Qian Qin

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3410368/publications.pdf

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24	2,173	516710 16	610901 24
papers	citations	h-index	g-index

26	26	26	4323
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Amplitude of low-frequency fluctuation may be an early predictor of delayed motor development due to neonatal hyperbilirubinemia: a fMRI study. Translational Pediatrics, 2021, 10, 1271-1284.	1.2	3
2	Current progress and potential opportunities to infer single-cell developmental trajectory and cell fate. Current Opinion in Systems Biology, 2021, 26, 1-11.	2.6	8
3	Single-cell imaging of T cell immunotherapy responses in vivo. Journal of Experimental Medicine, 2021, 218, .	8.5	16
4	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. Frontiers in Genetics, 2021, 12, 764170.	2.3	14
5	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. Genome Biology, 2020, 21, 198.	8.8	126
6	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
7	Functional annotation of genetic associations by transcriptome-wide association analysis provides insights into neutrophil development regulation. Communications Biology, 2020, 3, 790.	4.4	1
8	Clinical utility of 24-h rapid trio-exome sequencing for critically ill infants. Npj Genomic Medicine, 2020, 5, 20.	3.8	41
9	Lisa: inferring transcriptional regulators through integrative modeling of public chromatin accessibility and ChIP-seq data. Genome Biology, 2020, 21, 32.	8.8	161
10	Survival Motor Neuron Gene Copy Number Analysis by Exome Sequencing. Journal of Molecular Diagnostics, 2020, 22, 619-628.	2.8	17
11	Relationship between phenotype and genotype of 102 Chinese newborns with Praderâ€“Willi syndrome. Molecular Biology Reports, 2019, 46, 4717-4724.	2.3	12
12	Feeding difficulty is the dominant feature in 12 Chinese newborns with CHD7 pathogenic variants. BMC Medical Genetics, 2019, 20, 93.	2.1	6
13	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. Nucleic Acids Research, 2019, 47, D729-D735.	14.5	527
14	Early-onset infant epileptic encephalopathy associated with a de novo PPP3CA gene mutation. Journal of Physical Education and Sports Management, 2018, 4, a002949.	1.2	8
15	Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. Cancer Research, 2017, 77, e19-e22.	0.9	130
16	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. Nucleic Acids Research, 2017, 45, D658-D662.	14.5	451
17	Imputation for transcription factor binding predictions based on deep learning. PLoS Computational Biology, 2017, 13, e1005403.	3.2	87
18	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. BMC Bioinformatics, 2016, 17, 404.	2.6	100

#	Article	IF	Citations
19	CRISPR-DO for genome-wide CRISPR design and optimization. Bioinformatics, 2016, 32, 3336-3338.	4.1	46
20	High-dimensional genomic data bias correction and data integration using MANCIE. Nature Communications, 2016, 7, 11305.	12.8	52
21	Modeling cis-regulation with a compendium of genome-wide histone H3K27ac profiles. Genome Research, 2016, 26, 1417-1429.	5.5	75
22	Integrative Analysis Reveals the Transcriptional Collaboration between EZH2 and E2F1 in the Regulation of Cancer-Related Gene Expression. Molecular Cancer Research, 2016, 14, 163-172.	3.4	34
23	CR Cistrome: a ChIP-Seq database for chromatin regulators and histone modification linkages in human and mouse. Nucleic Acids Research, 2014, 42, D450-D458.	14.5	42
24	MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. Genome Biology, 2014, 15, 419.	8.8	87