

Qihui Wang

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

9,506
citations

136740

32
h-index

102304

66
g-index

71
all docs

71
docs citations

71
times ranked

15495
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and Functional Basis of SARS-CoV-2 Entry by Using Human ACE2. <i>Cell</i> , 2020, 181, 894-904.e9.	13.5	2,443
2	A human neutralizing antibody targets the receptor-binding site of SARS-CoV-2. <i>Nature</i> , 2020, 584, 120-124.	13.7	1,237
3	A noncompeting pair of human neutralizing antibodies block COVID-19 virus binding to its receptor ACE2. <i>Science</i> , 2020, 368, 1274-1278.	6.0	964
4	Cryo-EM structures of MERS-CoV and SARS-CoV spike glycoproteins reveal the dynamic receptor binding domains. <i>Nature Communications</i> , 2017, 8, 15092.	5.8	649
5	Molecular basis of binding between novel human coronavirus MERS-CoV and its receptor CD26. <i>Nature</i> , 2013, 500, 227-231.	13.7	582
6	Bat-to-human: spike features determining "host jump"™ of coronaviruses SARS-CoV, MERS-CoV, and beyond. <i>Trends in Microbiology</i> , 2015, 23, 468-478.	3.5	521
7	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. <i>Cell</i> , 2021, 184, 4380-4391.e14.	13.5	261
8	Bat Origins of MERS-CoV Supported by Bat Coronavirus HKU4's Usage of Human Receptor CD26. <i>Cell Host and Microbe</i> , 2014, 16, 328-337.	5.1	252
9	Molecular determinants of human neutralizing antibodies isolated from a patient infected with Zika virus. <i>Science Translational Medicine</i> , 2016, 8, 369ra179.	5.8	194
10	An unexpected N-terminal loop in PD-1 dominates binding by nivolumab. <i>Nature Communications</i> , 2017, 8, 14369.	5.8	192
11	Structure of the Fusion Core and Inhibition of Fusion by a Heptad Repeat Peptide Derived from the S Protein of Middle East Respiratory Syndrome Coronavirus. <i>Journal of Virology</i> , 2013, 87, 13134-13140.	1.5	144
12	A humanized neutralizing antibody against MERS-CoV targeting the receptor-binding domain of the spike protein. <i>Cell Research</i> , 2015, 25, 1237-1249.	5.7	137
13	Broad host range of SARS-CoV-2 and the molecular basis for SARS-CoV-2 binding to cat ACE2. <i>Cell Discovery</i> , 2020, 6, 68.	3.1	132
14	Molecular insights into receptor binding of recent emerging SARS-CoV-2 variants. <i>Nature Communications</i> , 2021, 12, 6103.	5.8	117
15	CD8 ⁺ T Cell Immune Response in Immunocompetent Mice during Zika Virus Infection. <i>Journal of Virology</i> , 2017, 91, .	1.5	102
16	Binding and molecular basis of the bat coronavirus RaTG13 virus to ACE2 in humans and other species. <i>Cell</i> , 2021, 184, 3438-3451.e10.	13.5	100
17	MERS-CoV spike protein: Targets for vaccines and therapeutics. <i>Antiviral Research</i> , 2016, 133, 165-177.	1.9	94
18	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. <i>PLoS Pathogens</i> , 2016, 12, e1005883.	2.1	92

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19	Cross-species recognition of SARS-CoV-2 to bat ACE2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	73
20	Recombinant Chimpanzee Adenovirus Vaccine AdC7-M/E Protects against Zika Virus Infection and Testis Damage. Journal of Virology, 2018, 92, .	1.5	72
21	A motif in LILRB2 critical for Angptl2 binding and activation. Blood, 2014, 124, 924-935.	0.6	68
22	A single-dose mRNA vaccine provides a long-term protection for hACE2 transgenic mice from SARS-CoV-2. Nature Communications, 2021, 12, 776.	5.8	65
23	Atlas of currently available human neutralizing antibodies against SARS-CoV-2 and escape by Omicron sub-variants BA.1/BA.1.1/BA.2/BA.3. Immunity, 2022, 55, 1501-1514.e3.	6.6	59
24	Molecular basis of cross-species ACE2 interactions with SARS-CoV-2-like viruses of pangolin origin. EMBO Journal, 2021, 40, e107786.	3.5	46
25	Genomic Perspectives on the Emerging SARS-CoV-2 Omicron Variant. Genomics, Proteomics and Bioinformatics, 2022, 20, 60-69.	3.0	46
26	Neutralisation of ZF2001-elicited antisera to SARS-CoV-2 variants. Lancet Microbe, The, 2021, 2, e494.	3.4	45
27	The molecular basis for SARS-CoV-2 binding to dog ACE2. Nature Communications, 2021, 12, 4195.	5.8	43
28	Molecular basis of antibody-mediated neutralization and protection against flavivirus. IUBMB Life, 2016, 68, 783-791.	1.5	42
29	Protective T Cell Responses Featured by Concordant Recognition of Middle East Respiratory Syndrome Coronavirus-Derived CD8+ T Cell Epitopes and Host MHC. Journal of Immunology, 2017, 198, 873-882.	0.4	42
30	Neutralization mechanism of human monoclonal antibodies against Rift Valley fever virus. Nature Microbiology, 2019, 4, 1231-1241.	5.9	39
31	Transcriptome profiling in swine macrophages infected with African swine fever virus at single-cell resolution. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2201288119.	3.3	39
32	Structures of the four- β -like domain LILRB2 and the four-domain LILRB1 and HLA-G1 complex. Cellular and Molecular Immunology, 2020, 17, 966-975.	4.8	38
33	The mysterious origins of the Omicron variant of SARS-CoV-2. Innovation(China), 2022, 3, 100206.	5.2	38
34	Monoclonal Antibodies against Zika Virus: Therapeutics and Their Implications for Vaccine Design. Journal of Virology, 2017, 91, .	1.5	36
35	Vertical Transmission of the Zika Virus Causes Neurological Disorders in Mouse Offspring. Scientific Reports, 2018, 8, 3541.	1.6	36
36	Limited Cross-Linking of 4-1BB by 4-1BB Ligand and the Agonist Monoclonal Antibody Utomilumab. Cell Reports, 2018, 25, 909-920.e4.	2.9	33

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37	Lentil lectin derived from <i>Lens culinaris</i> exhibit broad antiviral activities against SARS-CoV-2 variants. <i>Emerging Microbes and Infections</i> , 2021, 10, 1519-1529.	3.0	30
38	The identification of a CD47-blocking "hotspot" and design of a CD47/PD-L1 dual-specific antibody with limited hemagglutination. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 16.	7.1	29
39	Structural basis of HCoV-19 fusion core and an effective inhibition peptide against virus entry. <i>Emerging Microbes and Infections</i> , 2020, 9, 1238-1241.	3.0	26
40	PILRÎ± and PILRÎ² have a siglec fold and provide the basis of binding to sialic acid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8221-8226.	3.3	25
41	Tracing the origins of SARS-CoV-2: lessons learned from the past. <i>Cell Research</i> , 2021, 31, 1139-1141.	5.7	25
42	Protective Zika vaccines engineered to eliminate enhancement of dengue infection via immunodominance switch. <i>Nature Immunology</i> , 2021, 22, 958-968.	7.0	23
43	Broader-species receptor binding and structural bases of Omicron SARS-CoV-2 to both mouse and palm-civet ACE2s. <i>Cell Discovery</i> , 2022, 8, .	3.1	23
44	Putative Receptor Binding Domain of Bat-Derived Coronavirus HKU9 Spike Protein: Evolution of Betacoronavirus Receptor Binding Motifs. <i>Biochemistry</i> , 2016, 55, 5977-5988.	1.2	22
45	On the origin of SARS-CoV-2â€”The blind watchmaker argument. <i>Science China Life Sciences</i> , 2021, 64, 1560-1563.	2.3	18
46	VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. <i>Nucleic Acids Research</i> , 2022, 50, D888-D897.	6.5	18
47	Molecular Basis of Binding between Middle East Respiratory Syndrome Coronavirus and CD26 from Seven Bat Species. <i>Journal of Virology</i> , 2020, 94, .	1.5	16
48	Binding and structural basis of equine ACE2 to RBDs from SARS-CoV, SARS-CoV-2 and related coronaviruses. <i>Nature Communications</i> , 2022, 13, .	5.8	16
49	Crystal structures of the two membrane-proximal Ig-like domains (D3D4) of LILRB1/B2: alternative models for their involvement in peptide-HLA binding. <i>Protein and Cell</i> , 2013, 4, 761-770.	4.8	14
50	Structure of the S1 subunit C-terminal domain from bat-derived coronavirus HKU5 spike protein. <i>Virology</i> , 2017, 507, 101-109.	1.1	13
51	HBxâ€”upregulated MAFCâ€”AS1 promotes cell proliferation and migration of hepatoma cells by enhancing MAFG expression and stabilizing nonmuscle myosin IIA. <i>FASEB Journal</i> , 2021, 35, e21529.	0.2	13
52	The origins of viruses: discovery takes time, international resources, and cooperation. <i>Lancet</i> , The, 2021, 398, 1401-1402.	6.3	12
53	Zika Virus Envelope Protein and Antibody Complexes. <i>Sub-Cellular Biochemistry</i> , 2018, 88, 147-168.	1.0	10
54	Zika virus induces myocardial immune response and myocarditis in mice. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 148, 103-105.	0.9	10

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55	Cross-species recognition and molecular basis of SARS-CoV-2 and SARS-CoV binding to ACE2s of marine animals. <i>National Science Review</i> , 2022, 9, .	4.6	10
56	The antigenicity of SARS-CoV-2 Delta variants aggregated 10 high-frequency mutations in RBD has not changed sufficiently to replace the current vaccine strain. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 18.	7.1	9
57	Molecular basis of pangolin ACE2 engaged by COVID-19 virus. <i>Chinese Science Bulletin</i> , 2021, 66, 73-84.	0.4	8
58	A binding-enhanced but enzymatic activity-eliminated human ACE2 efficiently neutralizes SARS-CoV-2 variants. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 10.	7.1	8
59	Both structure and function of human monoclonal antibodies contribute to enhancement of Zika virus infectivity in vitro. <i>Science China Life Sciences</i> , 2017, 60, 1396-1398.	2.3	6
60	Aggregation of high-frequency RBD mutations of SARS-CoV-2 with three VOCs did not cause significant antigenic drift. <i>Journal of Medical Virology</i> , 2022, , .	2.5	5
61	CRISPR-Based Genetic Switches and Other Complex Circuits: Research and Application. <i>Life</i> , 2021, 11, 1255.	1.1	5
62	The crystal structure of the emerging human-infecting hepatitis E virus E2s protein. <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 25-31.	1.0	3
63	Machine Learning Approach Effectively Predicts Binding Between SARS-CoV-2 Spike and ACE2 Across Mammalian Species " Worldwide, 2021. <i>China CDC Weekly</i> , 2021, 3, 967-972.	1.0	2
64	Isolation of Monoclonal Antibodies from Zika Virus-Infected Patient Samples. <i>Methods in Molecular Biology</i> , 2020, 2142, 261-288.	0.4	1
65	Pinpointing the animal origins of SARS-CoV-2: a genomic approach. <i>Journal of Genetics and Genomics</i> , 2022, 49, 900-902.	1.7	1