

Li-Fang Chu

List of Publications by Year in Descending Order

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Version: 2024-04-27

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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.

28

papers

1,699

citations

16

h-index

31

g-index

31

ext. papers

2,188

ext. citations

13.3

avg, IF

4.34

L-index

#	Paper	IF	Citations
28	Network inference with Granger causality ensembles on single-cell transcriptomics.. <i>Cell Reports</i> , 2022 , 38, 110333	10.6	5
27	Enhancing biological signals and detection rates in single-cell RNA-seq experiments with cDNA library equalization. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
26	Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis. <i>PLoS ONE</i> , 2020 , 15, e0239711	3.7	2
25	An In Vitro Human Segmentation Clock Model Derived from Embryonic Stem Cells. <i>Cell Reports</i> , 2019 , 28, 2247-2255.e5	10.6	21
24	Epithelial DNA methyltransferase-1 regulates cell survival, growth and maturation in developing prostatic buds. <i>Developmental Biology</i> , 2019 , 447, 157-169	3.1	2
23	A folic acid-enriched diet attenuates prostate involution in response to androgen deprivation. <i>Prostate</i> , 2019 , 79, 183-194	4.2	2
22	Spatial patterns of gene expression are unveiled in the chick primitive streak by ordering single-cell transcriptomes. <i>Developmental Biology</i> , 2018 , 439, 30-41	3.1	4
21	In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 8394-8399	11.5	12
20	A Novel Approach to Single Cell RNA-Sequence Analysis Facilitates In Silico Gene Reporting of Human Pluripotent Stem Cell-Derived Retinal Cell Types. <i>Stem Cells</i> , 2018 , 36, 313-324	5.8	37
19	Trendy: segmented regression analysis of expression dynamics in high-throughput ordered profiling experiments. <i>BMC Bioinformatics</i> , 2018 , 19, 380	3.6	16
18	SCnorm: robust normalization of single-cell RNA-seq data. <i>Nature Methods</i> , 2017 , 14, 584-586	21.6	189
17	Functional characterization of human pluripotent stem cell-derived arterial endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E6072-E6078	11.5	70
16	Single-cell RNA-seq reveals novel regulators of human embryonic stem cell differentiation to definitive endoderm. <i>Genome Biology</i> , 2016 , 17, 173	18.3	195
15	A statistical approach for identifying differential distributions in single-cell RNA-seq experiments. <i>Genome Biology</i> , 2016 , 17, 222	18.3	133
14	OEFinder: a user interface to identify and visualize ordering effects in single-cell RNA-seq data. <i>Bioinformatics</i> , 2016 , 32, 1408-10	7.2	17
13	Mouse mutation reveals a mechanism involving mitochondrial dynamics that leads to age-dependent retinal pathologies. <i>ELife</i> , 2016 , 5,	8.9	32
12	Oscope identifies oscillatory genes in unsynchronized single-cell RNA-seq experiments. <i>Nature Methods</i> , 2015 , 12, 947-950	21.6	116

11	An expandable, inducible hemangioblast state regulated by fibroblast growth factor. <i>Stem Cell Reports</i> , 2014 , 3, 1043-57	8	18
10	Efficient genome engineering in human pluripotent stem cells using Cas9 from <i>Neisseria meningitidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 15644-9	11.5	508
9	Comparative RNA-seq analysis in the unsequenced axolotl: the oncogene burst highlights early gene expression in the blastema. <i>PLoS Computational Biology</i> , 2013 , 9, e1002936	5	92
8	Blimp1 expression predicts embryonic stem cell development in vitro. <i>Current Biology</i> , 2011 , 21, 1759-65	6.3	39
7	Ronin is essential for embryogenesis and the pluripotency of mouse embryonic stem cells. <i>Cell</i> , 2008 , 133, 1162-74	56.2	148
6	Expression of FoxP2 during zebrafish development and in the adult brain. <i>International Journal of Developmental Biology</i> , 2006 , 50, 435-8	1.9	22
5	scDD: A statistical approach for identifying differential distributions in single-cell RNA-seq experiments		5
4	SCPattern: A statistical approach to identify and classify expression changes in single cell RNA-seq experiments with ordered conditions		2
3	Network Inference with Granger Causality Ensembles on Single-Cell Transcriptomic Data		8
2	SCnorm: A quantile-regression based approach for robust normalization of single-cell RNA-seq data		2
1	Human Pluripotent Cells: The Biology of Pluripotency		311-325