Zhengyu Liang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3979161/publications.pdf

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12 papers	837 citations	932766 10 h-index	1125271 13 g-index
14	14	14	1241
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Transcription Elongation Machinery Is a Druggable Dependency and Potentiates Immunotherapy in Glioblastoma Stem Cells. Cancer Discovery, 2022, 12, 502-521.	7.7	29
2	PRDM16 Is a Compact Myocardium-Enriched Transcription Factor Required to Maintain Compact Myocardial Cardiomyocyte Identity in Left Ventricle. Circulation, 2022, 145, 586-602.	1.6	44
3	CTCF functions as an insulator for somatic genes and a chromatin remodeler for pluripotency genes during reprogramming. Cell Reports, 2022, 39, 110626.	2.9	22
4	3D genome encoded by LINE and SINE repeats. Cell Research, 2021, 31, 603-604.	5.7	4
5	Quantifying the phase separation property of chromatin-associated proteins under physiological conditions using an anti-1,6-hexanediol index. Genome Biology, 2021, 22, 229.	3.8	24
6	Mediator complex proximal Tail subunit MED30 is critical for Mediator core stability and cardiomyocyte transcriptional network. PLoS Genetics, 2021, 17, e1009785.	1.5	4
7	Reversing a model of Parkinson's disease with in situ converted nigral neurons. Nature, 2020, 582, 550-556.	13.7	316
8	Initiation of Parental Genome Reprogramming in Fertilized Oocyte by Splicing Kinase SRPK1-Catalyzed Protamine Phosphorylation. Cell, 2020, 180, 1212-1227.e14.	13.5	54
9	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. Cell, 2019, 178, 107-121.e18.	13.5	224
10	Alterations of specific chromatin conformation affect ATRA-induced leukemia cell differentiation. Cell Death and Disease, 2018, 9, 200.	2.7	29
11	BL-Hi-C is an efficient and sensitive approach for capturing structural and regulatory chromatin interactions. Nature Communications, 2017, 8, 1622.	5.8	60
12	3CPET: finding co-factor complexes from ChIA-PET data using a hierarchical Dirichlet process. Genome Biology, 2015, 16, 288.	3.8	20