

Peng Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2061367/publications.pdf>

Version: 2024-02-01

18
papers

1,570
citations

623734

14
h-index

839539

18
g-index

21
all docs

21
docs citations

21
times ranked

2269
citing authors

#	ARTICLE	IF	CITATIONS
1	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	14.5	364
2	MIWI and piRNA-mediated cleavage of messenger RNAs in mouse testes. <i>Cell Research</i> , 2015, 25, 193-207.	12.0	266
3	piRBase: a comprehensive database of piRNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D175-D180.	14.5	169
4	piRBase: a web resource assisting piRNA functional study. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau110.	3.0	132
5	BioCircos.js: an interactive Circos JavaScript library for biological data visualization on web applications. <i>Bioinformatics</i> , 2016, 32, 1740-1742.	4.1	119
6	NPInter v4.0: an integrated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2020, 48, D160-D165.	14.5	106
7	Genome-wide identification and differential analysis of translational initiation. <i>Nature Communications</i> , 2017, 8, 1749.	12.8	100
8	Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. <i>Genome Biology</i> , 2013, 14, R141.	9.6	85
9	NyuWa Genome resource: A deep whole-genome sequencing-based variation profile and reference panel for the Chinese population. <i>Cell Reports</i> , 2021, 37, 110017.	6.4	49
10	piRBase: integrating piRNA annotation in all aspects. <i>Nucleic Acids Research</i> , 2022, 50, D265-D272.	14.5	33
11	SmProt: A Reliable Repository with Comprehensive Annotation of Small Proteins Identified from Ribosome Profiling. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 602-610.	6.9	28
12	Predicting Housekeeping Genes Based on Fourier Analysis. <i>PLoS ONE</i> , 2011, 6, e21012.	2.5	26
13	Computational identification of piRNA targets on mouse mRNAs. <i>Bioinformatics</i> , 2016, 32, 1170-1177.	4.1	22
14	FGFR1-Activated Translation of WNT Pathway Components with Structured 5' UTRs Is Vulnerable to Inhibition of EIF4A-Dependent Translation Initiation. <i>Cancer Research</i> , 2018, 78, 4229-4240.	0.9	22
15	Characterizing mobile element insertions in 5675 genomes. <i>Nucleic Acids Research</i> , 2022, 50, 2493-2508.	14.5	16
16	Systematic functional interrogation of human pseudogenes using CRISPRi. <i>Genome Biology</i> , 2021, 22, 240.	8.8	13
17	New insights into the fungal community from the raw genomic sequence data of fig wasp <i>Ceratosolen solmsi</i> . <i>BMC Microbiology</i> , 2015, 15, 27.	3.3	5
18	Regulation of transcription factors on sexual dimorphism of fig wasps. <i>Scientific Reports</i> , 2015, 5, 10696.	3.3	2