

# Qian Qin

## List of Publications by Year in descending order

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

Version: 2024-02-01

24  
papers

2,173  
citations

516710

16  
h-index

610901

24  
g-index

26  
all docs

26  
docs citations

26  
times ranked

4323  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cistrome Data Browser: expanded datasets and new tools for gene regulatory analysis. <i>Nucleic Acids Research</i> , 2019, 47, D729-D735.	14.5	527
2	Cistrome Data Browser: a data portal for ChIP-Seq and chromatin accessibility data in human and mouse. <i>Nucleic Acids Research</i> , 2017, 45, D658-D662.	14.5	451
3	Lisa: inferring transcriptional regulators through integrative modeling of public chromatin accessibility and ChIP-seq data. <i>Genome Biology</i> , 2020, 21, 32.	8.8	161
4	Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. <i>Cancer Research</i> , 2017, 77, e19-e22.	0.9	130
5	Integrative analyses of single-cell transcriptome and regulome using MAESTRO. <i>Genome Biology</i> , 2020, 21, 198.	8.8	126
6	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
7	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	2.6	100
8	MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. <i>Genome Biology</i> , 2014, 15, 419.	8.8	87
9	Imputation for transcription factor binding predictions based on deep learning. <i>PLoS Computational Biology</i> , 2017, 13, e1005403.	3.2	87
10	Modeling cis-regulation with a compendium of genome-wide histone H3K27ac profiles. <i>Genome Research</i> , 2016, 26, 1417-1429.	5.5	75
11	High-dimensional genomic data bias correction and data integration using MANCIE. <i>Nature Communications</i> , 2016, 7, 11305.	12.8	52
12	CRISPR-DO for genome-wide CRISPR design and optimization. <i>Bioinformatics</i> , 2016, 32, 3336-3338.	4.1	46
13	CR Cistrome: a ChIP-Seq database for chromatin regulators and histone modification linkages in human and mouse. <i>Nucleic Acids Research</i> , 2014, 42, D450-D458.	14.5	42
14	Clinical utility of 24-h rapid trio-exome sequencing for critically ill infants. <i>Npj Genomic Medicine</i> , 2020, 5, 20.	3.8	41
15	Integrative Analysis Reveals the Transcriptional Collaboration between EZH2 and E2F1 in the Regulation of Cancer-Related Gene Expression. <i>Molecular Cancer Research</i> , 2016, 14, 163-172.	3.4	34
16	Survival Motor Neuron Gene Copy Number Analysis by Exome Sequencing. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 619-628.	2.8	17
17	Single-cell imaging of T cell immunotherapy responses in vivo. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	16
18	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. <i>Frontiers in Genetics</i> , 2021, 12, 764170.	2.3	14

#	ARTICLE	IF	CITATIONS
19	Relationship between phenotype and genotype of 102 Chinese newborns with Prader-Willi syndrome. <i>Molecular Biology Reports</i> , 2019, 46, 4717-4724.	2.3	12
20	Early-onset infant epileptic encephalopathy associated with a de novo <i>PPP3CA</i> gene mutation. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002949.	1.2	8
21	Current progress and potential opportunities to infer single-cell developmental trajectory and cell fate. <i>Current Opinion in Systems Biology</i> , 2021, 26, 1-11.	2.6	8
22	Feeding difficulty is the dominant feature in 12 Chinese newborns with CHD7 pathogenic variants. <i>BMC Medical Genetics</i> , 2019, 20, 93.	2.1	6
23	Amplitude of low-frequency fluctuation may be an early predictor of delayed motor development due to neonatal hyperbilirubinemia: a fMRI study. <i>Translational Pediatrics</i> , 2021, 10, 1271-1284.	1.2	3
24	Functional annotation of genetic associations by transcriptome-wide association analysis provides insights into neutrophil development regulation. <i>Communications Biology</i> , 2020, 3, 790.	4.4	1