

Shuai Jiang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5612681/publications.pdf>

Version: 2024-02-01

12
papers

765
citations

1307594

7
h-index

1281871

11
g-index

13
all docs

13
docs citations

13
times ranked

936
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	An expanded landscape of human long noncoding RNA. <i>Nucleic Acids Research</i> , 2019, 47, 7842-7856.	14.5	92
3	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 749-759.	6.9	88
4	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. <i>Genome Research</i> , 2019, 29, 682-696.	5.5	67
5	An online coronavirus analysis platform from the National Genomics Data Center. <i>Zoological Research</i> , 2020, 41, 705-708.	2.1	62
6	LncExpDB: an expression database of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2021, 49, D962-D968.	14.5	55
7	Accurately annotate compound effects of genetic variants using a context-sensitive framework. <i>Nucleic Acids Research</i> , 2017, 45, e82-e82.	14.5	9
8	LocExpress: a web server for efficiently estimating expression of novel transcripts. <i>BMC Genomics</i> , 2016, 17, 1023.	2.8	6
9	Multi-omics annotation of human long non-coding RNAs. <i>Biochemical Society Transactions</i> , 2020, 48, 1545-1556.	3.4	6
10	CompoDynamics: a comprehensive database for characterizing sequence composition dynamics. <i>Nucleic Acids Research</i> , 2022, 50, D962-D969.	14.5	6
11	Systematic identification and annotation of multiple-variant compound effects at transcription factor binding sites in human genome. <i>Journal of Genetics and Genomics</i> , 2018, 45, 373-379.	3.9	5
12	Quantitative model suggests both intrinsic and contextual features contribute to the transcript coding ability determination in cells. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	0