

Taijiao Jiang

List of Publications by Year in descending order

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93
papers

5,261
citations

249298

26
h-index

111975

67
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99
all docs

99
docs citations

99
times ranked

11581
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.	5.1	1,860
2	The deadly coronaviruses: The 2003 SARS pandemic and the 2020 novel coronavirus epidemic in China. <i>Journal of Autoimmunity</i> , 2020, 109, 102434.	3.0	704
3	A magnetic protein biocompass. <i>Nature Materials</i> , 2016, 15, 217-226.	13.3	250
4	From Mosquitos to Humans: Genetic Evolution of Zika Virus. <i>Cell Host and Microbe</i> , 2016, 19, 561-565.	5.1	199
5	Management and Treatment of COVID-19: The Chinese Experience. <i>Canadian Journal of Cardiology</i> , 2020, 36, 915-930.	0.8	147
6	Sequential Reassortments Underlie Diverse Influenza H7N9 Genotypes in China. <i>Cell Host and Microbe</i> , 2013, 14, 446-452.	5.1	141
7	Inference of immune cell composition on the expression profiles of mouse tissue. <i>Scientific Reports</i> , 2017, 7, 40508.	1.6	132
8	Mapping of H3N2 influenza antigenic evolution in China reveals a strategy for vaccine strain recommendation. <i>Nature Communications</i> , 2012, 3, 709.	5.8	88
9	Epigallocatechin-3-gallate, an active ingredient of Traditional Chinese Medicines, inhibits the 3CLpro activity of SARS-CoV-2. <i>International Journal of Biological Macromolecules</i> , 2021, 176, 1-12.	3.6	77
10	Comparative Transcriptome Analysis Reveals the Intensive Early Stage Responses of Host Cells to SARS-CoV-2 Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 593857.	1.5	62
11	Single-Cell Transcriptome Analysis of Uniparental Embryos Reveals Parent-of-Origin Effects on Human Preimplantation Development. <i>Cell Stem Cell</i> , 2019, 25, 697-712.e6.	5.2	61
12	One year of SARS-CoV-2 evolution. <i>Cell Host and Microbe</i> , 2021, 29, 503-507.	5.1	60
13	Clinical Pathway for Early Diagnosis of COVID-19: Updates from Experience to Evidence-Based Practice. <i>Clinical Reviews in Allergy and Immunology</i> , 2020, 59, 89-100.	2.9	59
14	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.	1.0	55
15	A Fast and Refined Cancer Regions Segmentation Framework in Whole-slide Breast Pathological Images. <i>Scientific Reports</i> , 2019, 9, 882.	1.6	55
16	Intracellular CD24 disrupts the ARF-NPM interaction and enables mutational and viral oncogene-mediated p53 inactivation. <i>Nature Communications</i> , 2015, 6, 5909.	5.8	54
17	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. <i>Bioinformatics</i> , 2011, 27, 785-790.	1.8	52
18	Prokaryotic virus host predictor: a Gaussian model for host prediction of prokaryotic viruses in metagenomics. <i>BMC Biology</i> , 2021, 19, 5.	1.7	50

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19	Antigenic Patterns and Evolution of the Human Influenza A (H1N1) Virus. <i>Scientific Reports</i> , 2015, 5, 14171.	1.6	47
20	Networks of genomic co-occurrence capture characteristics of human influenza A (H3N2) evolution. <i>Genome Research</i> , 2008, 18, 178-187.	2.4	44
21	Origin of the Reflectin Gene and Hierarchical Assembly of Its Protein. <i>Current Biology</i> , 2017, 27, 2833-2842.e6.	1.8	39
22	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.	3.2	37
23	<i>SNHG16</i> as the miRNA <i>let-7b-5p</i> sponge facilitates the G2/M and epithelial-mesenchymal transition by regulating <i>CDC25B</i> and <i>HMGA2</i> expression in hepatocellular carcinoma. <i>Journal of Cellular Biochemistry</i> , 2020, 121, 2543-2558.	1.2	35
24	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.	1.5	35
25	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.	1.5	31
26	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.	1.8	31
27	Human BDCA2+CD123+CD56+ dendritic cells (DCs) related to blastic plasmacytoid dendritic cell neoplasm represent a unique myeloid DC subset. <i>Protein and Cell</i> , 2015, 6, 297-306.	4.8	29
28	SARS-CoV-2: Mechanism of infection and emerging technologies for future prospects. <i>Reviews in Medical Virology</i> , 2021, 31, e2168.	3.9	28
29	Quantitative proteomics reveals ER \pm involvement in CD146-induced epithelial-mesenchymal transition in breast cancer cells. <i>Journal of Proteomics</i> , 2014, 103, 153-169.	1.2	26
30	Homologous recombination shapes the genetic diversity of African swine fever viruses. <i>Veterinary Microbiology</i> , 2019, 236, 108380.	0.8	26
31	Compositional diversity and evolutionary pattern of coronavirus accessory proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, 1267-1278.	3.2	26
32	Heterosubtypic Protections against Human-Infecting Avian Influenza Viruses Correlate to Biased Cross-T-Cell Responses. <i>MBio</i> , 2018, 9, .	1.8	25
33	Generation of a Live Attenuated Influenza Vaccine that Elicits Broad Protection in Mice and Ferrets. <i>Cell Host and Microbe</i> , 2017, 21, 334-343.	5.1	24
34	A universal computational model for predicting antigenic variants of influenza A virus based on conserved antigenic structures. <i>Scientific Reports</i> , 2017, 7, 42051.	1.6	22
35	Classification and characterization of multigene family proteins of African swine fever viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	22
36	EF4 disengages the peptidyl-tRNA CCA end and facilitates back-translocation on the 70S ribosome. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 125-131.	3.6	21

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37	Continual Antigenic Diversification in China Leads to Global Antigenic Complexity of Avian Influenza H5N1 Viruses. <i>Scientific Reports</i> , 2017, 7, 43566.	1.6	21
38	Evolutionary genotypes of influenza A (H7N9) viruses over five epidemic waves in China. <i>Infection, Genetics and Evolution</i> , 2017, 55, 269-276.	1.0	21
39	Regulation of Early Host Immune Responses Shapes the Pathogenicity of Avian Influenza A Virus. <i>Frontiers in Microbiology</i> , 2019, 10, 2007.	1.5	21
40	Functional comparison of SARS-CoV-2 with closely related pangolin and bat coronaviruses. <i>Cell Discovery</i> , 2021, 7, 21.	3.1	20
41	Deamidation Shunts RelA from Mediating Inflammation to Aerobic Glycolysis. <i>Cell Metabolism</i> , 2020, 31, 937-955.e7.	7.2	19
42	Predicting the host of influenza viruses based on the word vector. <i>PeerJ</i> , 2017, 5, e3579.	0.9	19
43	Recombinant Murine Gamma Herpesvirus 68 Carrying KSHV G Protein-Coupled Receptor Induces Angiogenic Lesions in Mice. <i>PLoS Pathogens</i> , 2015, 11, e1005001.	2.1	18
44	A novel index of protein-protein interface propensity improves interface residue recognition. <i>BMC Systems Biology</i> , 2016, 10, 112.	3.0	18
45	Co-mutation modules capture the evolution and transmission patterns of SARS-CoV-2. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	18
46	Network of co-mutations in Ebola virus genome predicts the disease lethality. <i>Cell Research</i> , 2015, 25, 753-756.	5.7	17
47	Inferring the antigenic epitopes for highly pathogenic avian influenza H5N1 viruses. <i>Vaccine</i> , 2014, 32, 671-676.	1.7	15
48	Monitoring infectious diseases in the big data era. <i>Science Bulletin</i> , 2015, 60, 144-145.	4.3	13
49	GAAP: Genome-organization-framework-Assisted Assembly Pipeline for prokaryotic genomes. <i>BMC Genomics</i> , 2017, 18, 952.	1.2	13
50	Cluster-Transition Determining Sites Underlying the Antigenic Evolution of Seasonal Influenza Viruses. <i>Molecular Biology and Evolution</i> , 2019, 36, 1172-1186.	3.5	13
51	Network-based methods for gene function prediction. <i>Briefings in Functional Genomics</i> , 2021, 20, 249-257.	1.3	13
52	Functional Genomics Reveals Linkers Critical for Influenza Virus Polymerase. <i>Journal of Virology</i> , 2016, 90, 2938-2947.	1.5	12
53	Screening for Novel Small-Molecule Inhibitors Targeting the Assembly of Influenza Virus Polymerase Complex by a Bimolecular Luminescence Complementation-Based Reporter System. <i>Journal of Virology</i> , 2017, 91, .	1.5	12
54	Plasma from patients with anti-glomerular basement membrane disease could recognize microbial peptides. <i>PLoS ONE</i> , 2017, 12, e0174553.	1.1	12

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55	Phage protein receptors have multiple interaction partners and high expressions. <i>Bioinformatics</i> , 2020, 36, 2975-2979.	1.8	12
56	Influenza activity during the outbreak of coronavirus disease 2019 in Chinese mainland. <i>Biosafety and Health</i> , 2020, 2, 206-209.	1.2	11
57	Prediction of the Receptorome for the Human-Infecting Virome. <i>Virologica Sinica</i> , 2021, 36, 133-140.	1.2	11
58	Prediction of antiviral drugs against African swine fever viruses based on protein-protein interaction analysis. <i>PeerJ</i> , 2020, 8, e8855.	0.9	11
59	Analysis of interactions between SNARE proteins using imaging ellipsometer coupled with microfluidic array. <i>Scientific Reports</i> , 2014, 4, 5341.	1.6	10
60	Protein interactome of the deamidase phosphoribosylformylglycinamide synthetase (PFAS) by LC-MS/MS. <i>Biochemical and Biophysical Research Communications</i> , 2019, 513, 746-752.	1.0	10
61	Improvement in Low-Homology Template-Based Modeling by Employing a Model Evaluation Method with Focus on Topology. <i>PLoS ONE</i> , 2014, 9, e89935.	1.1	10
62	MetaDP: a comprehensive web server for disease prediction of 16S rRNA metagenomic datasets. <i>Biophysics Reports</i> , 2016, 2, 106-115.	0.2	9
63	FluReassort: a database for the study of genomic reassortments among influenza viruses. <i>Briefings in Bioinformatics</i> , 2020, 21, 2126-2132.	3.2	9
64	DeepSSV: detecting somatic small variants in paired tumor and normal sequencing data with convolutional neural network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
65	Host E3 ligase HUWE1 attenuates the proapoptotic activity of the MERS-CoV accessory protein ORF3 by promoting its ubiquitin-dependent degradation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101584.	1.6	9
66	Integrating computational modeling and functional assays to decipher the structure-function relationship of influenza virus PB1 protein. <i>Scientific Reports</i> , 2015, 4, 7192.	1.6	8
67	Detection and typing of human-infecting influenza viruses in China by using a multiplex DNA biochip assay. <i>Journal of Virological Methods</i> , 2016, 234, 178-185.	1.0	8
68	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.	1.0	7
69	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.	2.3	7
70	LATTE: A knowledge-based method to normalize various expressions of laboratory test results in free text of Chinese electronic health records. <i>Journal of Biomedical Informatics</i> , 2020, 102, 103372.	2.5	7
71	FluPhenotype—a one-stop platform for early warnings of the influenza A virus. <i>Bioinformatics</i> , 2020, 36, 3251-3253.	1.8	7
72	Constructing High-Fidelity Phenotype Knowledge Graphs for Infectious Diseases With a Fine-Grained Semantic Information Model: Development and Usability Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e26892.	2.1	7

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73	Exploring protein domain organization by recognition of secondary structure packing interfaces. <i>Bioinformatics</i> , 2014, 30, 2440-2446.	1.8	6
74	An atlas of human viruses provides new insights into diversity and tissue tropism of human viruses. <i>Bioinformatics</i> , 2022, 38, 3087-3093.	1.8	6
75	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.	1.8	5
76	A population of innate myelolymphoblastoid effector cell expanded by inactivation of mTOR complex 1 in mice. <i>ELife</i> , 2017, 6, .	2.8	5
77	Genome-wide RNA-seq identifies Fas-mediated tumoricidal activity of embryonic stem cells. <i>International Journal of Cancer</i> , 2018, 142, 1829-1841.	2.3	5
78	Trap1a is an X-linked and cell-intrinsic regulator of thymocyte development. <i>Cellular and Molecular Immunology</i> , 2017, 14, 685-692.	4.8	4
79	cooccurNet: an R package for co-occurrence network construction and analysis. <i>Bioinformatics</i> , 2017, 33, 1881-1882.	1.8	4
80	Progress and Challenge in Computational Identification of Influenza Virus Reassortment. <i>Virologica Sinica</i> , 2021, 36, 1273-1283.	1.2	4
81	Mapping Genetic Events of SARS-CoV-2 Variants. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
82	New targets for controlling Ebola virus disease. <i>National Science Review</i> , 2015, 2, 266-267.	4.6	3
83	Hydrogen Bond Variations of Influenza A Viruses During Adaptation in Human. <i>Scientific Reports</i> , 2017, 7, 14295.	1.6	3
84	Landscape of the genome and host cell response of <i>Mycobacterium shigaense</i> reveals pathogenic features. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	3.0	3
85	Identification of genome-wide nucleotide sites associated with mammalian virulence in influenza A viruses. <i>Biosafety and Health</i> , 2020, 2, 32-38.	1.2	3
86	The evolution of zebrafish RAG2 protein is required for adapting to the elevated body temperature of the higher endothermic vertebrates. <i>Scientific Reports</i> , 2020, 10, 4126.	1.6	2
87	Large discrepancy between the two-way rNHT distances in hemagglutinin-inhibition assay. <i>Virologica Sinica</i> , 2016, 31, 441-443.	1.2	1
88	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.	2.3	1
89	Automated recommendation of the seasonal influenza vaccine strain with PREDAC. <i>Biosafety and Health</i> , 2020, 2, 117-119.	1.2	1
90	DSDatlas: disorders of sex development atlas for reproductive endocrinological-related gene discovery in integrative omics platforms. <i>F&S Science</i> , 2022, 3, 108-117.	0.5	1

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91	PIAT: An Evolutionarily Intelligent System for Deep Phenotyping of Chinese Electronic Health Records. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 4142-4152.	3.9	1
92	Web-Weka Meets D3.js in Web Based Medical Data Mining. , 2015, , .		0
93	Prediction of influenza epidemics at the province level in China using search query from "Haosou", 2015, , .		0