

Amos Tanay

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

18,383
citations

57758

44
h-index

106344

65
g-index

74
all docs

74
docs citations

74
times ranked

25565
citing authors

#	ARTICLE	IF	CITATIONS
1	Three-Dimensional Folding and Functional Organization Principles of the Drosophila Genome. <i>Cell</i> , 2012, 148, 458-472.	28.9	1,728
2	Massively Parallel Single-Cell RNA-Seq for Marker-Free Decomposition of Tissues into Cell Types. <i>Science</i> , 2014, 343, 776-779.	12.6	1,563
3	Single-cell Hi-C reveals cell-to-cell variability in chromosome structure. <i>Nature</i> , 2013, 502, 59-64.	27.8	1,347
4	Multiscale 3D Genome Rewiring during Mouse Neural Development. <i>Cell</i> , 2017, 171, 557-572.e24.	28.9	1,060
5	Derivation of novel human ground state naive pluripotent stem cells. <i>Nature</i> , 2013, 504, 282-286.	27.8	924
6	Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors. <i>Cell</i> , 2015, 163, 1663-1677.	28.9	875
7	Dysfunctional CD8 T Cells Form a Proliferative, Dynamically Regulated Compartment within Human Melanoma. <i>Cell</i> , 2019, 176, 775-789.e18.	28.9	760
8	Comparative Hi-C Reveals that CTCF Underlies Evolution of Chromosomal Domain Architecture. <i>Cell Reports</i> , 2015, 10, 1297-1309.	6.4	648
9	Cell-cycle dynamics of chromosomal organization at single-cell resolution. <i>Nature</i> , 2017, 547, 61-67.	27.8	636
10	Scaling single-cell genomics from phenomenology to mechanism. <i>Nature</i> , 2017, 541, 331-338.	27.8	633
11	Prediction of acute myeloid leukaemia risk in healthy individuals. <i>Nature</i> , 2018, 559, 400-404.	27.8	617
12	Dissecting Immune Circuits by Linking CRISPR-Pooled Screens with Single-Cell RNA-Seq. <i>Cell</i> , 2016, 167, 1883-1896.e15.	28.9	604
13	Probabilistic modeling of Hi-C contact maps eliminates systematic biases to characterize global chromosomal architecture. <i>Nature Genetics</i> , 2011, 43, 1059-1065.	21.4	582
14	Deterministic direct reprogramming of somatic cells to pluripotency. <i>Nature</i> , 2013, 502, 65-70.	27.8	471
15	The Spectrum and Regulatory Landscape of Intestinal Innate Lymphoid Cells Are Shaped by the Microbiome. <i>Cell</i> , 2016, 166, 1231-1246.e13.	28.9	465
16	Robust 4C-seq data analysis to screen for regulatory DNA interactions. <i>Nature Methods</i> , 2012, 9, 969-972.	19.0	357
17	Cnidarian Cell Type Diversity and Regulation Revealed by Whole-Organism Single-Cell RNA-Seq. <i>Cell</i> , 2018, 173, 1520-1534.e20.	28.9	284
18	Functional Anatomy of Polycomb and Trithorax Chromatin Landscapes in Drosophila Embryos. <i>PLoS Biology</i> , 2009, 7, e1000013.	5.6	281

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19	Single-cell characterization of haematopoietic progenitors and their trajectories in homeostasis and perturbed haematopoiesis. <i>Nature Cell Biology</i> , 2018, 20, 836-846.	10.3	267
20	Epigenetic polymorphism and the stochastic formation of differentially methylated regions in normal and cancerous tissues. <i>Nature Genetics</i> , 2012, 44, 1207-1214.	21.4	262
21	Early metazoan cell type diversity and the evolution of multicellular gene regulation. <i>Nature Ecology and Evolution</i> , 2018, 2, 1176-1188.	7.8	226
22	Extensive low-affinity transcriptional interactions in the yeast genome. <i>Genome Research</i> , 2006, 16, 962-972.	5.5	222
23	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. <i>Cell Reports</i> , 2014, 8, 798-806.	6.4	219
24	Single-cell epigenomics: techniques and emerging applications. <i>Nature Reviews Genetics</i> , 2015, 16, 716-726.	16.3	219
25	MetaCell: analysis of single-cell RNA-seq data using K-nn graph partitions. <i>Genome Biology</i> , 2019, 20, 206.	8.8	218
26	MARS-seq2.0: an experimental and analytical pipeline for indexed sorting combined with single-cell RNA sequencing. <i>Nature Protocols</i> , 2019, 14, 1841-1862.	12.0	200
27	Dissecting cellular crosstalk by sequencing physically interacting cells. <i>Nature Biotechnology</i> , 2020, 38, 629-637.	17.5	187
28	Single cell dissection of plasma cell heterogeneity in symptomatic and asymptomatic myeloma. <i>Nature Medicine</i> , 2018, 24, 1867-1876.	30.7	179
29	Hyperconserved CpG domains underlie Polycomb-binding sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5521-5526.	7.1	162
30	Comparative Analysis of DNA Replication Timing Reveals Conserved Large-Scale Chromosomal Architecture. <i>PLoS Genetics</i> , 2010, 6, e1001011.	3.5	158
31	Dynamic and static maintenance of epigenetic memory in pluripotent and somatic cells. <i>Nature</i> , 2014, 513, 115-119.	27.8	143
32	Single-cell Hi-C for genome-wide detection of chromatin interactions that occur simultaneously in a single cell. <i>Nature Protocols</i> , 2015, 10, 1986-2003.	12.0	135
33	Primate CpG Islands Are Maintained by Heterogeneous Evolutionary Regimes Involving Minimal Selection. <i>Cell</i> , 2011, 145, 773-786.	28.9	128
34	Capturing pairwise and multi-way chromosomal conformations using chromosomal walks. <i>Nature</i> , 2016, 540, 296-300.	27.8	128
35	Single-cell transcriptomic analyses provide insights into the developmental origins of neuroblastoma. <i>Nature Genetics</i> , 2021, 53, 683-693.	21.4	128
36	A single-embryo, single-cell time-resolved model for mouse gastrulation. <i>Cell</i> , 2021, 184, 2825-2842.e22.	28.9	114

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37	A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. <i>Cell</i> , 2021, 184, 2973-2987.e18.	28.9	111
38	LifeTime and improving European healthcare through cell-based interceptive medicine. <i>Nature</i> , 2020, 587, 377-386.	27.8	108
39	The interaction of CD4+ helper T cells with dendritic cells shapes the tumor microenvironment and immune checkpoint blockade response. <i>Nature Cancer</i> , 2022, 3, 303-317.	13.2	85
40	UMI-4C for quantitative and targeted chromosomal contact profiling. <i>Nature Methods</i> , 2016, 13, 685-691.	19.0	78
41	Cooperativity, Specificity, and Evolutionary Stability of Polycomb Targeting in <i>Drosophila</i> . <i>Cell Reports</i> , 2014, 9, 219-233.	6.4	69
42	Single-cell analysis of clonal maintenance of transcriptional and epigenetic states in cancer cells. <i>Nature Genetics</i> , 2020, 52, 709-718.	21.4	66
43	Suppressors and activators of JAK-STAT signaling at diagnosis and relapse of acute lymphoblastic leukemia in Down syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4030-E4039.	7.1	62
44	Chromosomal domains: epigenetic contexts and functional implications of genomic compartmentalization. <i>Current Opinion in Genetics and Development</i> , 2013, 23, 197-203.	3.3	61
45	A single-cell view on alga-virus interactions reveals sequential transcriptional programs and infection states. <i>Science Advances</i> , 2020, 6, eaba4137.	10.3	55
46	Hormone seasonality in medical records suggests circannual endocrine circuits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	55
47	p53 is essential for DNA methylation homeostasis in naïve embryonic stem cells, and its loss promotes clonal heterogeneity. <i>Genes and Development</i> , 2017, 31, 959-972.	5.9	48
48	Deterministic Somatic Cell Reprogramming Involves Continuous Transcriptional Changes Governed by Myc and Epigenetic-Driven Modules. <i>Cell Stem Cell</i> , 2019, 24, 328-341.e9.	11.1	44
49	Evolutionary cell type mapping with single-cell genomics. <i>Trends in Genetics</i> , 2021, 37, 919-932.	6.7	43
50	Sequence context affects the rate of short insertions and deletions in flies and primates. <i>Genome Biology</i> , 2008, 9, R37.	9.6	41
51	Widespread Compensatory Evolution Conserves DNA-Encoded Nucleosome Organization in Yeast. <i>PLoS Computational Biology</i> , 2010, 6, e1001039.	3.2	36
52	The mutation spectrum in genomic late replication domains shapes mammalian GC content. <i>Nucleic Acids Research</i> , 2016, 44, 4222-4232.	14.5	29
53	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. <i>Nature Communications</i> , 2021, 12, 5406.	12.8	29
54	Dissection of floral transition by single-meristem transcriptomes at high temporal resolution. <i>Nature Plants</i> , 2021, 7, 800-813.	9.3	26

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55	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	4.2	24
56	Recurrent deletions in clonal hematopoiesis are driven by microhomology-mediated end joining. <i>Nature Communications</i> , 2021, 12, 2455.	12.8	23
57	Global DNA methylation reflects spatial heterogeneity and molecular evolution of lung adenocarcinomas. <i>International Journal of Cancer</i> , 2019, 144, 1061-1072.	5.1	22
58	Metacell-2: a divide-and-conquer metacell algorithm for scalable scRNA-seq analysis. <i>Genome Biology</i> , 2022, 23, 100.	8.8	20
59	Evolution and Selection in Yeast Promoters: Analyzing the Combined Effect of Diverse Transcription Factor Binding Sites. <i>PLoS Computational Biology</i> , 2008, 4, e7.	3.2	19
60	Personalized lab test models to quantify disease potentials in healthy individuals. <i>Nature Medicine</i> , 2021, 27, 1582-1591.	30.7	16
61	Single-cell analysis of regions of interest (SCARI) using a photosensitive tag. <i>Nature Chemical Biology</i> , 2021, 17, 1139-1147.	8.0	13
62	Drosophila Functional Elements Are Embedded in Structurally Constrained Sequences. <i>PLoS Genetics</i> , 2013, 9, e1003512.	3.5	10
63	Inferring Divergence of Context-Dependent Substitution Rates in Drosophila Genomes with Applications to Comparative Genomics. <i>Molecular Biology and Evolution</i> , 2012, 29, 1769-1780.	8.9	7
64	Voices in methods development. <i>Nature Methods</i> , 2019, 16, 945-951.	19.0	5
65	Umi-4C: A Quantitative, Robust and Multiplexed Method to Study the Regulatory Three Dimensional Chromatin Organization - Application for the Mgaeryocytic-Eythroid Lineage. <i>Blood</i> , 2015, 126, 1183-1183.	1.4	0