

Yousong Peng

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,913
citations

394390

19
h-index

206102

48
g-index

54
all docs

54
docs citations

54
times ranked

5799
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Composition and Divergence of the Novel Coronavirus (2019-nCoV) Originating in China. <i>Cell Host and Microbe</i> , 2020, 27, 325-328.	11.0	1,860
2	Sequential Reassortments Underlie Diverse Influenza H7N9 Genotypes in China. <i>Cell Host and Microbe</i> , 2013, 14, 446-452.	11.0	141
3	Mapping of H3N2 influenza antigenic evolution in China reveals a strategy for vaccine strain recommendation. <i>Nature Communications</i> , 2012, 3, 709.	12.8	88
4	Nematode-Encoded RALF Peptide Mimics Facilitate Parasitism of Plants through the FERONIA Receptor Kinase. <i>Molecular Plant</i> , 2020, 13, 1434-1454.	8.3	67
5	Predicting the receptor-binding domain usage of the coronavirus based on kmer frequency on spike protein. <i>Infection, Genetics and Evolution</i> , 2018, 61, 183-184.	2.3	55
6	Prokaryotic virus host predictor: a Gaussian model for host prediction of prokaryotic viruses in metagenomics. <i>BMC Biology</i> , 2021, 19, 5.	3.8	50
7	A comprehensive surveillance of adamantane resistance among human influenza A virus isolated from mainland China between 1956 and 2009. <i>Antiviral Therapy</i> , 2010, 15, 853-860.	1.0	48
8	Antigenic Patterns and Evolution of the Human Influenza A (H1N1) Virus. <i>Scientific Reports</i> , 2015, 5, 14171.	3.3	47
9	Identification and characterization of circRNAs encoded by MERS-CoV, SARS-CoV-1 and SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, 1297-1308.	6.5	37
10	VirusCircBase: a database of virus circular RNAs. <i>Briefings in Bioinformatics</i> , 2021, 22, 2182-2190.	6.5	36
11	Microbiome Profiling Using Shotgun Metagenomic Sequencing Identified Unique Microorganisms in COVID-19 Patients With Altered Gut Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 712081.	3.5	35
12	New Insights into the Nonconserved Noncoding Region of the Subtype-Determinant Hemagglutinin and Neuraminidase Segments of Influenza A Viruses. <i>Journal of Virology</i> , 2014, 88, 11493-11503.	3.4	31
13	Cell membrane proteins with high N-glycosylation, high expression and multiple interaction partners are preferred by mammalian viruses as receptors. <i>Bioinformatics</i> , 2019, 35, 723-728.	4.1	31
14	Rapid identification of human-infecting viruses. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 2517-2522.	3.0	31
15	Homologous recombination shapes the genetic diversity of African swine fever viruses. <i>Veterinary Microbiology</i> , 2019, 236, 108380.	1.9	26
16	Compositional diversity and evolutionary pattern of coronavirus accessory proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, 1267-1278.	6.5	26
17	A universal computational model for predicting antigenic variants of influenza A virus based on conserved antigenic structures. <i>Scientific Reports</i> , 2017, 7, 42051.	3.3	22
18	Classification and characterization of multigene family proteins of African swine fever viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	22

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19	Correlation of Influenza Virus Excess Mortality with Antigenic Variation: Application to Rapid Estimation of Influenza Mortality Burden. <i>PLoS Computational Biology</i> , 2010, 6, e1000882.	3.2	21
20	Continual Antigenic Diversification in China Leads to Global Antigenic Complexity of Avian Influenza H5N1 Viruses. <i>Scientific Reports</i> , 2017, 7, 43566.	3.3	21
21	Predicting the host of influenza viruses based on the word vector. <i>PeerJ</i> , 2017, 5, e3579.	2.0	19
22	Network of co-mutations in Ebola virus genome predicts the disease lethality. <i>Cell Research</i> , 2015, 25, 753-756.	12.0	17
23	Inferring the antigenic epitopes for highly pathogenic avian influenza H5N1 viruses. <i>Vaccine</i> , 2014, 32, 671-676.	3.8	15
24	RAEdb: a database of enhancers identified by high-throughput reporter assays. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
25	Monitoring infectious diseases in the big data era. <i>Science Bulletin</i> , 2015, 60, 144-145.	9.0	13
26	Cluster-Transition Determining Sites Underlying the Antigenic Evolution of Seasonal Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2019, 36, 1172-1186.	8.9	13
27	Computed Tomography-Based Machine Learning Differentiates Adrenal Pheochromocytoma From Lipid-Poor Adenoma. <i>Frontiers in Endocrinology</i> , 2022, 13, 833413.	3.5	13
28	Phage protein receptors have multiple interaction partners and high expressions. <i>Bioinformatics</i> , 2020, 36, 2975-2979.	4.1	12
29	Prediction of the Receptorome for the Human-Infecting Virome. <i>Virologica Sinica</i> , 2021, 36, 133-140.	3.0	11
30	Prediction of antiviral drugs against African swine fever viruses based on protein-protein interaction analysis. <i>PeerJ</i> , 2020, 8, e8855.	2.0	11
31	Integrating computational modeling and functional assays to decipher the structure-function relationship of influenza virus PB1 protein. <i>Scientific Reports</i> , 2015, 4, 7192.	3.3	8
32	PREDAC-H5: A user-friendly tool for the automated surveillance of antigenic variants for the HPAI H5N1 virus. <i>Infection, Genetics and Evolution</i> , 2014, 28, 62-63.	2.3	7
33	Antigenic variation of the human influenza A (H3N2) virus during the 2014-2015 winter season. <i>Science China Life Sciences</i> , 2015, 58, 882-888.	4.9	7
34	FluPhenotype—a one-stop platform for early warnings of the influenza A virus. <i>Bioinformatics</i> , 2020, 36, 3251-3253.	4.1	7
35	Influenza A virus utilizes a suboptimal Kozak sequence to fine-tune virus replication and host response. <i>Journal of General Virology</i> , 2015, 96, 756-766.	2.9	6
36	An atlas of human viruses provides new insights into diversity and tissue tropism of human viruses. <i>Bioinformatics</i> , 2022, 38, 3087-3093.	4.1	6

#	ARTICLE	IF	CITATIONS
37	PREDAC-H3: a user-friendly platform for antigenic surveillance of human influenza a(H3N2) virus based on hemagglutinin sequences. <i>Bioinformatics</i> , 2016, 32, 2526-2527.	4.1	5
38	virusMED: an atlas of hotspots of viral proteins. <i>IUCr</i> , 2021, 8, 931-942.	2.2	5
39	Prediction of coronavirus 3C-like protease cleavage sites using machine-learning algorithms. <i>Virologica Sinica</i> , 2022, 37, 437-444.	3.0	5
40	cooccurNet: an R package for co-occurrence network construction and analysis. <i>Bioinformatics</i> , 2017, 33, 1881-1882.	4.1	4
41	Progress and Challenge in Computational Identification of Influenza Virus Reassortment. <i>Virologica Sinica</i> , 2021, 36, 1273-1283.	3.0	4
42	Identification of a Type-Specific Promoter Element That Differentiates between Influenza A and B Viruses. <i>Journal of Virology</i> , 2019, 93, .	3.4	3
43	Identification of genome-wide nucleotide sites associated with mammalian virulence in influenza A viruses. <i>Biosafety and Health</i> , 2020, 2, 32-38.	2.7	3
44	Computational Viromics: Applications of the Computational Biology in Viromics Studies. <i>Virologica Sinica</i> , 2021, 36, 1256-1260.	3.0	3
45	A comprehensive microsatellite landscape of human Y-DNA at kilobase resolution. <i>BMC Genomics</i> , 2021, 22, 76.	2.8	3
46	Large discrepancy between the two-way rNHT distances in hemagglutinin-inhibition assay. <i>Virologica Sinica</i> , 2016, 31, 441-443.	3.0	1
47	PREDAV-H1: a user-friendly web server for predicting antigenic variants of influenza H1N1 viruses. <i>Science China Life Sciences</i> , 2019, 62, 426-427.	4.9	1
48	Automated recommendation of the seasonal influenza vaccine strain with PREDAC. <i>Biosafety and Health</i> , 2020, 2, 117-119.	2.7	1
49	Web-Weka Meets D3.js in Web Based Medical Data Mining. , 2015, , .		0
50	Prediction of influenza epidemics at the province level in China using search query from "Haosou", 2015, , .		0
51	EVIHVR: A platform for analysis of expression, variation and identification of human virus receptors. , 2022, , .		0