

# Xiangxi Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7484917/publications.pdf>

Version: 2024-02-01

64  
papers

9,101  
citations

136885

32  
h-index

110317

64  
g-index

84  
all docs

84  
docs citations

84  
times ranked

11910  
citing authors

#	ARTICLE	IF	CITATIONS
1	Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies. <i>Nature</i> , 2022, 602, 657-663.	13.7	1,350
2	Development of an inactivated vaccine candidate for SARS-CoV-2. <i>Science</i> , 2020, 369, 77-81.	6.0	1,180
3	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
4	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
5	Structural basis for neutralization of SARS-CoV-2 and SARS-CoV by a potent therapeutic antibody. <i>Science</i> , 2020, 369, 1505-1509.	6.0	358
6	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
7	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
8	Architecture of African swine fever virus and implications for viral assembly. <i>Science</i> , 2019, 366, 640-644.	6.0	252
9	SARS-CoV-2 spike protein interacts with and activates TLR41. <i>Cell Research</i> , 2021, 31, 818-820.	5.7	225
10	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015, 517, 85-88.	13.7	158
11	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013, 4, 1929.	5.8	148
12	Human-IgG-Neutralizing Monoclonal Antibodies Block the SARS-CoV-2 Infection. <i>Cell Reports</i> , 2020, 32, 107918.	2.9	148
13	Memory B cell repertoire from triple vaccinees against diverse SARS-CoV-2 variants. <i>Nature</i> , 2022, 603, 919-925.	13.7	146
14	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
15	The architecture of the SARS-CoV-2 RNA genome inside virion. <i>Nature Communications</i> , 2021, 12, 3917.	5.8	122
16	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017, 8, 14.	5.8	117
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	Molecular mechanism of SCARB2-mediated attachment and uncoating of EV71. <i>Protein and Cell</i> , 2014, 5, 692-703.	4.8	95

#	ARTICLE	IF	CITATIONS
19	Cryo-EM structure of a herpesvirus capsid at 3.1 Å... Science, 2018, 360, .	6.0	93
20	Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies. Nature, 0, , .	13.7	90
21	Characterization and structural basis of a lethal mouse-adapted SARS-CoV-2. Nature Communications, 2021, 12, 5654.	5.8	89
22	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. Nature Structural and Molecular Biology, 2014, 21, 282-288.	3.6	88
23	Pushing the resolution limit by correcting the Ewald sphere effect in single-particle Cryo-EM reconstructions. Nature Communications, 2018, 9, 1552.	5.8	83
24	Rational development of a human antibody cocktail that deploys multiple functions to confer Pan-SARS-CoVs protection. Cell Research, 2021, 31, 25-36.	5.7	76
25	Structure-based development of human antibody cocktails against SARS-CoV-2. Cell Research, 2021, 31, 101-103.	5.7	75
26	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. Nature Microbiology, 2019, 4, 414-419.	5.9	73
27	Structures of Coxsackievirus A16 Capsids with Native Antigenicity: Implications for Particle Expansion, Receptor Binding, and Immunogenicity. Journal of Virology, 2015, 89, 10500-10511.	1.5	58
28	Architecture of the herpesvirus genome-packaging complex and implications for DNA translocation. Protein and Cell, 2020, 11, 339-351.	4.8	53
29	Structures of Coxsackievirus A10 unveil the molecular mechanisms of receptor binding and viral uncoating. Nature Communications, 2018, 9, 4985.	5.8	52
30	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
31	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. Nature Communications, 2015, 6, 8316.	5.8	43
32	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
33	Structural basis for neutralization of Japanese encephalitis virus by two potent therapeutic antibodies. Nature Microbiology, 2018, 3, 287-294.	5.9	42
34	Structure of human Aichi virus and implications for receptor binding. Nature Microbiology, 2016, 1, 16150.	5.9	36
35	A proof of concept for neutralizing antibody-guided vaccine design against SARS-CoV-2. National Science Review, 2021, 8, nwab053.	4.6	36
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

#	ARTICLE	IF	CITATIONS
37	Structure of the herpes simplex virus type 2 C-capsid with capsid-vertex-specific component. <i>Nature Communications</i> , 2018, 9, 3668.	5.8	31
38	Nanometer-resolution in situ structure of the SARS-CoV-2 postfusion spike protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	30
39	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. <i>Nature Communications</i> , 2020, 11, 38.	5.8	28
40	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. <i>MBio</i> , 2018, 9, .	1.8	26
41	Structure-based development of three- and four-antibody cocktails against SARS-CoV-2 via multiple mechanisms. <i>Cell Research</i> , 2021, 31, 597-600.	5.7	26
42	Double lock of a potent human therapeutic monoclonal antibody against SARS-CoV-2. <i>National Science Review</i> , 2021, 8, nwaa297.	4.6	24
43	<scp>Cryoâ€</scp>electron microscopy structure of human <scp>ABCB6</scp> transporter. <i>Protein Science</i> , 2020, 29, 2363-2374.	3.1	22
44	Cryo-EM structure of Type III-A CRISPR effector complex. <i>Cell Research</i> , 2018, 28, 1195-1197.	5.7	21
45	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
46	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
47	The binding of a monoclonal antibody to the apical region of SCARB2 blocks EV71 infection. <i>Protein and Cell</i> , 2017, 8, 590-600.	4.8	18
48	Hepatitis A Virus Capsid Structure. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a031807.	2.9	18
49	Structures of Echovirus 30 in complex with its receptors inform a rational prediction for enterovirus receptor usage. <i>Nature Communications</i> , 2020, 11, 4421.	5.8	18
50	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. <i>Nature Communications</i> , 2019, 10, 1456.	5.8	17
51	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
52	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
53	Serotype specific epitopes identified by neutralizing antibodies underpin immunogenic differences in Enterovirus B. <i>Nature Communications</i> , 2020, 11, 4419.	5.8	13
54	Structural basis for neutralization of hepatitis A virus informs a rational design of highly potent inhibitors. <i>PLoS Biology</i> , 2019, 17, e3000229.	2.6	12

#	ARTICLE	IF	CITATIONS
55	Design, Synthesis, and Evaluation of Novel Enterovirus 71 Inhibitors as Therapeutic Drug Leads for the Treatment of Human Hand, Foot, and Mouth Disease. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 1233-1244.	2.9	12
56	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
57	A single residue in the $\hat{I}\pm B$ helix of the E protein is critical for Zika virus thermostability. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-15.	3.0	6
58	A Heat-Induced Mutation on VP1 of Foot-and-Mouth Disease Virus Serotype O Enhanced Capsid Stability and Immunogenicity. <i>Journal of Virology</i> , 2021, 95, e0017721.	1.5	5
59	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
60	Atomic Structures of Coxsackievirus B5 Provide Key Information on Viral Evolution and Survival. <i>Journal of Virology</i> , 2022, , e0010522.	1.5	5
61	Structural basis for neutralization of an anicteric hepatitis associated echovirus by a potent neutralizing antibody. <i>Cell Discovery</i> , 2021, 7, 35.	3.1	2
62	Uncovering Drug Mechanism of Action by Proteome Wide- Identification of Drug-Binding Proteins. <i>Medicinal Chemistry</i> , 2017, 13, 526-535.	0.7	2
63	Structural Insights into Alphavirus Assembly Revealed by the Cryo-EM Structure of Getah Virus. <i>Viruses</i> , 2022, 14, 327.	1.5	2
64	Virion Assembly: From Small Picornaviruses (Picornaviridae) to Large Herpesviruses (Herpesviridae). , 2021, , 480-487.		0