

# Xinquan Wang

## List of Publications by Year in descending order

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73  
papers

14,490  
citations

126708

33  
h-index

79541

73  
g-index

95  
all docs

95  
docs citations

95  
times ranked

25158  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor. <i>Nature</i> , 2020, 581, 215-220.	13.7	4,948
2	Mammalian WTAP is a regulatory subunit of the RNA N6-methyladenosine methyltransferase. <i>Cell Research</i> , 2014, 24, 177-189.	5.7	1,719
3	Human neutralizing antibodies elicited by SARS-CoV-2 infection. <i>Nature</i> , 2020, 584, 115-119.	13.7	1,524
4	Detection of SARS-CoV-2-Specific Humoral and Cellular Immunity in COVID-19 Convalescent Individuals. <i>Immunity</i> , 2020, 52, 971-977.e3.	6.6	979
5	Cryo-EM structure of the SARS coronavirus spike glycoprotein in complex with its host cell receptor ACE2. <i>PLoS Pathogens</i> , 2018, 14, e1007236.	2.1	716
6	Structure of MERS-CoV spike receptor-binding domain complexed with human receptor DPP4. <i>Cell Research</i> , 2013, 23, 986-993.	5.7	588
7	Cryo-electron microscopy structures of the SARS-CoV spike glycoprotein reveal a prerequisite conformational state for receptor binding. <i>Cell Research</i> , 2017, 27, 119-129.	5.7	547
8	BMP restricts stemness of intestinal Lgr5+ stem cells by directly suppressing their signature genes. <i>Nature Communications</i> , 2017, 8, 13824.	5.8	214
9	Potent Neutralization of MERS-CoV by Human Neutralizing Monoclonal Antibodies to the Viral Spike Glycoprotein. <i>Science Translational Medicine</i> , 2014, 6, 234ra59.	5.8	194
10	Analysis of SARS-CoV-2 variant mutations reveals neutralization escape mechanisms and the ability to use ACE2 receptors from additional species. <i>Immunity</i> , 2021, 54, 1611-1621.e5.	6.6	190
11	Functional and genetic analysis of viral receptor ACE2 orthologs reveals a broad potential host range of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	168
12	Kinesin 1 Drives Autolysosome Tubulation. <i>Developmental Cell</i> , 2016, 37, 326-336.	3.1	129
13	Structural definition of a neutralization epitope on the N-terminal domain of MERS-CoV spike glycoprotein. <i>Nature Communications</i> , 2019, 10, 3068.	5.8	122
14	Cryo-EM structure of the exocyst complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 139-146.	3.6	119
15	Antibody neutralization of SARS-CoV-2 through ACE2 receptor mimicry. <i>Nature Communications</i> , 2021, 12, 250.	5.8	108
16	Characterization and structural basis of a lethal mouse-adapted SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 5654.	5.8	89
17	The humoral response and antibodies against SARS-CoV-2 infection. <i>Nature Immunology</i> , 2022, 23, 1008-1020.	7.0	84
18	Potent and protective IGHV3-53/3-66 public antibodies and their shared escape mutant on the spike of SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 4210.	5.8	82

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19	Ultra-fast and onsite interrogation of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in waters via surface enhanced Raman scattering (SERS). <i>Water Research</i> , 2021, 200, 117243.	5.3	77
20	Bat and pangolin coronavirus spike glycoprotein structures provide insights into SARS-CoV-2 evolution. <i>Nature Communications</i> , 2021, 12, 1607.	5.8	76
21	Antibodies and vaccines against Middle East respiratory syndrome coronavirus. <i>Emerging Microbes and Infections</i> , 2019, 8, 841-856.	3.0	71
22	Enfuvirtide (T20)-Based Lipopeptide Is a Potent HIV-1 Cell Fusion Inhibitor: Implications for Viral Entry and Inhibition. <i>Journal of Virology</i> , 2017, 91, .	1.5	65
23	Structural basis for the neutralization of MERS-CoV by a human monoclonal antibody MERS-27. <i>Scientific Reports</i> , 2015, 5, 13133.	1.6	63
24	Ultrapotent Human Neutralizing Antibody Repertoires Against Middle East Respiratory Syndrome Coronavirus From a Recovered Patient. <i>Journal of Infectious Diseases</i> , 2018, 218, 1249-1260.	1.9	63
25	Structural studies of GDNF family ligands with their receptors—Insights into ligand recognition and activation of receptor tyrosine kinase RET. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2205-2212.	1.1	59
26	Structural Definition of a Unique Neutralization Epitope on the Receptor-Binding Domain of MERS-CoV Spike Glycoprotein. <i>Cell Reports</i> , 2018, 24, 441-452.	2.9	57
27	Structural insights into the SARS-CoV-2 Omicron RBD-ACE2 interaction. <i>Cell Research</i> , 2022, 32, 593-595.	5.7	55
28	Structural basis for bivalent binding and inhibition of SARS-CoV-2 infection by human potent neutralizing antibodies. <i>Cell Research</i> , 2021, 31, 517-525.	5.7	54
29	Interleukin-17D regulates group 3 innate lymphoid cell function through its receptor CD93. <i>Immunity</i> , 2021, 54, 673-686.e4.	6.6	53
30	Cryo-EM structures of HKU2 and SARS-CoV spike glycoproteins provide insights into coronavirus evolution. <i>Nature Communications</i> , 2020, 11, 3070.	5.8	44
31	Mutation Y453F in the spike protein of SARS-CoV-2 enhances interaction with the mink ACE2 receptor for host adaption. <i>PLoS Pathogens</i> , 2021, 17, e1010053.	2.1	43
32	From crystal structure of Î±-conotoxin G1C in complex with Ac-AChBP to molecular determinants of its high selectivity for Î±3Î²2 nAChR. <i>Scientific Reports</i> , 2016, 6, 22349.	1.6	41
33	Structural and functional characterization of HIV-1 cell fusion inhibitor T20. <i>Aids</i> , 2019, 33, 1-11.	1.0	38
34	Single intranasal immunization with chimpanzee adenovirus-based vaccine induces sustained and protective immunity against MERS-CoV infection. <i>Emerging Microbes and Infections</i> , 2019, 8, 760-772.	3.0	36
35	Comprehensive analysis of antibody recognition in convalescent humans from highly pathogenic avian influenza H5N1 infection. <i>Nature Communications</i> , 2015, 6, 8855.	5.8	35
36	ULK1 phosphorylates Exo70 to suppress breast cancer metastasis. <i>Nature Communications</i> , 2020, 11, 117.	5.8	35

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37	Comparative analysis reveals the species-specific genetic determinants of ACE2 required for SARS-CoV-2 entry. <i>PLoS Pathogens</i> , 2021, 17, e1009392.	2.1	34
38	Structural Insights on PHA Binding Protein PhaP from <i>Aeromonas hydrophila</i> . <i>Scientific Reports</i> , 2016, 6, 39424.	1.6	30
39	Tumor Necrosis Factor Receptor 2 (TNFR2)–Interleukin-17 Receptor D (IL-17RD) Heteromerization Reveals a Novel Mechanism for NF- $\kappa$ B Activation. <i>Journal of Biological Chemistry</i> , 2015, 290, 861-871.	1.6	27
40	Exceptional potency and structural basis of a T1249-derived lipopeptide fusion inhibitor against HIV-1, HIV-2, and simian immunodeficiency virus. <i>Journal of Biological Chemistry</i> , 2018, 293, 5323-5334.	1.6	27
41	The crystal structure of Ac-AChBP in complex with $\alpha$ -conotoxin Lv1A reveals the mechanism of its selectivity towards different nAChR subtypes. <i>Protein and Cell</i> , 2017, 8, 675-685.	4.8	25
42	Nuclear glutaredoxin 3 is critical for protection against oxidative stress-induced cell death. <i>Free Radical Biology and Medicine</i> , 2015, 85, 197-206.	1.3	24
43	The <i>Rhinolophus affinis</i> bat ACE2 and multiple animal orthologs are functional receptors for bat coronavirus RaTG13 and SARS-CoV-2. <i>Science Bulletin</i> , 2021, 66, 1215-1227.	4.3	24
44	Loss of Spike N370 glycosylation as an important evolutionary event for the enhanced infectivity of SARS-CoV-2. <i>Cell Research</i> , 2022, 32, 315-318.	5.7	24
45	Targeted inhibition of activated protein C by a non-active-site inhibitory antibody to treat hemophilia. <i>Nature Communications</i> , 2020, 11, 2992.	5.8	23
46	Susceptibilities of Human ACE2 Genetic Variants in Coronavirus Infection. <i>Journal of Virology</i> , 2022, 96, JV0149221.	1.5	22
47	Characterization of SARS-CoV-2 Variants B.1.617.1 (Kappa), B.1.617.2 (Delta), and B.1.618 by Cell Entry and Immune Evasion. <i>MBio</i> , 2022, 13, e0009922.	1.8	22
48	Structural basis for the specific recognition of IL-18 by its alpha receptor. <i>FEBS Letters</i> , 2014, 588, 3838-3843.	1.3	21
49	Selective oxidation of aliphatic C–H bonds in alkylphenols by a chemomimetic biocatalytic system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5129-E5137.	3.3	19
50	RBD trimer mRNA vaccine elicits broad and protective immune responses against SARS-CoV-2 variants. <i>IScience</i> , 2022, 25, 104043.	1.9	19
51	High Selectivity of an $\alpha$ -Conotoxin Lv1A Analogue for $\alpha$ 3 $\beta$ 2 Nicotinic Acetylcholine Receptors Is Mediated by $\beta$ 2 Functionally Important Residues. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 13656-13668.	2.9	18
52	A potent and protective human neutralizing antibody targeting a novel vulnerable site of Epstein-Barr virus. <i>Nature Communications</i> , 2021, 12, 6624.	5.8	18
53	Structural insights into the substrate specificity of a glycoside hydrolase family 5 lichenase from <i>Caldicellulosiruptor</i> sp. F32. <i>Biochemical Journal</i> , 2017, 474, 3373-3389.	1.7	17
54	One-step homozygosity in precise gene editing by an improved CRISPR/Cas9 system. <i>Cell Research</i> , 2016, 26, 633-636.	5.7	15

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55	Cardiac-specific ablation of glutaredoxin 3 leads to cardiac hypertrophy and heart failure. <i>Physiological Reports</i> , 2019, 7, e14071.	0.7	15
56	A Potent and Protective Human Neutralizing Antibody Against SARS-CoV-2 Variants. <i>Frontiers in Immunology</i> , 2021, 12, 766821.	2.2	15
57	Structural Insights into the Mechanisms of Action of Short-Peptide HIV-1 Fusion Inhibitors Targeting the Gp41 Pocket. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 51.	1.8	14
58	Crystal Structure of Human ISG15 Protein in Complex with Influenza B Virus NS1B. <i>Journal of Biological Chemistry</i> , 2011, 286, 30258-30262.	1.6	13
59	A novel mechanism underlies caspase-dependent conversion of the dicer ribonuclease into a deoxyribonuclease during apoptosis. <i>Cell Research</i> , 2014, 24, 218-232.	5.7	13
60	Complementary recognition of the receptor-binding site of highly pathogenic H5N1 influenza viruses by two human neutralizing antibodies. <i>Journal of Biological Chemistry</i> , 2018, 293, 16503-16517.	1.6	11
61	Conformational Sampling and Binding Site Assessment of Suppression of Tumorigenicity 2 Ectodomain. <i>PLoS ONE</i> , 2016, 11, e0146522.	1.1	11
62	Structural insight into a GH1 $\beta$ -glucosidase from the oleaginous microalga, <i>Nannochloropsis oceanica</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 170, 196-206.	3.6	10
63	Structural basis of tetanus toxin neutralization by native human monoclonal antibodies. <i>Cell Reports</i> , 2021, 35, 109070.	2.9	10
64	Modelling of microbial polyhydroxyalkanoate surface binding protein PhaP for rational mutagenesis. <i>Microbial Biotechnology</i> , 2017, 10, 1400-1411.	2.0	8
65	Structural basis of severe acute respiratory syndrome coronavirus 2 infection. <i>Current Opinion in HIV and AIDS</i> , 2021, 16, 74-81.	1.5	7
66	Functional Relevance of Interleukin-1 Receptor Inter-domain Flexibility for Cytokine Binding and Signaling. <i>Structure</i> , 2019, 27, 1296-1307.e5.	1.6	6
67	The spike glycoprotein of highly pathogenic human coronaviruses: structural insights for understanding infection, evolution and inhibition. <i>FEBS Open Bio</i> , 2022, 12, 1602-1622.	1.0	6
68	Structural and functional definition of a vulnerable site on the hemagglutinin of highly pathogenic avian influenza A virus H5N1. <i>Journal of Biological Chemistry</i> , 2019, 294, 4290-4303.	1.6	5
69	Structural insights into the species preference of the influenza B virus NS1 protein in ISG15 binding. <i>Protein and Cell</i> , 2019, 10, 681-687.	4.8	5
70	A shedding-soluble form of interleukin-17 receptor D exacerbates collagen-induced arthritis through facilitating TNF-dependent receptor clustering. <i>Cellular and Molecular Immunology</i> , 2020, 18, 1883-1895.	4.8	4
71	CEBIT screening for inhibitors of the interaction between SARS-CoV-2 spike and ACE2. <i>Fundamental Research</i> , 2022, 2, 562-569.	1.6	2
72	From Crystal Structures of RgIA4 in Complex with Ac-AChBP to Molecular Determinants of Its High Potency of $10^{-9}$ nAChR. <i>Marine Drugs</i> , 2021, 19, 709.	2.2	1

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73	Crystallization and Structural Determination of the Receptor-Binding Domain of MERS-CoV Spike Glycoprotein. <i>Methods in Molecular Biology</i> , 2020, 2099, 39-50.	0.4	0