Samantha A Morris

List of Publications by Year
in descending order

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	Capybara: A computational tool to measure cell identity and fate transitions. Cell Stem Cell, 2022, 29, 635-649.e11.	11.1	24
2	New dual-channel system records lineage in high definition. Nature Methods, 2022, 19, 38-39.	19.0	1
3	Identification of a retinoic acid-dependent haemogenic endothelial progenitor from human pluripotent stem cells. Nature Cell Biology, 2022, 24, 616-624.	10.3	12
4	Anniversary reflections: Inspiring discoveries and the future of the field. Cell Stem Cell, 2022, 29, 879-881.	11.1	1
5	In preprints: the fast-paced field of single-cell lineage tracing. Development (Cambridge), 2022, 149, .	2.5	4
6	Next-Generation Lineage Tracing and Fate Mapping to Interrogate Development. Developmental Cell, 2021, 56, 7-21.	7.0	69
7	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. Cell Stem Cell, 2021, 28, 127-140.e9.	11.1	39
8	Computational Stem Cell Biology: Open Questions and Guiding Principles. Cell Stem Cell, 2021, 28, 20-32.	11.1	18
9	Challenges for Computational Stem Cell Biology: A Discussion for the Field. Stem Cell Reports, 2021, 16, 3-9.	4.8	4
10	Localized EMT reprograms glial progenitors to promote spinal cord repair. Developmental Cell, 2021, 56, 613-626.e7.	7.0	40
11	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
12	The coding and long noncoding single-cell atlas of the developing human fetal striatum. Science, 2021, 372, .	12.6	40
13	Basal epithelial stem cells cross an alarmin checkpoint for postviral lung disease. Journal of Clinical Investigation, 2021, 131, .	8.2	30
14	Single cell biologyâ€"a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	3.8	3
15	Self-Reporting Transposons Enable SimultaneousÂReadout of Gene Expression and TranscriptionÂFactor Binding in Single Cells. Cell, 2020, 182, 992-1008.e21.	28.9	54
16	Single-Cell Analysis of Neonatal HSC Ontogeny Reveals Gradual and Uncoordinated Transcriptional Reprogramming that Begins before Birth. Cell Stem Cell, 2020, 27, 732-747.e7.	11.1	53
17	CellTagging: combinatorial indexing to simultaneously map lineage and identity at single-cell resolution. Nature Protocols, 2020, 15, 750-772.	12.0	49
18	High-resolution transcriptional and morphogenetic profiling of cells from micropatterned human ESC gastruloid cultures. ELife, 2020, 9, .	6.0	62

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19	3022 â€“ GENERATION OF RETINOIC ACID-DEPENDENT HEMOGENIC ENDOTHELIAL PROGENITORS FROM HUMAN PLURIPOTENT STEM CELLS. Experimental Hematology, 2020, 88, S45.	0.4	0
20	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
21	The evolving concept of cell identity in the single cell era. Development (Cambridge), 2019, 146, .	2.5	115
22	Cell identity reprogrammed. Nature, 2019, 575, 44-45.	27.8	2
23	Pinpointing a spatial address for RNA profiles in tissues. Nature, 2019, 569, 197-199.	27.8	2
24	CellTag Indexing: genetic barcode-based sample multiplexing for single-cell genomics. Genome Biology, 2019, 20, 90.	8.8	61
25	Breaking New Ground in the Landscape of Single-Cell Analysis. Cell Systems, 2018, 6, 5-7.	6.2	4
26	Comparative Analysis and Refinement of Human PSC-Derived Kidney Organoid Differentiation with Single-Cell Transcriptomics. Cell Stem Cell, 2018, 23, 869-881.e8.	11.1	419
27	Evaluation of Wu etÂal.: Comprehending Global and Local Structure of Single-Cell Datasets. Cell Systems, 2018, 7, 565-566.	6.2	1
28	Tracing the Origins of Axolotl Limb Regeneration. Developmental Cell, 2018, 47, 675-677.	7.0	3
29	Single-cell mapping of lineage and identity in direct reprogramming. Nature, 2018, 564, 219-224.	27.8	255
30	HSCs Transition from Fetal to Adult Transcriptional States through Gradual Epigenomic Reprogramming That Begins Shortly after Birth. Blood, 2018, 132, 172-172.	1.4	0
31	Human embryos cultured<i>in vitro</i>to 14 days. Open Biology, 2017, 7, 170003.	3.6	7
32	Engineering cell identity: establishing new gene regulatory and chromatin landscapes. Current Opinion in Genetics and Development, 2017, 46, 50-57.	3.3	29
33	Direct lineage reprogramming via pioneer factors; a detour through developmental gene regulatory networks. Development (Cambridge), 2016, 143, 2696-2705.	2.5	67
34	Single-Cell RNA-Seq Steps Up to the Growth Plate. Trends in Biotechnology, 2016, 34, 525-527.	9.3	3
35	Biomechanical forces promote blood development through prostaglandin E2 and the cAMPâ€“PKA signaling axis. Journal of Experimental Medicine, 2015, 212, 665-680.	8.5	74
36	Defining cellular identity through network biology. Cell Cycle, 2014, 13, 3313-3314.	2.6	6

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37	CellNet: Network Biology Applied to Stem Cell Engineering. Cell, 2014, 158, 903-915.	28.9	490
38	Dissecting Engineered Cell Types and Enhancing Cell Fate Conversion via CellNet. Cell, 2014, 158, 889-902.	28.9	238
39	A blueprint for engineering cell fate: current technologies to reprogram cell identity. Cell Research, 2013, 23, 33-48.	12.0	108
40	The differential response to Fgf signalling in cells internalized at different times influences lineage segregation in preimplantation mouse embryos. Open Biology, 2013, 3, 130104.	3.6	67
41	Zcchc11 Uridylates Mature miRNAs to Enhance Neonatal IGF-1 Expression, Growth, and Survival. PLoS Genetics, 2012, 8, e1003105.	3.5	49
42	Dynamics of anteriorâ€"posterior axis formation in the developing mouse embryo. Nature Communications, 2012, 3, 673.	12.8	86
43	Formation of Distinct Cell Types in the Mouse Blastocyst. Results and Problems in Cell Differentiation, 2012, 55, 203-217.	0.7	14
44	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
45	Reply: Cell fate in the early mouse embryo: Sorting out the influence of developmental history on lineage choice. Reproductive BioMedicine Online, 2011, 22, 528.	2.4	0
46	Origin and formation of the first two distinct cell types of the inner cell mass in the mouse embryo. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6364-6369.	7.1	269
47	Making a firm decision: multifaceted regulation of cell fate in the early mouse embryo. Nature Reviews Genetics, 2009, 10, 467-477.	16.3	275
48	Active cell movements coupled to positional induction are involved in lineage segregation in the mouse blastocyst. Developmental Biology, 2009, 331, 210-221.	2.0	152
49	Tsukushi Modulates Xnr2, FGF and BMP Signaling: Regulation of Xenopus Germ Layer Formation. PLoS ONE, 2007, 2, e1004.	2.5	35
50	Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs. SSRN Electronic Journal, 0, , .	0.4	0