

Cole Trapnell

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67 papers	13,436 citations	35 h-index	77 g-index
77 ext. papers	20,102 ext. citations	22.6 avg, IF	6.87 L-index

#	Paper	IF	Citations
67	Systematic reconstruction of cellular trajectories across mouse embryogenesis.. <i>Nature Genetics</i> , 2022 , 54, 328-341	36.3	3
66	Engineering a niche supporting hematopoietic stem cell development using integrated single-cell transcriptomics.. <i>Nature Communications</i> , 2022 , 13, 1584	17.4	3
65	Nuclear oligo hashing improves differential analysis of single-cell RNA-seq.. <i>Nature Communications</i> , 2022 , 13, 2666	17.4	
64	Embryo-scale, single-cell spatial transcriptomics. <i>Science</i> , 2021 , 373, 111-117	33.3	29
63	Multipotent progenitors and hematopoietic stem cells arise independently from hemogenic endothelium in the mouse embryo. <i>Cell Reports</i> , 2021 , 36, 109675	10.6	5
62	Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation. <i>Genome Biology</i> , 2021 , 22, 279	18.3	2
61	The promise of single-cell genomics in plants. <i>Current Opinion in Plant Biology</i> , 2020 , 54, 114-121	9.9	18
60	Inferring Causal Gene Regulatory Networks from Coupled Single-Cell Expression Dynamics Using Scribe. <i>Cell Systems</i> , 2020 , 10, 265-274.e11	10.6	36
59	Dimensionality reduction by UMAP to visualize physical and genetic interactions. <i>Nature Communications</i> , 2020 , 11, 1537	17.4	43
58	Sci-fate characterizes the dynamics of gene expression in single cells. <i>Nature Biotechnology</i> , 2020 , 38, 980-988	44.5	34
57	IL-2 enhances ex vivo-expanded regulatory T-cell persistence after adoptive transfer. <i>Blood Advances</i> , 2020 , 4, 1594-1605	7.8	13
56	Distinct Transcriptional Signatures Distinguish the Emergence of Multipotent Progenitors and Hematopoietic Stem Cells from Endothelial Precursors in the Murine Embryo. <i>Blood</i> , 2020 , 136, 7-8	2.2	
55	High-throughput, microscope-based sorting to dissect cellular heterogeneity. <i>Molecular Systems Biology</i> , 2020 , 16, e9442	12.2	17
54	Massively multiplex chemical transcriptomics at single-cell resolution. <i>Science</i> , 2020 , 367, 45-51	33.3	67
53	A human cell atlas of fetal chromatin accessibility. <i>Science</i> , 2020 , 370,	33.3	75
52	A human cell atlas of fetal gene expression. <i>Science</i> , 2020 , 370,	33.3	130
51	Trajectory analysis quantifies transcriptional plasticity during macrophage polarization. <i>Scientific Reports</i> , 2020 , 10, 12273	4.9	15

50	A lineage-resolved molecular atlas of embryogenesis at single-cell resolution. <i>Science</i> , 2019 , 365,	33.3	141
49	A pooled single-cell genetic screen identifies regulatory checkpoints in the continuum of the epithelial-to-mesenchymal transition. <i>Nature Genetics</i> , 2019 , 51, 1389-1398	36.3	79
48	Supervised classification enables rapid annotation of cell atlases. <i>Nature Methods</i> , 2019 , 16, 983-986	21.6	157
47	Wnt Signaling Separates the Progenitor and Endocrine Compartments during Pancreas Development. <i>Cell Reports</i> , 2019 , 27, 2281-2291.e5	10.6	57
46	Dynamics of Gene Expression in Single Root Cells of. <i>Plant Cell</i> , 2019 , 31, 993-1011	11.6	133
45	The accessible chromatin landscape of the murine hippocampus at single-cell resolution. <i>Genome Research</i> , 2019 , 29, 857-869	9.7	43
44	Integrated Single Cell Transcriptomics Defines an Engineered Niche Supporting Hematopoietic Stem Cell Development Ex Vivo. <i>Blood</i> , 2019 , 134, 3699-3699	2.2	1
43	Thyroid hormone regulates distinct paths to maturation in pigment cell lineages. <i>ELife</i> , 2019 , 8,	8.9	54
42	The single-cell transcriptional landscape of mammalian organogenesis. <i>Nature</i> , 2019 , 566, 496-502	50.4	826
41	A Genome-wide Framework for Mapping Gene Regulation via Cellular Genetic Screens. <i>Cell</i> , 2019 , 176, 377-390.e19	56.2	188
40	A Peninsular Structure Coordinates Asynchronous Differentiation with Morphogenesis to Generate Pancreatic Islets. <i>Cell</i> , 2019 , 176, 790-804.e13	56.2	59
39	Highly scalable generation of DNA methylation profiles in single cells. <i>Nature Biotechnology</i> , 2018 , 36, 428-431	44.5	125
38	On the design of CRISPR-based single-cell molecular screens. <i>Nature Methods</i> , 2018 , 15, 271-274	21.6	96
37	The cis-regulatory dynamics of embryonic development at single-cell resolution. <i>Nature</i> , 2018 , 555, 538-544	54.4	199
36	A Single-Cell Atlas of In Vivo Mammalian Chromatin Accessibility. <i>Cell</i> , 2018 , 174, 1309-1324.e18	56.2	331
35	Cicero Predicts cis-Regulatory DNA Interactions from Single-Cell Chromatin Accessibility Data. <i>Molecular Cell</i> , 2018 , 71, 858-871.e8	17.6	247
34	Single-Cell Multi-omics: An Engine for New Quantitative Models of Gene Regulation. <i>Trends in Genetics</i> , 2018 , 34, 653-665	8.5	63
33	Activated CARD11 accelerates germinal center kinetics, promoting mTORC1 and terminal differentiation. <i>Journal of Experimental Medicine</i> , 2018 , 215, 2445-2461	16.6	9

32	Single Cell Transcriptomics Maps the Embryonic Emergence of HSC and Identifies Intercellular Interactions Regulating HSC Genesis. <i>Blood</i> , 2018 , 132, 5086-5086	2.2	1
31	Author response: Extreme heterogeneity of influenza virus infection in single cells 2018 ,		5
30	IL2 and Rapamycin Enhance Persistence of Adoptively-Transferred Ex-Vivo Expanded T Regulatory Cells. <i>Blood</i> , 2018 , 132, 2049-2049	2.2	
29	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018 , 7, 258-268.e3	10.6	40
28	Joint profiling of chromatin accessibility and gene expression in thousands of single cells. <i>Science</i> , 2018 , 361, 1380-1385	33.3	381
27	Extreme heterogeneity of influenza virus infection in single cells. <i>ELife</i> , 2018 , 7,	8.9	122
26	Single-cell mRNA quantification and differential analysis with Census. <i>Nature Methods</i> , 2017 , 14, 309-315	11.6	612
25	Reversed graph embedding resolves complex single-cell trajectories. <i>Nature Methods</i> , 2017 , 14, 979-982	21.6	1207
24	Comprehensive single-cell transcriptional profiling of a multicellular organism. <i>Science</i> , 2017 , 357, 661-665	33.3	645
23	LIN28 Regulates Stem Cell Metabolism and Conversion to Primed Pluripotency. <i>Cell Stem Cell</i> , 2016 , 19, 66-80	18	192
22	Single-cell transcriptome sequencing: recent advances and remaining challenges. <i>F1000Research</i> , 2016 , 5,	3.6	149
21	Multiplex single cell profiling of chromatin accessibility by combinatorial cellular indexing. <i>Science</i> , 2015 , 348, 910-4	33.3	668
20	Defining cell types and states with single-cell genomics. <i>Genome Research</i> , 2015 , 25, 1491-8	9.7	421
19	The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. <i>Nature Biotechnology</i> , 2014 , 32, 381-386	44.5	2466
18	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 198-206	17.6	455
17	Pulmonary macrophage transplantation therapy. <i>Nature</i> , 2014 , 514, 450-4	50.4	195
16	Differential analysis of gene regulation at transcript resolution with RNA-seq. <i>Nature Biotechnology</i> , 2013 , 31, 46-53	44.5	2465
15	TransMPRA: A framework for assaying the role of many trans-acting factors at many enhancers		1

14	On the design of CRISPR-based single cell molecular screens	4
13	Reversed graph embedding resolves complex single-cell developmental trajectories	32
12	Aligning single-cell developmental and reprogramming trajectories identifies molecular determinants of reprogramming outcome	4
11	Chromatin accessibility dynamics of myogenesis at single cell resolution	12
10	Scalable and efficient single-cell DNA methylation sequencing by combinatorial indexing	5
9	crisprQTL mapping as a genome-wide association framework for cellular genetic screens	3
8	The accessible chromatin landscape of the hippocampus at single-cell resolution	2
7	Towards inferring causal gene regulatory networks from single cell expression Measurements	13
6	Dynamics of gene expression in single root cells of <i>A. thaliana</i>	4
5	Supervised classification enables rapid annotation of cell atlases	15
4	A lineage-resolved molecular atlas of <i>C. elegans</i> embryogenesis at single cell resolution	11
3	Characterizing the temporal dynamics of gene expression in single cells with sci-fate	5
2	Dimensionality reduction by UMAP to visualize physical and genetic interactions	1
1	Visual Cell Sorting: A High-throughput, Microscope-based Method to Dissect Cellular Heterogeneity	1