domains and subdomains by Gaussian Mixture model And Proportion test. Nature Communications, 2017, 8, 535.	12.8	58
24	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
25	Modeling disease progression using dynamics of pathway connectivity. Bioinformatics, 2014, 30, 2343-2350.	4.1	56
26	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
27	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
28	CytoTalk: De novo construction of signal transduction networks using single-cell transcriptomic data. Science Advances, 2021, 7, .	10.3	51
29	Combinatorial chromatin modification patterns in the human genome revealed by subspace clustering. Nucleic Acids Research, 2011, 39, 4063-4075.	14.5	49
30	Genome-wide studies of the multi-zinc finger Drosophila Suppressor of Hairy-wing protein in the ovary. Nucleic Acids Research, 2012, 40, 5415-5431.	14.5	47
31	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
32	Spatial Genome Re-organization between Fetal and Adult Hematopoietic Stem Cells. Cell Reports, 2019, 29, 4200-4211.e7.	6.4	46
33	Dynamic HoxB4-regulatory network during embryonic stem cell differentiation to hematopoietic cells. Blood, 2012, 119, e139-e147.	1.4	45
34	Revealing Pathway Dynamics in Heart Diseases by Analyzing Multiple Differential Networks. PLoS Computational Biology, 2015, 11, e1004332.	3.2	43
35	Prostaglandin E1 and Its Analog Misoprostol Inhibit Human CML Stem Cell Self-Renewal via EP4 Receptor Activation and Repression of AP-1. Cell Stem Cell, 2017, 21, 359-373.e5.	11.1	40
36	Runx1 negatively regulates inflammatory cytokine production by neutrophils in response to Toll-like receptor signaling. Blood Advances, 2020, 4, 1145-1158.	5.2	39

#	ARTICLE	IF	CITATIONS
37	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. Genomics, 2008, 91, 219-231.	2.9	38
38	Evolutionary divergence in the fungal response to fluconazole revealed by soft clustering. Genome Biology, 2010, 11, R77.	9.6	38
39	Optimal control nodes in disease-perturbed networks as targets for combination therapy. Nature Communications, 2019, 10, 2180.	12.8	37
40	Single-cell multiomics reveals increased plasticity, resistant populations, and stem-cellâ€“like blasts in <i>KMT2A</i>-rearranged leukemia. Blood, 2022, 139, 2198-2211.	1.4	37
41	Exploiting genetic variation to uncover rules of transcription factor binding and chromatin accessibility. Nature Communications, 2018, 9, 782.	12.8	36
42	Identifying noncoding risk variants using disease-relevant gene regulatory networks. Nature Communications, 2018, 9, 702.	12.8	35
43	Understanding transcriptional regulatory networks using computational models. Current Opinion in Genetics and Development, 2016, 37, 101-108.	3.3	34
44	Risk variants disrupting enhancers of T _H 1 and T _{REG} cells in type 1 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7581-7590.	7.1	33
45	Transcriptional regulatory network controlling the ontogeny of hematopoietic stem cells. Genes and Development, 2020, 34, 950-964.	5.9	33
46	scATAC-pro: a comprehensive workbench for single-cell chromatin accessibility sequencing data. Genome Biology, 2020, 21, 94.	8.8	28
47	Multi-Analyte Network Markers for Tumor Prognosis. PLoS ONE, 2012, 7, e52973.	2.5	22
48	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
49	Epigenetic state determines inflammatory sensing in neuroblastoma. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	21
50	Dynamic Transcriptional and Epigenetic Changes Drive Cellular Plasticity in the Liver. Hepatology, 2021, 74, 444-457.	7.3	20
51	Maturation of hematopoietic stem cells from prehematopoietic stem cells is accompanied by up-regulation of PD-L1. Journal of Experimental Medicine, 2018, 215, 645-659.	8.5	19
52	Discover context-specific combinatorial transcription factor interactions by integrating diverse ChIP-Seq data sets. Nucleic Acids Research, 2014, 42, e24-e24.	14.5	18
53	CD27 marks murine embryonic hematopoietic stem cells and type II prehematopoietic stem cells. Blood, 2017, 130, 372-376.	1.4	18
54	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23626-23635.	7.1	18

#	ARTICLE	IF	CITATIONS
55	Dissecting the Tumorâ€“Immune Landscape in Chimeric Antigen Receptor T-cell Therapy: Key Challenges and Opportunities for a Systems Immunology Approach. Clinical Cancer Research, 2020, 26, 3505-3513.	7.0	18
56	RUNX-1 haploinsufficiency causes a marked deficiency of megakaryocyte-biased hematopoietic progenitor cells. Blood, 2021, 137, 2662-2675.	1.4	16
57	Mechanisms of Entrectinib Resistance in a Neuroblastoma Xenograft Model. Molecular Cancer Therapeutics, 2020, 19, 920-926.	4.1	15
58	Diverse noncoding mutations contribute to deregulation of cis-regulatory landscape in pediatric cancers. Science Advances, 2020, 6, eaba3064.	10.3	14
59	Discover Protein Complexes in Protein-Protein Interaction Networks Using Parametric Local Modularity. BMC Bioinformatics, 2010, 11, 521.	2.6	13
60	Finding combinatorial histone code by semi-supervised biclustering. BMC Genomics, 2012, 13, 301.	2.8	12
61	Predictive modeling of single-cell DNA methylome data enhances integration with transcriptome data. Genome Research, 2021, 31, 101-109.	5.5	12
62	FLAGS: A Flexible and Adaptive Association Test for Gene Sets Using Summary Statistics. Genetics, 2016, 202, 919-929.	2.9	11
63	Efficient hemogenic endothelial cell specification by RUNX1 is dependent on baseline chromatin accessibility of RUNX1-regulated TGFÎ² target genes. Genes and Development, 2021, 35, 1475-1489.	5.9	11
64	Transcriptome and unique cytokine microenvironment of Castleman disease. Modern Pathology, 2022, 35, 451-461.	5.5	10
65	Endothelial MEKK3-KLF2/4 signaling integrates inflammatory and hemodynamic signals during definitive hematopoiesis. Blood, 2022, 139, 2942-2957.	1.4	9
66	Network Analysis Reveals Synergistic Genetic Dependencies for Rational Combination Therapy in Philadelphia Chromosomeâ€“Like Acute Lymphoblastic Leukemia. Clinical Cancer Research, 2021, 27, 5109-5122.	7.0	8
67	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	28.9	4
68	Kikuchi-Fujimoto disease is mediated by an aberrant type I interferon response. Modern Pathology, 2022, 35, 462-469.	5.5	4
69	B cell targeting in CAR T cell therapy: Side effect or driver of CAR T cell function?. Science Translational Medicine, 2022, 14, .	12.4	4
70	Analysis of multiple gene co-expression networks to discover interactions favoring CFTR biogenesis and Î”F508-CFTR rescue. BMC Medical Genomics, 2021, 14, 258.	1.5	2
71	Decade-Long Remissions of Leukemia Sustained By the Persistence of Activated CD4+ CAR T-Cells. Blood, 2021, 138, 166-166.	1.4	2
72	Discovering distal regulatory elements by integrating multiple types of chromatin state maps. , 2012, , .		1

#	Article	IF	Citations
73	The Inherited Platelet Disorder of RUNX1 Haploinsufficiency (Familial Platelet Disorder with) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Hematopoietic Progenitor Cells: Mechanistic Studies and Drug Correction. Blood, 2019, 134, 220-220.	1.4	0
74	Developmental Biology of the Blood System. Blood, 2019, 134, SCI-29-SCI-29.	1.4	0
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