

Xiangxi Wang

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

9,101
citations

136740

32
h-index

110170

64
g-index

84
all docs

84
docs citations

84
times ranked

11910
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and molecular basis for foot-and-mouth disease virus neutralization by two potent protective antibodies. <i>Protein and Cell</i> , 2022, 13, 446-453.	4.8	19
2	Memory B cell repertoire from triple vaccinees against diverse SARS-CoV-2 variants. <i>Nature</i> , 2022, 603, 919-925.	13.7	146
3	Structural and functional characterizations of infectivity and immune evasion of SARS-CoV-2 Omicron. <i>Cell</i> , 2022, 185, 860-871.e13.	13.5	310
4	Structural Insights into Alphavirus Assembly Revealed by the Cryo-EM Structure of Getah Virus. <i>Viruses</i> , 2022, 14, 327.	1.5	2
5	Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies. <i>Nature</i> , 2022, 602, 657-663.	13.7	1,350
6	Replication is the key barrier during the dual-host adaptation of mosquito-borne flaviviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2110491119.	3.3	7
7	A highly immunogenic live-attenuated vaccine candidate prevents SARS-CoV-2 infection and transmission in hamsters. <i>Innovation(China)</i> , 2022, 3, 100221.	5.2	5
8	Atomic Structures of Coxsackievirus B5 Provide Key Information on Viral Evolution and Survival. <i>Journal of Virology</i> , 2022, , e0010522.	1.5	5
9	Sequential immunizations confer cross-protection against variants of SARS-CoV-2, including Omicron in Rhesus macaques. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 124.	7.1	15
10	BA.2.12.1, BA.4 and BA.5 escape antibodies elicited by Omicron infection. <i>Nature</i> , 2022, 608, 593-602.	13.7	889
11	Selection and structural bases of potent broadly neutralizing antibodies from 3-dose vaccinees that are highly effective against diverse SARS-CoV-2 variants, including Omicron sublineages. <i>Cell Research</i> , 2022, 32, 691-694.	5.7	14
12	Rational development of a human antibody cocktail that deploys multiple functions to confer Pan-SARS-CoVs protection. <i>Cell Research</i> , 2021, 31, 25-36.	5.7	76
13	Structure-based development of human antibody cocktails against SARS-CoV-2. <i>Cell Research</i> , 2021, 31, 101-103.	5.7	75
14	Safety, tolerability, and immunogenicity of an inactivated SARS-CoV-2 vaccine in healthy adults aged 18–59 years: a randomised, double-blind, placebo-controlled, phase 1/2 clinical trial. <i>Lancet Infectious Diseases</i> , 2021, 21, 181-192.	4.6	1,104
15	Virion Assembly: From Small Picornaviruses (Picornaviridae) to Large Herpesviruses (Herpesviridae). , 2021, , 480-487.		0
16	Induction of alarmin S100A8/A9 mediates activation of aberrant neutrophils in the pathogenesis of COVID-19. <i>Cell Host and Microbe</i> , 2021, 29, 222-235.e4.	5.1	145
17	Enhancement versus neutralization by SARS-CoV-2 antibodies from a convalescent donor associates with distinct epitopes on the RBD. <i>Cell Reports</i> , 2021, 34, 108699.	2.9	110
18	SARS-CoV-2 spike protein interacts with and activates TLR41. <i>Cell Research</i> , 2021, 31, 818-820.	5.7	225

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19	A proof of concept for neutralizing antibody-guided vaccine design against SARS-CoV-2. National Science Review, 2021, 8, nwab053.	4.6	36
20	Structure-based development of three- and four-antibody cocktails against SARS-CoV-2 via multiple mechanisms. Cell Research, 2021, 31, 597-600.	5.7	26
21	Structural basis for neutralization of an anicteric hepatitis associated echovirus by a potent neutralizing antibody. Cell Discovery, 2021, 7, 35.	3.1	2
22	The architecture of the SARS-CoV-2 RNA genome inside virion. Nature Communications, 2021, 12, 3917.	5.8	122
23	A Heat-Induced Mutation on VP1 of Foot-and-Mouth Disease Virus Serotype O Enhanced Capsid Stability and Immunogenicity. Journal of Virology, 2021, 95, e0017721.	1.5	5
24	Characterization and structural basis of a lethal mouse-adapted SARS-CoV-2. Nature Communications, 2021, 12, 5654.	5.8	89
25	Double lock of a potent human therapeutic monoclonal antibody against SARS-CoV-2. National Science Review, 2021, 8, nwaa297.	4.6	24
26	Nanometer-resolution in situ structure of the SARS-CoV-2 postfusion spike protein. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	30
27	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. Nature Communications, 2020, 11, 38.	5.8	28
28	Cryo-electron microscopy structure of human ABCB6 transporter. Protein Science, 2020, 29, 2363-2374.	3.1	22
29	Structural basis for neutralization of SARS-CoV-2 and SARS-CoV by a potent therapeutic antibody. Science, 2020, 369, 1505-1509.	6.0	358
30	Serotype specific epitopes identified by neutralizing antibodies underpin immunogenic differences in Enterovirus B. Nature Communications, 2020, 11, 4419.	5.8	13
31	Structures of Echovirus 30 in complex with its receptors inform a rational prediction for enterovirus receptor usage. Nature Communications, 2020, 11, 4421.	5.8	18
32	Development of an inactivated vaccine candidate for SARS-CoV-2. Science, 2020, 369, 77-81.	6.0	1,180
33	Human-IgG-Neutralizing Monoclonal Antibodies Block the SARS-CoV-2 Infection. Cell Reports, 2020, 32, 107918.	2.9	148
34	Design, Synthesis, and Evaluation of Novel Enterovirus 71 Inhibitors as Therapeutic Drug Leads for the Treatment of Human Hand, Foot, and Mouth Disease. Journal of Medicinal Chemistry, 2020, 63, 1233-1244.	2.9	12
35	Architecture of the herpesvirus genome-packaging complex and implications for DNA translocation. Protein and Cell, 2020, 11, 339-351.	4.8	53
36	Structures of the portal vertex reveal essential protein-protein interactions for Herpesvirus assembly and maturation. Protein and Cell, 2020, 11, 366-373.	4.8	33

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37	Hepatitis A Virus Capsid Structure. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a031807.	2.9	18
38	Architecture of African swine fever virus and implications for viral assembly. Science, 2019, 366, 640-644.	6.0	252
39	Structural basis for neutralization of hepatitis A virus informs a rational design of highly potent inhibitors. PLoS Biology, 2019, 17, e3000229.	2.6	12
40	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. Nature Communications, 2019, 10, 1456.	5.8	17
41	Double Lock of a Human Neutralizing and Protective Monoclonal Antibody Targeting the Yellow Fever Virus Envelope. Cell Reports, 2019, 26, 438-446.e5.	2.9	49
42	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. Nature Microbiology, 2019, 4, 414-419.	5.9	73
43	Pushing the resolution limit by correcting the Ewald sphere effect in single-particle Cryo-EM reconstructions. Nature Communications, 2018, 9, 1552.	5.8	83
44	Cryo-EM structure of a herpesvirus capsid at 3.1 Å... Science, 2018, 360, .	6.0	93
45	Structural basis for neutralization of Japanese encephalitis virus by two potent therapeutic antibodies. Nature Microbiology, 2018, 3, 287-294.	5.9	42
46	A single residue in the $\hat{\pm}$ B helix of the E protein is critical for Zika virus thermostability. Emerging Microbes and Infections, 2018, 7, 1-15.	3.0	6
47	Structures of Coxsackievirus A10 unveil the molecular mechanisms of receptor binding and viral uncoating. Nature Communications, 2018, 9, 4985.	5.8	52
48	Cryo-EM structure of Type III-A CRISPR effector complex. Cell Research, 2018, 28, 1195-1197.	5.7	21
49	Structure of the herpes simplex virus type 2 C-capsid with capsid-vertex-specific component. Nature Communications, 2018, 9, 3668.	5.8	31
50	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. MBio, 2018, 9, .	1.8	26
51	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 770-775.	3.3	42
52	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. Nature Communications, 2017, 8, 14.	5.8	117
53	The binding of a monoclonal antibody to the apical region of SCARB2 blocks EV71 infection. Protein and Cell, 2017, 8, 590-600.	4.8	18
54	Uncovering Drug Mechanism of Action by Proteome Wide- Identification of Drug-Binding Proteins. Medicinal Chemistry, 2017, 13, 526-535.	0.7	2

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55	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016, 1, 16150.	5.9	36
56	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. <i>Nature Communications</i> , 2015, 6, 8316.	5.8	43
57	Structures of Coxsackievirus A16 Capsids with Native Antigenicity: Implications for Particle Expansion, Receptor Binding, and Immunogenicity. <i>Journal of Virology</i> , 2015, 89, 10500-10511.	1.5	58
58	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015, 517, 85-88.	13.7	158
59	Structure Elucidation of Coxsackievirus A16 in Complex with GPP3 Informs a Systematic Review of Highly Potent Capsid Binders to Enteroviruses. <i>PLoS Pathogens</i> , 2015, 11, e1005165.	2.1	20
60	Molecular mechanism of SCARB2-mediated attachment and uncoating of EV71. <i>Protein and Cell</i> , 2014, 5, 692-703.	4.8	95
61	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 282-288.	3.6	88
62	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013, 4, 1929.	5.8	148
63	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 424-429.	3.6	347
64	Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies. <i>Nature</i> , 0, , .	13.7	90