

# Samantha A Morris

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

3,505  
citations

236925

25  
h-index

243625

44  
g-index

67  
all docs

67  
docs citations

67  
times ranked

5304  
citing authors

#	ARTICLE	IF	CITATIONS
1	CellNet: Network Biology Applied to Stem Cell Engineering. <i>Cell</i> , 2014, 158, 903-915.	28.9	490
2	Comparative Analysis and Refinement of Human PSC-Derived Kidney Organoid Differentiation with Single-Cell Transcriptomics. <i>Cell Stem Cell</i> , 2018, 23, 869-881.e8.	11.1	419
3	Making a firm decision: multifaceted regulation of cell fate in the early mouse embryo. <i>Nature Reviews Genetics</i> , 2009, 10, 467-477.	16.3	275
4	Origin and formation of the first two distinct cell types of the inner cell mass in the mouse embryo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6364-6369.	7.1	269
5	Single-cell mapping of lineage and identity in direct reprogramming. <i>Nature</i> , 2018, 564, 219-224.	27.8	255
6	Dissecting Engineered Cell Types and Enhancing Cell Fate Conversion via CellNet. <i>Cell</i> , 2014, 158, 889-902.	28.9	238
7	Active cell movements coupled to positional induction are involved in lineage segregation in the mouse blastocyst. <i>Developmental Biology</i> , 2009, 331, 210-221.	2.0	152
8	The evolving concept of cell identity in the single cell era. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	115
9	A blueprint for engineering cell fate: current technologies to reprogram cell identity. <i>Cell Research</i> , 2013, 23, 33-48.	12.0	108
10	Dynamics of anterior-posterior axis formation in the developing mouse embryo. <i>Nature Communications</i> , 2012, 3, 673.	12.8	86
11	Biomechanical forces promote blood development through prostaglandin E2 and the cAMP-PKA signaling axis. <i>Journal of Experimental Medicine</i> , 2015, 212, 665-680.	8.5	74
12	Next-Generation Lineage Tracing and Fate Mapping to Interrogate Development. <i>Developmental Cell</i> , 2021, 56, 7-21.	7.0	69
13	The differential response to Fgf signalling in cells internalized at different times influences lineage segregation in preimplantation mouse embryos. <i>Open Biology</i> , 2013, 3, 130104.	3.6	67
14	Direct lineage reprogramming via pioneer factors; a detour through developmental gene regulatory networks. <i>Development (Cambridge)</i> , 2016, 143, 2696-2705.	2.5	67
15	High-resolution transcriptional and morphogenetic profiling of cells from micropatterned human ESC gastruloid cultures. <i>ELife</i> , 2020, 9, .	6.0	62
16	CellTag Indexing: genetic barcode-based sample multiplexing for single-cell genomics. <i>Genome Biology</i> , 2019, 20, 90.	8.8	61
17	Self-Reporting Transposons Enable Simultaneous Readout of Gene Expression and Transcription Factor Binding in Single Cells. <i>Cell</i> , 2020, 182, 992-1008.e21.	28.9	54
18	Single-Cell Analysis of Neonatal HSC Ontogeny Reveals Gradual and Uncoordinated Transcriptional Reprogramming that Begins before Birth. <i>Cell Stem Cell</i> , 2020, 27, 732-747.e7.	11.1	53

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19	Zcchc11 Uridylates Mature miRNAs to Enhance Neonatal IGF-1 Expression, Growth, and Survival. PLoS Genetics, 2012, 8, e1003105.	3.5	49
20	CellTagging: combinatorial indexing to simultaneously map lineage and identity at single-cell resolution. Nature Protocols, 2020, 15, 750-772.	12.0	49
21	Localized EMT reprograms glial progenitors to promote spinal cord repair. Developmental Cell, 2021, 56, 613-626.e7.	7.0	40
22	The coding and long noncoding single-cell atlas of the developing human fetal striatum. Science, 2021, 372, .	12.6	40
23	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. Cell Stem Cell, 2021, 28, 127-140.e9.	11.1	39
24	Tsukushi Modulates Xnr2, FGF and BMP Signaling: Regulation of Xenopus Germ Layer Formation. PLoS ONE, 2007, 2, e1004.	2.5	35
25	Basal epithelial stem cells cross an alarmin checkpoint for postviral lung disease. Journal of Clinical Investigation, 2021, 131, .	8.2	30
26	Engineering cell identity: establishing new gene regulatory and chromatin landscapes. Current Opinion in Genetics and Development, 2017, 46, 50-57.	3.3	29
27	Cell fate in the early mouse embryo: sorting out the influence of developmental history on lineage choice. Reproductive BioMedicine Online, 2011, 22, 521-524.	2.4	26
28	Single-Cell Analysis Reveals Regional Reprogramming During Adaptation to Massive Small Bowel Resection in Mice. Cellular and Molecular Gastroenterology and Hepatology, 2019, 8, 407-426.	4.5	24
29	Capybara: A computational tool to measure cell identity and fate transitions. Cell Stem Cell, 2022, 29, 635-649.e11.	11.1	24
30	Computational Stem Cell Biology: Open Questions and Guiding Principles. Cell Stem Cell, 2021, 28, 20-32.	11.1	18
31	Gene expression dynamics underlying cell fate emergence in 2D micropatterned human embryonic stem cell gastruloids. Stem Cell Reports, 2021, 16, 1210-1227.	4.8	18
32	Formation of Distinct Cell Types in the Mouse Blastocyst. Results and Problems in Cell Differentiation, 2012, 55, 203-217.	0.7	14
33	Identification of a retinoic acid-dependent haemogenic endothelial progenitor from human pluripotent stem cells. Nature Cell Biology, 2022, 24, 616-624.	10.3	12
34	Human embryos cultured <i>in vitro</i> to 14 days. Open Biology, 2017, 7, 170003.	3.6	7
35	Defining cellular identity through network biology. Cell Cycle, 2014, 13, 3313-3314.	2.6	6
36	Breaking New Ground in the Landscape of Single-Cell Analysis. Cell Systems, 2018, 6, 5-7.	6.2	4

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37	Challenges for Computational Stem Cell Biology: A Discussion for the Field. <i>Stem Cell Reports</i> , 2021, 16, 3-9.	4.8	4
38	In preprints: the fast-paced field of single-cell lineage tracing. <i>Development (Cambridge)</i> , 2022, 149, .	2.5	4
39	Single-Cell RNA-Seq Steps Up to the Growth Plate. <i>Trends in Biotechnology</i> , 2016, 34, 525-527.	9.3	3
40	Tracing the Origins of Axolotl Limb Regeneration. <i>Developmental Cell</i> , 2018, 47, 675-677.	7.0	3
41	Single cell biologyâ€™a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	3.8	3
42	Cell identity reprogrammed. <i>Nature</i> , 2019, 575, 44-45.	27.8	2
43	Pinpointing a spatial address for RNA profiles in tissues. <i>Nature</i> , 2019, 569, 197-199.	27.8	2
44	Evaluation of Wu etÂal.: Comprehending Global and Local Structure of Single-Cell Datasets. <i>Cell Systems</i> , 2018, 7, 565-566.	6.2	1
45	New dual-channel system records lineage in high definition. <i>Nature Methods</i> , 2022, 19, 38-39.	19.0	1
46	Anniversary reflections: Inspiring discoveries and the future of the field. <i>Cell Stem Cell</i> , 2022, 29, 879-881.	11.1	1
47	Reply: Cell fate in the early mouse embryo: Sorting out the influence of developmental history on lineage choice. <i>Reproductive BioMedicine Online</i> , 2011, 22, 528.	2.4	0
48	HSCs Transition from Fetal to Adult Transcriptional States through Gradual Epigenomic Reprogramming That Begins Shortly after Birth. <i>Blood</i> , 2018, 132, 172-172.	1.4	0
49	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
50	3022 â€“ GENERATION OF RETINOIC ACID-DEPENDENT HEMOGENIC ENDOTHELIAL PROGENITORS FROM HUMAN PLURIPOTENT STEM CELLS. <i>Experimental Hematology</i> , 2020, 88, S45.	0.4	0