Taijiao Jiang

List of Publications by Year
in descending order

93	5,261	218677	98798
papers	citations	26	67
		h-index	g-index

99	99	99	10734
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Host E3 ligase HUWE1 attenuates the proapoptotic activity of the MERS-CoV accessory protein ORF3 by promoting its ubiquitin-dependent degradation. Journal of Biological Chemistry, 2022, 298, 101584.	3.4	9
2	DSDatlas: disorders of sex development atlas for reproductive endocrinological-related gene discovery in integrative omics platforms. F&S Science, 2022, 3, 108-117.	0.9	1
3	An atlas of human viruses provides new insights into diversity and tissue tropism of human viruses. Bioinformatics, 2022, 38, 3087-3093.	4.1	6
4	PIAT: An Evolutionarily Intelligent System for Deep Phenotyping of Chinese Electronic Health Records. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 4142-4152.	6.3	1
5	Classification and characterization of multigene family proteins of African swine fever viruses. Briefings in Bioinformatics, 2021, 22, .	6.5	22
6	DeepSSV: detecting somatic small variants in paired tumor and normal sequencing data with convolutional neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	9
7	Prediction of the Receptorome for the Human-Infecting Virome. Virologica Sinica, 2021, 36, 133-140.	3.0	11
8	Identification and characterization of circRNAs encoded by MERS-CoV, SARS-CoV-1 and SARS-CoV-2. Briefings in Bioinformatics, 2021, 22, 1297-1308.	6.5	37
9	Compositional diversity and evolutionary pattern of coronavirus accessory proteins. Briefings in Bioinformatics, 2021, 22, 1267-1278.	6.5	26
10	SARSâ€CoVâ€2: Mechanism of infection and emerging technologies for future prospects. Reviews in Medical Virology, 2021, 31, e2168.	8.3	28
11	Prokaryotic virus host predictor: a Gaussian model for host prediction of prokaryotic viruses in metagenomics. BMC Biology, 2021, 19, 5.	3.8	50
12	Network-based methods for gene function prediction. Briefings in Functional Genomics, 2021, 20, 249-257.	2.7	13
13	Functional comparison of SARS-CoV-2 with closely related pangolin and bat coronaviruses. Cell Discovery, 2021, 7, 21.	6.7	20
14	One year of SARS-CoV-2 evolution. Cell Host and Microbe, 2021, 29, 503-507.	11.0	60
15	Epigallocatechin-3-gallate, an active ingredient of Traditional Chinese Medicines, inhibits the 3CLpro activity of SARS-CoV-2. International Journal of Biological Macromolecules, 2021, 176, 1-12.	7.5	77
16	Progress and Challenge in Computational Identification of Influenza Virus Reassortment. Virologica Sinica, 2021, 36, 1273-1283.	3.0	4
17	Constructing High-Fidelity Phenotype Knowledge Graphs for Infectious Diseases With a Fine-Grained Semantic Information Model: Development and Usability Study. Journal of Medical Internet Research, 2021, 23, e26892.	4.3	7
18	Co-mutation modules capture the evolution and transmission patterns of SARS-CoV-2. Briefings in Bioinformatics, 2021, 22, .	6.5	18

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19	Microbiome Profiling Using Shotgun Metagenomic Sequencing Identified Unique Microorganisms in COVID-19 Patients With Altered Gut Microbiota. Frontiers in Microbiology, 2021, 12, 712081.	3.5	35
20	*SNHG16* as the miRNA *let‑7b‑5p* sponge facilitates the G2/M and epithelial‑mesenchymal transition by regulating *CDC25B* and *HMGA2* expression in hepatocellular carcinoma. Journal of Cellular Biochemistry, 2020, 121, 2543-2558.	2.6	35
21	LATTE: A knowledge-based method to normalize various expressions of laboratory test results in free text of Chinese electronic health records. Journal of Biomedical Informatics, 2020, 102, 103372.	4.3	7
22	FluReassort: a database for the study of genomic reassortments among influenza viruses. Briefings in Bioinformatics, 2020, 21, 2126-2132.	6.5	9
23	Influenza activity during the outbreak of coronavirus disease 2019 in Chinese mainland. Biosafety and Health, 2020, 2, 206-209.	2.7	11
24	Comparative Transcriptome Analysis Reveals the Intensive Early Stage Responses of Host Cells to SARS-CoV-2 Infection. Frontiers in Microbiology, 2020, 11, 593857.	3.5	62
25	The evolution of zebrafish RAG2 protein is required for adapting to the elevated body temperature of the higher endothermic vertebrates. Scientific Reports, 2020, 10, 4126.	3.3	2
26	Identification of genome-wide nucleotide sites associated with mammalian virulence in influenza A viruses. Biosafety and Health, 2020, 2, 32-38.	2.7	3
27	Automated recommendation of the seasonal influenza vaccine strain with PREDAC. Biosafety and Health, 2020, 2, 117-119.	2.7	1
28	Phage protein receptors have multiple interaction partners and high expressions. Bioinformatics, 2020, 36, 2975-2979.	4.1	12
29	The deadly coronaviruses: The 2003 SARS pandemic and the 2020 novel coronavirus epidemic in China. Journal of Autoimmunity, 2020, 109, 102434.	6.5	704
30	FluPhenotype—a one-stop platform for early warnings of the influenza A virus. Bioinformatics, 2020, 36, 3251-3253.	4.1	7
31	Genome Composition and Divergence of the Novel Coronavirus (2019-nCoV) Originating in China. Cell Host and Microbe, 2020, 27, 325-328.	11.0	1,860
32	Clinical Pathway for Early Diagnosis of COVID-19: Updates from Experience to Evidence-Based Practice. Clinical Reviews in Allergy and Immunology, 2020, 59, 89-100.	6.5	59
33	Deamidation Shunts RelA from Mediating Inflammation to Aerobic Glycolysis. Cell Metabolism, 2020, 31, 937-955.e7.	16.2	19
34	Management and Treatment of COVID-19: The Chinese Experience. Canadian Journal of Cardiology, 2020, 36, 915-930.	1.7	147
35	Prediction of antiviral drugs against African swine fever viruses based on protein–protein interaction analysis. PeerJ, 2020, 8, e8855.	2.0	11
36	Cell membrane proteins with high N-glycosylation, high expression and multiple interaction partners are preferred by mammalian viruses as receptors. Bioinformatics, 2019, 35, 723-728.	4.1	31

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37	Regulation of Early Host Immune Responses Shapes the Pathogenicity of Avian Influenza A Virus. Frontiers in Microbiology, 2019, 10, 2007.	3.5	21
38	Homologous recombination shapes the genetic diversity of African swine fever viruses. Veterinary Microbiology, 2019, 236, 108380.	1.9	26
39	Single-Cell Transcriptome Analysis of Uniparental Embryos Reveals Parent-of-Origin Effects on Human Preimplantation Development. Cell Stem Cell, 2019, 25, 697-712.e6.	11.1	61
40	A Fast and Refined Cancer Regions Segmentation Framework in Whole-slide Breast Pathological Images. Scientific Reports, 2019, 9, 882.	3.3	55
41	Cluster-Transition Determining Sites Underlying the Antigenic Evolution of Seasonal Influenza Viruses. Molecular Biology and Evolution, 2019, 36, 1172-1186.	8.9	13
42	Protein interactome of the deamidase phosphoribosylformylglycinamidine synthetase (PFAS) by LC-MS/MS. Biochemical and Biophysical Research Communications, 2019, 513, 746-752.	2.1	10
43	PREDAV-H1: a user-friendly web server for predicting antigenic variants of influenza H1N1 viruses. Science China Life Sciences, 2019, 62, 426-427.	4.9	1
44	Predicting the receptor-binding domain usage of the coronavirus based on kmer frequency on spike protein. Infection, Genetics and Evolution, 2018, 61, 183-184.	2.3	55
45	Genome–wide RNA–Seq identifies *Fas*/*FasL*–mediated tumoricidal activity of embryonic stem cells. International Journal of Cancer, 2018, 142, 1829-1841.	5.1	5
46	Landscape of the genome and host cell response of *Mycobacterium shigaense* reveals pathogenic features. Emerging Microbes and Infections, 2018, 7, 1-13.	6.5	3
47	Heterosubtypic Protections against Human-Infecting Avian Influenza Viruses Correlate to Biased Cross-T-Cell Responses. MBio, 2018, 9, .	4.1	25
48	Trap1a is an X-linked and cell-intrinsic regulator of thymocyte development. Cellular and Molecular Immunology, 2017, 14, 685-692.	10.5	4
49	Inference of immune cell composition on the expression profiles of mouse tissue. Scientific Reports, 2017, 7, 40508.	3.3	132
50	Generation of a Live Attenuated Influenza Vaccine that Elicits Broad Protection in Mice and Ferrets. Cell Host and Microbe, 2017, 21, 334-343.	11.0	24
51	A universal computational model for predicting antigenic variants of influenza A virus based on conserved antigenic structures. Scientific Reports, 2017, 7, 42051.	3.3	22
52	Continual Antigenic Diversification in China Leads to Global Antigenic Complexity of Avian Influenza H5N1 Viruses. Scientific Reports, 2017, 7, 43566.	3.3	21
53	cooccurNet: an R package for co-occurrence network construction and analysis. Bioinformatics, 2017, 33, 1881-1882.	4.1	4
54	Screening for Novel Small-Molecule Inhibitors Targeting the Assembly of Influenza Virus Polymerase Complex by a Bimolecular Luminescence Complementation-Based Reporter System. Journal of Virology, 2017, 91, .	3.4	12

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55	Evolutionary genotypes of influenza A (H7N9) viruses over five epidemic waves in China. Infection, Genetics and Evolution, 2017, 55, 269-276.	2.3	21
56	Hydrogen Bond Variations of Influenza A Viruses During Adaptation in Human. Scientific Reports, 2017, 7, 14295.	3.3	3
57	Origin of the Reflectin Gene and Hierarchical Assembly of Its Protein. Current Biology, 2017, 27, 2833-2842.e6.	3.9	39
58	GAAP: Genome-organization-framework-Assisted Assembly Pipeline for prokaryotic genomes. BMC Genomics, 2017, 18, 952.	2.8	13
59	A population of innate myelolymphoblastoid effector cell expanded by inactivation of mTOR complex 1 in mice. ELife, 2017, 6, .	6.0	5
60	Plasma from patients with anti-glomerular basement membrane disease could recognize microbial peptides. PLoS ONE, 2017, 12, e0174553.	2.5	12
61	Predicting the host of influenza viruses based on the word vector. PeerJ, 2017, 5, e3579.	2.0	19
62	MetaDP: a comprehensive web server for disease prediction of 16S rRNA metagenomic datasets. Biophysics Reports, 2016, 2, 106-115.	0.8	9
63	From Mosquitos to Humans: Genetic Evolution of Zika Virus. Cell Host and Microbe, 2016, 19, 561-565.	11.0	199
64	PREDAC-H3: a user-friendly platform for antigenic surveillance of human influenza a(H3N2) virus based on hemagglutinin sequences. Bioinformatics, 2016, 32, 2526-2527.	4.1	5
65	Detection and typing of human-infecting influenza viruses in China by using a multiplex DNA biochip assay. Journal of Virological Methods, 2016, 234, 178-185.	2.1	8
66	Large discrepancy between the two-way rNHT distances in hemagglutinin-inhibition assay. Virologica Sinica, 2016, 31, 441-443.	3.0	1
67	A novel index of protein-protein interface propensity improves interface residue recognition. BMC Systems Biology, 2016, 10, 112.	3.0	18
68	EF4 disengages the peptidyl-tRNA CCA end and facilitates back-translocation on the 70S ribosome. Nature Structural and Molecular Biology, 2016, 23, 125-131.	8.2	21
69	Functional Genomics Reveals Linkers Critical for Influenza Virus Polymerase. Journal of Virology, 2016, 90, 2938-2947.	3.4	12
70	A magnetic protein biocompass. Nature Materials, 2016, 15, 217-226.	27.5	250
71	Integrating computational modeling and functional assays to decipher the structure-function relationship of influenza virus PB1 protein. Scientific Reports, 2015, 4, 7192.	3.3	8
72	Antigenic Patterns and Evolution of the Human Influenza A (H1N1) Virus. Scientific Reports, 2015, 5, 14171.	3.3	47

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73	Web-Weka Meets D3.js in Web Based Medical Data Mining. , 2015, , .		0
74	Recombinant Murine Gamma Herpesvirus 68 Carrying KSHV G Protein-Coupled Receptor Induces Angiogenic Lesions in Mice. PLoS Pathogens, 2015, 11, e1005001.	4.7	18
75	Network of co-mutations in Ebola virus genome predicts the disease lethality. Cell Research, 2015, 25, 753-756.	12.0	17
76	Prediction of influenza epidemics at the province level in China using search query from â€œHaosouâ€, 2015, , .		0
77	Monitoring infectious diseases in the big data era. Science Bulletin, 2015, 60, 144-145.	9.0	13
78	Human BDCA2+CD123+CD56+ dendritic cells (DCs) related to blastic plasmacytoid dendritic cell neoplasm represent a unique myeloid DC subset. Protein and Cell, 2015, 6, 297-306.	11.0	29
79	New targets for controlling Ebola virus disease. National Science Review, 2015, 2, 266-267.	9.5	3
80	Intracellular CD24 disrupts the ARFâ€"NPM interaction and enables mutational and viral oncogene-mediated p53 inactivation. Nature Communications, 2015, 6, 5909.	12.8	54
81	Antigenic variation of the human influenza A (H3N2) virus during the 2014â€"2015 winter season. Science China Life Sciences, 2015, 58, 882-888.	4.9	7
82	Analysis of interactions between SNARE proteins using imaging ellipsometer coupled with microfluidic array. Scientific Reports, 2014, 4, 5341.	3.3	10
83	PREDAC-H5: A user-friendly tool for the automated surveillance of antigenic variants for the HPAI H5N1 virus. Infection, Genetics and Evolution, 2014, 28, 62-63.	2.3	7
84	New Insights into the Nonconserved Noncoding Region of the Subtype-Determinant Hemagglutinin and Neuraminidase Segments of Influenza A Viruses. Journal of Virology, 2014, 88, 11493-11503.	3.4	31
85	Inferring the antigenic epitopes for highly pathogenic avian influenza H5N1 viruses. Vaccine, 2014, 32, 671-676.	3.8	15
86	Quantitative proteomics reveals ER-α involvement in CD146-induced epithelial-mesenchymal transition in breast cancer cells. Journal of Proteomics, 2014, 103, 153-169.	2.4	26
87	Exploring protein domain organization by recognition of secondary structure packing interfaces. Bioinformatics, 2014, 30, 2440-2446.	4.1	6
88	Improvement in Low-Homology Template-Based Modeling by Employing a Model Evaluation Method with Focus on Topology. PLoS ONE, 2014, 9, e89935.	2.5	10
89	Sequential Reassortments Underlie Diverse Influenza H7N9 Genotypes in China. Cell Host and Microbe, 2013, 14, 446-452.	11.0	141
90	Mapping of H3N2 influenza antigenic evolution in China reveals a strategy for vaccine strain recommendation. Nature Communications, 2012, 3, 709.	12.8	88

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91	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. Bioinformatics, 2011, 27, 785-790.	4.1	52
92	Networks of genomic co-occurrence capture characteristics of human influenza A (H3N2) evolution. Genome Research, 2008, 18, 178-187.	5.5	44
93	Mapping Genetic Events of SARS-CoV-2 Variants. Frontiers in Microbiology, 0, 13, .	3.5	4