Xueqiu Lin

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11255146/publications.pdf

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16 papers	1,535 citations	14 h-index	940533 16 g-index
16	16	16	3181 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	Development of CRISPR as an Antiviral Strategy to Combat SARS-CoV-2 and Influenza. Cell, 2020, 181, 865-876.e12.	28.9	354
2	Broad H3K4me3 is associated with increased transcription elongation and enhancer activity at tumor-suppressor genes. Nature Genetics, 2015, 47, 1149-1157.	21.4	276
3	CRISPR-Mediated Programmable 3D Genome Positioning and Nuclear Organization. Cell, 2018, 175, 1405-1417.e14.	28.9	164
4	CRISPR Activation Screens Systematically Identify Factors that Drive Neuronal Fate and Reprogramming. Cell Stem Cell, 2018, 23, 758-771.e8.	11.1	161
5	DNMT3A and TET1 cooperate to regulate promoter epigenetic landscapes in mouse embryonic stem cells. Genome Biology, 2018, 19, 88.	8.8	120
6	DNMT3A Loss Drives Enhancer Hypomethylation in FLT3-ITD-Associated Leukemias. Cancer Cell, 2016, 29, 922-934.	16.8	107
7	Homeobox oncogene activation by pan-cancer DNA hypermethylation. Genome Biology, 2018, 19, 108.	8.8	94
8	BSeQC: quality control of bisulfite sequencing experiments. Bioinformatics, 2013, 29, 3227-3229.	4.1	45
9	A benchmark of algorithms for the analysis of pooled CRISPR screens. Genome Biology, 2020, 21, 62.	8.8	45
10	Multiplexed genome regulation in vivo with hyper-efficient Cas12a. Nature Cell Biology, 2022, 24, 590-600.	10.3	39
11	CRISPhieRmix: a hierarchical mixture model for CRISPR pooled screens. Genome Biology, 2018, 19, 159.	8.8	36
12	The disordered N-terminal domain of DNMT3A recognizes H2AK119ub and is required for postnatal development. Nature Genetics, 2022, 54, 625-636.	21.4	31
13	A comprehensive analysis and resource to use CRISPR-Cas13 for broad-spectrum targeting of RNA viruses. Cell Reports Medicine, 2021, 2, 100245.	6.5	23
14	Broad-spectrum CRISPR-mediated inhibition of SARS-CoV-2 variants and endemic coronaviruses in vitro. Nature Communications, 2022, 13, 2766.	12.8	20
15	Sparse conserved under-methylated CpGs are associated with high-order chromatin structure. Genome Biology, 2017, 18, 163.	8.8	16
16	Computational Methods for Analysis of Large-Scale CRISPR Screens. Annual Review of Biomedical Data Science, 2020, 3, 137-162.	6.5	4