

Xinquan Wang

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77
papers

9,048
citations

29
h-index

95
g-index

95
ext. papers

12,249
ext. citations

13
avg, IF

6.59
L-index

#	Paper	IF	Citations
77	Structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor. <i>Nature</i> , 2020 , 581, 215-220	50.4	2961
76	Mammalian WTAP is a regulatory subunit of the RNA N6-methyladenosine methyltransferase. <i>Cell Research</i> , 2014 , 24, 177-89	24.7	1061
75	Human neutralizing antibodies elicited by SARS-CoV-2 infection. <i>Nature</i> , 2020 , 584, 115-119	50.4	982
74	Detection of SARS-CoV-2-Specific Humoral and Cellular Immunity in COVID-19 Convalescent Individuals. <i>Immunity</i> , 2020 , 52, 971-977.e3	32.3	707
73	Cryo-EM structure of the SARS coronavirus spike glycoprotein in complex with its host cell receptor ACE2. <i>PLoS Pathogens</i> , 2018 , 14, e1007236	7.6	523
72	Structure of MERS-CoV spike receptor-binding domain complexed with human receptor DPP4. <i>Cell Research</i> , 2013 , 23, 986-93	24.7	459
71	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	24.7	410
70	Potent human neutralizing antibodies elicited by SARS-CoV-2 infection		211
69	Potent neutralization of MERS-CoV by human neutralizing monoclonal antibodies to the viral spike glycoprotein. <i>Science Translational Medicine</i> , 2014 , 6, 234ra59	17.5	165
68	BMP restricts stemness of intestinal Lgr5 stem cells by directly suppressing their signature genes. <i>Nature Communications</i> , 2017 , 8, 13824	17.4	142
67	Structural definition of a neutralization epitope on the N-terminal domain of MERS-CoV spike glycoprotein. <i>Nature Communications</i> , 2019 , 10, 3068	17.4	94
66	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	32.3	85
65	Kinesin 1 Drives Autolysosome Tubulation. <i>Developmental Cell</i> , 2016 , 37, 326-336	10.2	79
64	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,	11.5	73
63	Cryo-EM structure of the exocyst complex. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 139-146	17.6	69
62	Antibodies and vaccines against Middle East respiratory syndrome coronavirus. <i>Emerging Microbes and Infections</i> , 2019 , 8, 841-856	18.9	58
61	Structural basis for the neutralization of MERS-CoV by a human monoclonal antibody MERS-27. <i>Scientific Reports</i> , 2015 , 5, 13133	4.9	54

60	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	7	50
59	Antibody neutralization of SARS-CoV-2 through ACE2 receptor mimicry. <i>Nature Communications</i> , 2021 , 12, 250	17.4	45
58	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	10.6	43
57	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, 2205-12	4	40
56	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,	6.6	39
55	From crystal structure of ßconotoxin G1C in complex with Ac-AChBP to molecular determinants of its high selectivity for ß nAChR. <i>Scientific Reports</i> , 2016 , 6, 22349	4.9	35
54	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	12.5	34
53	Characterization and structural basis of a lethal mouse-adapted SARS-CoV-2. <i>Nature Communications</i> , 2021 , 12, 5654	17.4	32
52	Comprehensive analysis of antibody recognition in convalescent humans from highly pathogenic avian influenza H5N1 infection. <i>Nature Communications</i> , 2015 , 6, 8855	17.4	31
51	Bat and pangolin coronavirus spike glycoprotein structures provide insights into SARS-CoV-2 evolution. <i>Nature Communications</i> , 2021 , 12, 1607	17.4	31
50	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	18.9	30
49	Functional and Genetic Analysis of Viral Receptor ACE2 Orthologs Reveals a Broad Potential Host Range of SARS-CoV-2		30
48	Structural and functional characterization of HIV-1 cell fusion inhibitor T20. <i>Aids</i> , 2019 , 33, 1-11	3.5	29
47	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	17.4	23
46	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	5.4	22
45	Tumor necrosis factor receptor 2 (TNFR2)–Interleukin-17 receptor D (IL-17RD) heteromerization reveals a novel mechanism for NF-ß activation. <i>Journal of Biological Chemistry</i> , 2015 , 290, 861-71	5.4	22
44	Nuclear glutaredoxin 3 is critical for protection against oxidative stress-induced cell death. <i>Free Radical Biology and Medicine</i> , 2015 , 85, 197-206	7.8	20
43	Cryo-EM structures of HKU2 and SARS-CoV spike glycoproteins provide insights into coronavirus evolution. <i>Nature Communications</i> , 2020 , 11, 3070	17.4	20

42	ULK1 phosphorylates Exo70 to suppress breast cancer metastasis. <i>Nature Communications</i> , 2020 , 11, 117	17.4	20
41	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	24.7	20
40	Structural Insights on PHA Binding Protein PhaP from <i>Aeromonas hydrophila</i> . <i>Scientific Reports</i> , 2016 , 6, 39424	4.9	19
39	The crystal structure of Ac-AChBP in complex with α -conotoxin Lv1A reveals the mechanism of its selectivity towards different nAChR subtypes. <i>Protein and Cell</i> , 2017 , 8, 675-685	7.2	16
38	Characterization and structural basis of a lethal mouse-adapted SARS-CoV-2		16
37	Comparative analysis reveals the species-specific genetic determinants of ACE2 required for SARS-CoV-2 entry. <i>PLoS Pathogens</i> , 2021 , 17, e1009392	7.6	16
36	Structural insights into the substrate specificity of a glycoside hydrolase family 5 lichenase from sp. F32. <i>Biochemical Journal</i> , 2017 , 474, 3373-3389	3.8	14
35	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 ^{11.5}		13
34	Crystal structure of human ISG15 protein in complex with influenza B virus NS1B. <i>Journal of Biological Chemistry</i> , 2011 , 286, 30258-30262	5.4	13
33	Interleukin-17D regulates group 3 innate lymphoid cell function through its receptor CD93. <i>Immunity</i> , 2021 , 54, 673-686.e4	32.3	13
32	One-step homozygosity in precise gene editing by an improved CRISPR/Cas9 system. <i>Cell Research</i> , 2016 , 26, 633-6	24.7	12
31	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	5.9	11
30	Structural basis for the specific recognition of IL-18 by its alpha receptor. <i>FEBS Letters</i> , 2014 , 588, 3838-3843	5.8	11
29	Cardiac-specific ablation of glutaredoxin 3 leads to cardiac hypertrophy and heart failure. <i>Physiological Reports</i> , 2019 , 7, e14071	2.6	10
28	Targeted inhibition of activated protein C by a non-active-site inhibitory antibody to treat hemophilia. <i>Nature Communications</i> , 2020 , 11, 2992	17.4	10
27	A novel mechanism underlies caspase-dependent conversion of the dicer ribonuclease into a deoxyribonuclease during apoptosis. <i>Cell Research</i> , 2014 , 24, 218-32	24.7	10
26	The 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	10.6	9
25	SARS-CoV-2 variants resist antibody neutralization and broaden host ACE2 usage		8

24	Modelling of microbial polyhydroxyalkanoate surface binding protein PhaP for rational mutagenesis. <i>Microbial Biotechnology</i> , 2017 , 10, 1400-1411	6.3	7
23	Conformational Sampling and Binding Site Assessment of Suppression of Tumorigenicity 2 Ectodomain. <i>PLoS ONE</i> , 2016 , 11, e0146522	3.7	7
22	High Selectivity of an EConotoxin LvIA Analogue for $\beta\beta$ Nicotinic Acetylcholine Receptors Is Mediated by α Functionally Important Residues. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 13656-13668	8.3	7
21	Structural insights into the SARS-CoV-2 Omicron RBD-ACE2 interaction.. <i>Cell Research</i> , 2022 ,	24.7	7
20	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	7.6	6
19	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	5.4	6
18	A Potent and Protective Human Neutralizing Antibody Against SARS-CoV-2 Variants.. <i>Frontiers in Immunology</i> , 2021 , 12, 766821	8.4	5
17	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	7.2	5
16	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	5.4	4
15	Structural and computational insights into the SARS-CoV-2 Omicron RBD-ACE2 interaction		4
14	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> , 2021 , 18, 1883-1895	15.4	4
13	Structural basis of tetanus toxin neutralization by native human monoclonal antibodies. <i>Cell Reports</i> , 2021 , 35, 109070	10.6	4
12	A potent and protective human neutralizing antibody targeting a novel vulnerable site of Epstein-Barr virus. <i>Nature Communications</i> , 2021 , 12, 6624	17.4	3
11	Structural basis of severe acute respiratory syndrome coronavirus 2 infection. <i>Current Opinion in HIV and AIDS</i> , 2021 , 16, 74-81	4.2	3
10	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 , e0009922	7.8	3
9	RBD trimer mRNA vaccine elicits broad and protective immune responses against SARS-CoV-2 variants.. <i>IScience</i> , 2022 , 104043	6.1	3
8	Functional Relevance of Interleukin-1 Receptor Inter-domain Flexibility for Cytokine Binding and Signaling. <i>Structure</i> , 2019 , 27, 1296-1307.e5	5.2	2
7	Loss of Spike N370 glycosylation as an important evolutionary event for the enhanced infectivity of SARS-CoV-2.. <i>Cell Research</i> , 2022 ,	24.7	2

- 6 Susceptibilities of human ACE2 genetic variants in coronavirus infection. *Journal of Virology*, **2021**, JVI01492212
- 5 Structural basis for bivalent binding and inhibition of SARS-CoV-2 infection by human potent neutralizing antibodies 2
- 4 Structural insight into a GH1 α -glucosidase from the oleaginous microalga, *Nannochloropsis oceanica*. *International Journal of Biological Macromolecules*, **2021**, 170, 196-206 7.9 2
- 3 Characterization of SARS-CoV-2 variants B.1.617.1 (Kappa), B.1.617.2 (Delta) and B.1.618 on cell entry, host range, and sensitivity to convalescent plasma and ACE2 decoy receptor 2
- 2 Bat and pangolin coronavirus spike glycoprotein structures provide insights into SARS-CoV-2 evolution 1
- 1 Crystallization and Structural Determination of the Receptor-Binding Domain of MERS-CoV Spike Glycoprotein. *Methods in Molecular Biology*, **2020**, 2099, 39-50 1.4