

Qihui Wang

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

6,098

citations

25

h-index

71

g-index

71

ext. papers

8,006

ext. citations

15.9

avg, IF

5.99

L-index

#	Paper	IF	Citations
62	Structural and Functional Basis of SARS-CoV-2 Entry by Using Human ACE2. <i>Cell</i> , 2020 , 181, 894-904.e9	56.2	1513
61	A human neutralizing antibody targets the receptor-binding site of SARS-CoV-2. <i>Nature</i> , 2020 , 584, 120-124	57.4	844
60	A noncompeting pair of human neutralizing antibodies block COVID-19 virus binding to its receptor ACE2. <i>Science</i> , 2020 , 368, 1274-1278	33.3	682
59	Cryo-EM structures of MERS-CoV and SARS-CoV spike glycoproteins reveal the dynamic receptor binding domains. <i>Nature Communications</i> , 2017 , 8, 15092	17.4	484
58	Molecular basis of binding between novel human coronavirus MERS-CoV and its receptor CD26. <i>Nature</i> , 2013 , 500, 227-31	50.4	466
57	Bat-to-human: spike features determining host jump of coronaviruses SARS-CoV, MERS-CoV, and beyond. <i>Trends in Microbiology</i> , 2015 , 23, 468-78	12.4	363
56	Bat origins of MERS-CoV supported by bat coronavirus HKU4 usage of human receptor CD26. <i>Cell Host and Microbe</i> , 2014 , 16, 328-37	23.4	198
55	Molecular determinants of human neutralizing antibodies isolated from a patient infected with Zika virus. <i>Science Translational Medicine</i> , 2016 , 8, 369ra179	17.5	152
54	An unexpected N-terminal loop in PD-1 dominates binding by nivolumab. <i>Nature Communications</i> , 2017 , 8, 14369	17.4	128
53	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, 13134-40	6.6	118
52	A humanized neutralizing antibody against MERS-CoV targeting the receptor-binding domain of the spike protein. <i>Cell Research</i> , 2015 , 25, 1237-49	24.7	116
51	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	56.2	99
50	CD8 T Cell Immune Response in Immunocompetent Mice during Zika Virus Infection. <i>Journal of Virology</i> , 2017 , 91,	6.6	79
49	MERS-CoV spike protein: Targets for vaccines and therapeutics. <i>Antiviral Research</i> , 2016 , 133, 165-77	10.8	72
48	A Bat-Derived Putative Cross-Family Recombinant Coronavirus with a Reovirus Gene. <i>PLoS Pathogens</i> , 2016 , 12, e1005883	7.6	70
47	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	22.3	69
46	A motif in LILRB2 critical for Angptl2 binding and activation. <i>Blood</i> , 2014 , 124, 924-35	2.2	57

45	Recombinant Chimpanzee Adenovirus Vaccine AdC7-M/E Protects against Zika Virus Infection and Testis Damage. <i>Journal of Virology</i> , 2018 , 92,	6.6	55
44	Monoclonal Antibodies against Zika Virus: Therapeutics and Their Implications for Vaccine Design. <i>Journal of Virology</i> , 2017 , 91,	6.6	33
43	Protective T Cell Responses Featured by Concordant Recognition of Middle East Respiratory Syndrome Coronavirus-Derived CD8+ T Cell Epitopes and Host MHC. <i>Journal of Immunology</i> , 2017 , 198, 873-882	5.3	32
42	Cross-species recognition of SARS-CoV-2 to bat ACE2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	32
41	Molecular basis of antibody-mediated neutralization and protection against flavivirus. <i>IUBMB Life</i> , 2016 , 68, 783-91	4.7	31
40	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	56.2	30
39	A single-dose mRNA vaccine provides a long-term protection for hACE2 transgenic mice from SARS-CoV-2. <i>Nature Communications</i> , 2021 , 12, 776	17.4	26
38	Vertical Transmission of the Zika Virus Causes Neurological Disorders in Mouse Offspring. <i>Scientific Reports</i> , 2018 , 8, 3541	4.9	25
37	Molecular insights into receptor binding of recent emerging SARS-CoV-2 variants. <i>Nature Communications</i> , 2021 , 12, 6103	17.4	24
36	Neutralization mechanism of human monoclonal antibodies against Rift Valley fever virus. <i>Nature Microbiology</i> , 2019 , 4, 1231-1241	26.6	22
35	PILR and PILR 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, 8221-6	11.5	19
34	Structures of the four Ig-like domain LILRB2 and the four-domain LILRB1 and HLA-G1 complex. <i>Cellular and Molecular Immunology</i> , 2020 , 17, 966-975	15.4	19
33	The molecular basis for SARS-CoV-2 binding to dog ACE2. <i>Nature Communications</i> , 2021 , 12, 4195	17.4	17
32	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	21	16
31	Neutralisation of ZF2001-elicited antisera to SARS-CoV-2 variants. <i>Lancet Microbe, The</i> , 2021 , 2, e494	22.2	16
30	Putative Receptor Binding Domain of Bat-Derived Coronavirus HKU9 Spike Protein: Evolution of Betacoronavirus Receptor Binding Motifs. <i>Biochemistry</i> , 2016 , 55, 5977-5988	3.2	14
29	Limited Cross-Linking of 4-1BB by 4-1BB Ligand and the Agonist Monoclonal Antibody Utomilumab. <i>Cell Reports</i> , 2018 , 25, 909-920.e4	10.6	14
28	A non-competing pair of human neutralizing antibodies block COVID-19 virus binding to its receptor ACE2		13

27	Molecular basis of cross-species ACE2 interactions with SARS-CoV-2-like viruses of pangolin origin. <i>EMBO Journal</i> , 2021 , 40, e107786	13	13
26	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	18.9	12
25	Molecular Basis of Binding between Middle East Respiratory Syndrome Coronavirus and CD26 from Seven Bat Species. <i>Journal of Virology</i> , 2020 , 94,	6.6	12
24	Genomic perspectives on the emerging SARS-CoV-2 omicron variant.. <i>Genomics, Proteomics and Bioinformatics</i> , 2022 ,	6.5	12
23	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, 761-70	7.2	10
22	On the origin of SARS-CoV-2-The blind watchmaker argument. <i>Science China Life Sciences</i> , 2021 , 64, 1560-1563	10	10
21	Lentil lectin derived from exhibit broad antiviral activities against SARS-CoV-2 variants. <i>Emerging Microbes and Infections</i> , 2021 , 10, 1519-1529	18.9	10
20	Structure of the S1 subunit C-terminal domain from bat-derived coronavirus HKU5 spike protein. <i>Virology</i> , 2017 , 507, 101-109	3.6	9
19	Tracing the origins of SARS-CoV-2: lessons learned from the past. <i>Cell Research</i> , 2021 , 31, 1139-1141	24.7	7
18	Neutralization of recombinant RBD-subunit vaccine ZF2001-elicited antisera to SARS-CoV-2 variants including Delta		6
17	Zika Virus Envelope Protein and Antibody Complexes. <i>Sub-Cellular Biochemistry</i> , 2018 , 88, 147-168	5.5	5
16	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	8.5	5
15	Protective Zika vaccines engineered to eliminate enhancement of dengue infection via immunodominance switch. <i>Nature Immunology</i> , 2021 , 22, 958-968	19.1	4
14	Transcriptome profiling in swine macrophages infected with African swine fever virus at single-cell resolution.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2201288119	11.5	4
13	Molecular basis of pangolin ACE2 engaged by COVID-19 virus. <i>Chinese Science Bulletin</i> , 2021 , 66, 73-84	2.9	3
12	Zika virus induces myocardial immune response and myocarditis in mice. <i>Journal of Molecular and Cellular Cardiology</i> , 2020 , 148, 103-105	5.8	3
11	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	21	2
10	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 ,	19.7	2

9	HBx-upregulated MAFG-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	0.9	2
8	The origins of viruses: discovery takes time, international resources, and cooperation. <i>Lancet, The</i> , 2021 , 398, 1401-1402	4.0	2
7	VarEPS: an evaluation and prewarning system of known and virtual variations of SARS-CoV-2 genomes. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
6	The crystal structure of the emerging human-infecting hepatitis E virus E2s protein. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 532, 25-31	3.4	1
5	CRISPR-Based Genetic Switches and Other Complex Circuits: Research and Application. <i>Life</i> , 2021 , 11,	3	1
4	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	21	0
3	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	4	0
2	Isolation of Monoclonal Antibodies from Zika Virus-Infected Patient Samples. <i>Methods in Molecular Biology</i> , 2020 , 2142, 261-288	1.4	
1	Pinpointing the animal origins of SARS-CoV-2: a genomic approach. <i>Journal of Genetics and Genomics</i> , 2022 ,	4	