

# Aiping Wu

## List of Publications by Year in descending order

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53  
papers

3,425  
citations

394286

19  
h-index

168321

53  
g-index

54  
all docs

54  
docs citations

54  
times ranked

7507  
citing authors

#	ARTICLE	IF	CITATIONS
1	Conserved Pattern and Potential Role of Recurrent Deletions in SARS-CoV-2 Evolution. <i>Microbiology Spectrum</i> , 2022, 10, e0219121.	1.2	9
2	Detecting Potentially Adaptive Mutations from the Parallel and Fixed Patterns in SARS-CoV-2 Evolution. <i>Viruses</i> , 2022, 14, 1087.	1.5	4
3	SARS-CoV-2 Continuous Genetic Divergence and Changes in Multiplex RT-PCR Detection Pattern on Positive Retesting Median 150 Days after Initial Infection. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6254.	1.8	1
4	Prediction of the Receptorome for the Human-Infecting Virome. <i>Virologica Sinica</i> , 2021, 36, 133-140.	1.2	11
5	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
6	Compositional diversity and evolutionary pattern of coronavirus accessory proteins. <i>Briefings in Bioinformatics</i> , 2021, 22, 1267-1278.	3.2	26
7	The m6A methylome of SARS-CoV-2 in host cells. <i>Cell Research</i> , 2021, 31, 404-414.	5.7	95
8	Convergent evolution of SARS-CoV-2 in human and animals. <i>Protein and Cell</i> , 2021, 12, 832-835.	4.8	15
9	One year of SARS-CoV-2 evolution. <i>Cell Host and Microbe</i> , 2021, 29, 503-507.	5.1	60
10	Progress and Challenge in Computational Identification of Influenza Virus Reassortment. <i>Virologica Sinica</i> , 2021, 36, 1273-1283.	1.2	4
11	Transcriptome Analysis Reveals the Molecular Immunological Characteristics of Lesions in Patients with Halo Nevi When Compared to Stable Vitiligo, Normal Nevocytic Nevi and Cutaneous Melanoma. <i>Journal of Inflammation Research</i> , 2021, Volume 14, 4111-4124.	1.6	2
12	ImmuCellDB: An Indicative Database of Immune Cell Composition From Different Tissues and Disease Conditions in Mouse and Human. <i>Frontiers in Immunology</i> , 2021, 12, 670070.	2.2	2
13	Progress and challenge for computational quantification of tissue immune cells. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	9
14	Tissue-specific deconvolution of immune cell composition by integrating bulk and single-cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 819-827.	1.8	13
15	Identification of dynamic signatures associated with smoking-related squamous cell lung cancer and chronic obstructive pulmonary disease. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 1614-1625.	1.6	12
16	FluReassort: a database for the study of genomic reassortments among influenza viruses. <i>Briefings in Bioinformatics</i> , 2020, 21, 2126-2132.	3.2	9
17	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
18	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

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19	Automated recommendation of the seasonal influenza vaccine strain with PREDAC. <i>Biosafety and Health</i> , 2020, 2, 117-119.	1.2	1
20	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
21	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
22	Molecular surveillance of antimicrobial resistance and transmission pattern of <i>Mycobacterium leprae</i> in Chinese leprosy patients. <i>Emerging Microbes and Infections</i> , 2019, 8, 1479-1489.	3.0	16
23	Identification of Bridging Centrality in Complex Networks. <i>IEEE Access</i> , 2019, 7, 93123-93130.	2.6	14
24	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
25	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
26	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
27	Viral diseases meet omics: Time for systems virology. <i>Science China Life Sciences</i> , 2018, 61, 1274-1276.	2.3	1
28	seq-ImmuCC: Cell-Centric View of Tissue Transcriptome Measuring Cellular Compositions of Immune Microenvironment From Mouse RNA-Seq Data. <i>Frontiers in Immunology</i> , 2018, 9, 1286.	2.2	75
29	Inference of immune cell composition on the expression profiles of mouse tissue. <i>Scientific Reports</i> , 2017, 7, 40508.	1.6	132
30	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
31	cooccurNet: an R package for co-occurrence network construction and analysis. <i>Bioinformatics</i> , 2017, 33, 1881-1882.	1.8	4
32	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
33	Hydrogen Bond Variations of Influenza A Viruses During Adaptation in Human. <i>Scientific Reports</i> , 2017, 7, 14295.	1.6	3
34	From Mosquitos to Humans: Genetic Evolution of Zika Virus. <i>Cell Host and Microbe</i> , 2016, 19, 561-565.	5.1	199
35	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
36	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

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37	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
38	Antigenic Patterns and Evolution of the Human Influenza A (H1N1) Virus. <i>Scientific Reports</i> , 2015, 5, 14171.	1.6	47
39	Network of co-mutations in Ebola virus genome predicts the disease lethality. <i>Cell Research</i> , 2015, 25, 753-756.	5.7	17
40	Positive Feedback Regulation of Type I IFN Production by the IFN-Inducible DNA Sensor cGAS. <i>Journal of Immunology</i> , 2015, 194, 1545-1554.	0.4	141
41	Computational analysis of antigenic epitopes of avian influenza A (H7N9) viruses. <i>Science China Life Sciences</i> , 2015, 58, 687-693.	2.3	15
42	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
43	Coevolution signals capture the specific packing of secondary structures in protein architecture. <i>Protein and Cell</i> , 2014, 5, 480-483.	4.8	1
44	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
45	Sequential Reassortments Underlie Diverse Influenza H7N9 Genotypes in China. <i>Cell Host and Microbe</i> , 2013, 14, 446-452.	5.1	141
46	A peptide derived from the C-terminus of PB1 inhibits influenza virus replication by interfering with viral polymerase assembly. <i>FEBS Journal</i> , 2013, 280, 1139-1149.	2.2	29
47	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
48	Incorporation of Local Structural Preference Potential Improves Fold Recognition. <i>PLoS ONE</i> , 2011, 6, e17215.	1.1	13
49	Rapid Estimation of Binding Activity of Influenza Virus Hemagglutinin to Human and Avian Receptors. <i>PLoS ONE</i> , 2011, 6, e18664.	1.1	13
50	NCACO-score: An effective main-chain dependent scoring function for structure modeling. <i>BMC Bioinformatics</i> , 2011, 12, 208.	1.2	4
51	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.	1.5	21
52	Length-dependent regulation of the Kv1.2 channel activation by its C-terminus. <i>Molecular Membrane Biology</i> , 2009, 26, 186-193.	2.0	6
53	Networks of genomic co-occurrence capture characteristics of human influenza A (H3N2) evolution. <i>Genome Research</i> , 2008, 18, 178-187.	2.4	44