Xiannian Zhang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9734881/publications.pdf

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		933447	1125743
13	1,887	10	13
papers	citations	h-index	g-index
1.0	10	1.0	4760
13	13	13	4760
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Heightened Innate Immune Responses in the Respiratory Tract of COVID-19 Patients. Cell Host and Microbe, 2020, 27, 883-890.e2.	11.0	811
2	Comparative Analysis of Droplet-Based Ultra-High-Throughput Single-Cell RNA-Seq Systems. Molecular Cell, 2019, 73, 130-142.e5.	9.7	283
3	Microfluidic single-cell whole-transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7048-7053.	7.1	259
4	Chemoproteomics reveals baicalin activates hepatic CPT1 to ameliorate diet-induced obesity and hepatic steatosis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5896-E5905.	7.1	201
5	Dissecting esophageal squamous-cell carcinoma ecosystem by single-cell transcriptomic analysis. Nature Communications, 2021, 12, 5291.	12.8	98
6	Single-cell transcriptomic analysis in a mouse model deciphers cell transition states in the multistep development of esophageal cancer. Nature Communications, 2020, 11, 3715.	12.8	79
7	Establishment of intestinal organoid cultures modeling injury-associated epithelial regeneration. Cell Research, 2021, 31, 259-271.	12.0	54
8	A valve-less microfluidic peristaltic pumping method. Biomicrofluidics, 2015, 9, 014118.	2.4	35
9	High-throughput single-cell whole-genome amplification through centrifugal emulsification and eMDA. Communications Biology, 2019, 2, 147.	4.4	35
10	Microfluidic Device for Studying Controllable Hydrodynamic Flow Induced Cellular Responses. Analytical Chemistry, 2017, 89, 3710-3715.	6.5	17
11	Genomic Heterogeneity and Branched Evolution of Early Stage Primary Acral Melanoma Shown by Multiregional Microdissection Sequencing. Journal of Investigative Dermatology, 2019, 139, 1526-1534.	0.7	7
12	Integrating single-cell datasets with ambiguous batch information by incorporating molecular network features. Briefings in Bioinformatics, 2022, 23, .	6.5	5
13	Terminal transfer amplification and sequencing for high-efficiency and low-bias copy number profiling of fragmented DNA samples. Protein and Cell, 2019, 10, 229-233.	11.0	3