Antonio Scialdone

List of Publications by Year
in descending order

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39

papers

5,558

citations

331670

21

h-index

289244

40

g-index

53

all docs

53

docs citations

53

times ranked

9192

citing authors

#	ARTICLE	IF	CITATIONS
1	The role of cell geometry and cell-cell communication in gradient sensing. PLoS Computational Biology, 2022, 18, e1009552.	3.2	2
2	DNA replication fork speed underlies cell fate changes and promotes reprogramming. Nature Genetics, 2022, 54, 318-327.	21.4	38
3	A 3D transcriptomics atlas of the mouse nose sheds light on the anatomical logic of smell. Cell Reports, 2022, 38, 110547.	6.4	16
4	MitoHEAR: an R package for the estimation and downstream statistical analysis of the mitochondrial DNA heteroplasmy calculated from single-cell datasets. Journal of Open Source Software, 2022, 7, 4265.	4.6	0
5	Characterization of a common progenitor pool of the epicardium and myocardium. Science, 2021, 371, .	12.6	88
6	Retinoic acid signaling is critical during the totipotency window in early mammalian development. Nature Structural and Molecular Biology, 2021, 28, 521-532.	8.2	42
7	Cell competition acts as a purifying selection to eliminate cells with mitochondrial defects during early mouse development. Nature Metabolism, 2021, 3, 1091-1108.	11.9	33
8	Single-cell transcriptomic characterization of a gastrulating human embryo. Nature, 2021, 600, 285-289.	27.8	202
9	Measuring and Modeling Single-Cell Heterogeneity and Fate Decision in Mouse Embryos. Annual Review of Genetics, 2020, 54, 167-187.	7.6	14
10	COMUNET: a tool to explore and visualize intercellular communication. Bioinformatics, 2020, 36, 4296-4300.	4.1	22
11	Differential regulation of the immune system in a brain-liver-fats organ network during short-term fasting. Molecular Metabolism, 2020, 40, 101038.	6.5	7
12	Automatic identification of relevant genes from low-dimensional embeddings of single-cell RNA-seq data. Bioinformatics, 2020, 36, 4291-4295.	4.1	7
13	Epsteinâ€“Barr virus reprograms human B lymphocytes immediately in the prelatent phase of infection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16046-16055.	7.1	138
14	Interspecific variation of olfactory preferences in flies, mice, and humans. Chemical Senses, 2019, 44, 7-9.	2.0	5
15	Using singleâ€cell genomics to understand developmental processes and cell fate decisions. Molecular Systems Biology, 2018, 14, e8046.	7.2	190
16	Spatiotemporal patterning of EpCAM is important for murine embryonic endo- and mesodermal differentiation. Scientific Reports, 2018, 8, 1801.	3.3	20
17	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. Nature Cell Biology, 2018, 20, 127-134.	10.3	112
18	Complex multi-enhancer contacts captured by genome architecture mapping. Nature, 2017, 543, 519-524.	27.8	562

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19	Normalizing single-cell RNA sequencing data: challenges and opportunities. Nature Methods, 2017, 14, 565-571.	19.0	405
20	Adipocyte Accumulation in the Bone Marrow during Obesity and Aging Impairs Stem Cell-Based Hematopoietic and Bone Regeneration. Cell Stem Cell, 2017, 20, 771-784.e6.	11.1	566
21	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. Cell Reports, 2017, 20, 1215-1228.	6.4	290
22	Pluripotent state transitions coordinate morphogenesis in mouse and human embryos. Nature, 2017, 552, 239-243.	27.8	193
23	Mosaic autosomal aneuploidies are detectable from single-cell RNAseq data. BMC Genomics, 2017, 18, 904.	2.8	21
24	Resolving early mesoderm diversification through single-cell expression profiling. Nature, 2016, 535, 289-293.	27.8	261
25	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. Cell, 2016, 165, 61-74.	28.9	385
26	Hierarchical deconstruction of mouse olfactory sensory neurons: from whole mucosa to single-cell RNA-seq. Scientific Reports, 2015, 5, 18178.	3.3	148
27	Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. Nature Biotechnology, 2015, 33, 155-160.	17.5	1,068
28	Computational assignment of cell-cycle stage from single-cell transcriptome data. Methods, 2015, 85, 54-61.	3.8	381
29	How plants manage food reserves at night: quantitative models and open questions. Frontiers in Plant Science, 2015, 6, 204.	3.6	35
30	Polymer physics, scaling and heterogeneity in the spatial organisation of chromosomes in the cell nucleus. Soft Matter, 2013, 9, 8631.	2.7	15
31	Polymer models of chromatin organization. Frontiers in Genetics, 2013, 4, 113.	2.3	15
32	Arabidopsis plants perform arithmetic division to prevent starvation at night. ELife, 2013, 2, e00669.	6.0	134
33	Colocalization of Multiple DNA Loci: A Physical Mechanism. Biophysical Journal, 2012, 103, 2223-2232.	0.5	8
34	Conformation Regulation of the X Chromosome Inactivation Center: A Model. PLoS Computational Biology, 2011, 7, e1002229.	3.2	29
35	Diffusion-based DNA target colocalization by thermodynamic mechanisms. Development (Cambridge), 2010, 137, 3877-3885.	2.5	8
36	STATISTICAL MECHANICS MODELS FOR X-CHROMOSOME INACTIVATION. International Journal of Modeling, Simulation, and Scientific Computing, 2010, 13, 367-376.	1.4	0

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37	Passive DNA shuttling. Europhysics Letters, 2010, 92, 20002.	2.0	3
38	DNA Loci Cross-Talk through Thermodynamics. Journal of Biomedicine and Biotechnology, 2009, 2009, 1-8.	3.0	2
39	Mechanics and Dynamics of X-Chromosome Pairing at X Inactivation. PLoS Computational Biology, 2008, 4, e1000244.	3.2	20