

Yiming Bao

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

9,898
citations

172207

29
h-index

301761

39
g-index

47
all docs

47
docs citations

47
times ranked

19146
citing authors

#	ARTICLE	IF	CITATIONS
1	Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. <i>Nucleic Acids Research</i> , 2016, 44, D733-D745.	6.5	4,739
2	The Influenza Virus Resource at the National Center for Biotechnology Information. <i>Journal of Virology</i> , 2008, 82, 596-601.	1.5	888
3	NCBI Viral Genomes Resource. <i>Nucleic Acids Research</i> , 2015, 43, D571-D577.	6.5	541
4	The Genome Sequence Archive Family: Toward Explosive Data Growth and Diverse Data Types. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 578-583.	3.0	504
5	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016, 161, 2351-2360.	0.9	407
6	Virus Variation Resource “improved response to emergent viral outbreaks. <i>Nucleic Acids Research</i> , 2017, 45, D482-D490.	6.5	342
7	Reorganization and expansion of the nidoviral family Arteriviridae. <i>Archives of Virology</i> , 2016, 161, 755-768.	0.9	254
8	Taxonomy of the order Mononegavirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1967-1980.	0.9	224
9	Taxonomy of the order Mononegavirales: update 2017. <i>Archives of Virology</i> , 2017, 162, 2493-2504.	0.9	173
10	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	6.5	168
11	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D24-D33.	6.5	165
12	Past, present, and future of arenavirus taxonomy. <i>Archives of Virology</i> , 2015, 160, 1851-1874.	0.9	158
13	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310.	0.9	157
14	Improvements to pairwise sequence comparison (PASC): a genome-based web tool for virus classification. <i>Archives of Virology</i> , 2014, 159, 3293-3304.	0.9	143
15	Genome Warehouse: A Public Repository Housing Genome-scale Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 584-589.	3.0	104
16	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 749-759.	3.0	88
17	Nomenclature- and Database-Compatible Names for the Two Ebola Virus Variants that Emerged in Guinea and the Democratic Republic of the Congo in 2014. <i>Viruses</i> , 2014, 6, 4760-4799.	1.5	83
18	National Center for Biotechnology Information Viral Genomes Project. <i>Journal of Virology</i> , 2004, 78, 7291-7298.	1.5	64

#	ARTICLE	IF	CITATIONS
19	FLAN: a web server for influenza virus genome annotation. <i>Nucleic Acids Research</i> , 2007, 35, W280-W284.	6.5	60
20	Genomic Characterization of the Genus Nairovirus (Family Bunyaviridae). <i>Viruses</i> , 2016, 8, 164.	1.5	57
21	EWAS Data Hub: a resource of DNA methylation array data and metadata. <i>Nucleic Acids Research</i> , 2020, 48, D890-D895.	6.5	57
22	Genome Variation Map: a data repository of genome variations in BIG Data Center. <i>Nucleic Acids Research</i> , 2018, 46, D944-D949.	6.5	53
23	MethBank 3.0: a database of DNA methylomes across a variety of species. <i>Nucleic Acids Research</i> , 2018, 46, D288-D295.	6.5	50
24	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	1.5	49
25	Genomic Perspectives on the Emerging SARS-CoV-2 Omicron Variant. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 60-69.	3.0	46
26	Population Genetics of SARS-CoV-2: Disentangling Effects of Sampling Bias and Infection Clusters. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 640-647.	3.0	44
27	Comparative Plastomics of Ashwagandha (<i>Withania, Solanaceae</i>) and Identification of Mutational Hotspots for Barcoding Medicinal Plants. <i>Plants</i> , 2020, 9, 752.	1.6	37
28	A novel negative-stranded RNA virus mediates sex ratio in its parasitoid host. <i>PLoS Pathogens</i> , 2017, 13, e1006201.	2.1	35
29	PAirwise Sequence Comparison (PASC) and Its Application in the Classification of Filoviruses. <i>Viruses</i> , 2012, 4, 1318-1327.	1.5	33
30	iDog: an integrated resource for domestic dogs and wild canids. <i>Nucleic Acids Research</i> , 2019, 47, D793-D800.	6.5	33
31	Implementation of Objective PASC-Derived Taxon Demarcation Criteria for Official Classification of Filoviruses. <i>Viruses</i> , 2017, 9, 106.	1.5	22
32	Historical Outbreaks of Simian Hemorrhagic Fever in Captive Macaques Were Caused by Distinct Arteriviruses. <i>Journal of Virology</i> , 2015, 89, 8082-8087.	1.5	21
33	Exposure to air pollution and scarlet fever resurgence in China: a six-year surveillance study. <i>Nature Communications</i> , 2020, 11, 4229.	5.8	20
34	Gene Expression Nebulas (GEN): a comprehensive data portal integrating transcriptomic profiles across multiple species at both bulk and single-cell levels. <i>Nucleic Acids Research</i> , 2022, 50, D1016-D1024.	6.5	18
35	The Elements of Data Sharing. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 1-4.	3.0	13
36	Ongoing Positive Selection Drives the Evolution of SARS-CoV-2 Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1214-1223.	3.0	9

#	ARTICLE	IF	CITATIONS
37	Genomic Epidemiology of SARS-CoV-2 in Pakistan. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 727-740.	3.0	8
38	Identification of COVID-19-Associated DNA Methylation Variations by Integrating Methylation Array and scRNA-Seq Data at Cell-Type Resolution. <i>Genes</i> , 2022, 13, 1109.	1.0	6
39	Multiresolution approaches to representation and visualization of large influenza virus sequence datasets. , 2007, , .		1
40	Preliminary Classification of Novel Hemorrhagic Fever-Causing Viruses Using Sequence-Based PAirwise Sequence Comparison (PASC) Analysis. <i>Methods in Molecular Biology</i> , 2018, 1604, 43-53.	0.4	1