

Zhihua Ou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3103944/publications.pdf>

Version: 2024-02-01

13
papers

832
citations

1162367

8
h-index

1199166

12
g-index

22
all docs

22
docs citations

22
times ranked

1789
citing authors

#	ARTICLE	IF	CITATIONS
1	VThunter: a database for single-cell screening of virus target cells in the animal kingdom. <i>Nucleic Acids Research</i> , 2022, 50, D934-D942.	6.5	13
2	Viral receptor profiles of masked palm civet revealed by single-cell transcriptomics. <i>Journal of Genetics and Genomics</i> , 2022, , .	1.7	1
3	Genetic signatures for lineage/sublineage classification of HPV16, 18, 52 and 58 variants. <i>Virology</i> , 2021, 553, 62-69.	1.1	12
4	Population Bottlenecks and Intra-host Evolution During Human-to-Human Transmission of SARS-CoV-2. <i>Frontiers in Medicine</i> , 2021, 8, 585358.	1.2	28
5	Intra-host variation and evolutionary dynamics of SARS-CoV-2 populations in COVID-19 patients. <i>Genome Medicine</i> , 2021, 13, 30.	3.6	88
6	Mutation Profiles, Glycosylation Site Distribution and Codon Usage Bias of Human Papillomavirus Type 16. <i>Viruses</i> , 2021, 13, 1281.	1.5	3
7	Genetic characteristics of human papillomavirus type 16, 18, 52 and 58 in southern China. <i>Genomics</i> , 2021, 113, 3895-3906.	1.3	2
8	Single cell atlas for 11 non-model mammals, reptiles and birds. <i>Nature Communications</i> , 2021, 12, 7083.	5.8	32
9	A compromised specific humoral immune response against the SARS-CoV-2 receptor-binding domain is related to viral persistence and periodic shedding in the gastrointestinal tract. <i>Cellular and Molecular Immunology</i> , 2020, 17, 1119-1125.	4.8	67
10	A Path toward SARS-CoV-2 Attenuation: Metabolic Pressure on CTP Synthesis Rules the Virus Evolution. <i>Genome Biology and Evolution</i> , 2020, 12, 2467-2485.	1.1	22
11	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57.	3.6	104
12	Prevalence and evolution of avian H1 subtype influenza A viruses in Southern China. <i>Virus Evolution</i> , 2018, 4, .	2.2	0
13	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013, 502, 241-244.	13.7	429