

# Nianshuang Wang

## List of Publications by Year in Descending Order

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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.

29  
papers

9,708  
citations

22  
h-index

30  
g-index

30  
ext. papers

12,679  
ext. citations

21.2  
avg, IF

6.96  
L-index

#	Paper	IF	Citations
29	A Combination of Receptor-Binding Domain and N-Terminal Domain Neutralizing Antibodies Limits the Generation of SARS-CoV-2 Spike Neutralization-Escape Mutants. <i>MBio</i> , <b>2021</b> , 12, e0247321	7.8	11
28	Expression and characterization of SARS-CoV-2 spike proteins. <i>Nature Protocols</i> , <b>2021</b> , 16, 5339-5356	18.8	4
27	Synthetic repertoires derived from convalescent COVID-19 patients enable discovery of SARS-CoV-2 neutralizing antibodies and a novel quaternary binding modality <b>2021</b> ,		4
26	Prevalent, protective, and convergent IgG recognition of SARS-CoV-2 non-RBD spike epitopes. <i>Science</i> , <b>2021</b> , 372, 1108-1112	33.3	100
25	Cross-reactive coronavirus antibodies with diverse epitope specificities and Fc effector functions. <i>Cell Reports Medicine</i> , <b>2021</b> , 2, 100313	18	24
24	Structural Basis for Potent Neutralization of Betacoronaviruses by Single-Domain Camelid Antibodies. <i>Cell</i> , <b>2020</b> , 181, 1004-1015.e15	56.2	319
23	Broad neutralization of SARS-related viruses by human monoclonal antibodies. <i>Science</i> , <b>2020</b> , 369, 731-736	33.3	376
22	Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. <i>Science</i> , <b>2020</b> , 367, 1260-1263	33.3	5176
21	Cryo-EM Structure of the 2019-nCoV Spike in the Prefusion Conformation <b>2020</b> ,		143
20	Broad sarbecovirus neutralizing antibodies define a key site of vulnerability on the SARS-CoV-2 spike protein <b>2020</b> ,		18
19	Structure-based Design of Prefusion-stabilized SARS-CoV-2 Spikes <b>2020</b> ,		27
18	SARS-CoV-2 mRNA Vaccine Development Enabled by Prototype Pathogen Preparedness <b>2020</b> ,		62
17	Cross-reactive coronavirus antibodies with diverse epitope specificities and extra-neutralization functions <b>2020</b> ,		7
16	Prevalent, protective, and convergent IgG recognition of SARS-CoV-2 non-RBD spike epitopes in COVID-19 convalescent plasma <b>2020</b> ,		29
15	SARS-CoV-2 mRNA vaccine design enabled by prototype pathogen preparedness. <i>Nature</i> , <b>2020</b> , 586, 567-571	50.4	594
14	Structure-based design of prefusion-stabilized SARS-CoV-2 spikes. <i>Science</i> , <b>2020</b> , 369, 1501-1505	33.3	450
13	Structural Definition of a Neutralization-Sensitive Epitope on the MERS-CoV S1-NTD. <i>Cell Reports</i> , <b>2019</b> , 28, 3395-3405.e6	10.6	53

12	A high-throughput inhibition assay to study MERS-CoV antibody interactions using image cytometry. <i>Journal of Virological Methods</i> , <b>2019</b> , 265, 77-83	2.6	8
11	Importance of Neutralizing Monoclonal Antibodies Targeting Multiple Antigenic Sites on the Middle East Respiratory Syndrome Coronavirus Spike Glycoprotein To Avoid Neutralization Escape. <i>Journal of Virology</i> , <b>2018</b> , 92,	6.6	119
10	Global site-specific analysis of glycoprotein N-glycan processing. <i>Nature Protocols</i> , <b>2018</b> , 13, 1196-1212	18.8	40
9	Stabilized coronavirus spikes are resistant to conformational changes induced by receptor recognition or proteolysis. <i>Scientific Reports</i> , <b>2018</b> , 8, 15701	4.9	259
8	Immunogenicity and structures of a rationally designed prefusion MERS-CoV spike antigen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E7348-E7357	11.5	615
7	Pre-fusion structure of a human coronavirus spike protein. <i>Nature</i> , <b>2016</b> , 531, 118-21	50.4	474
6	Structural basis for the neutralization of MERS-CoV by a human monoclonal antibody MERS-27. <i>Scientific Reports</i> , <b>2015</b> , 5, 13133	4.9	54
5	Identification of residues on human receptor DPP4 critical for MERS-CoV binding and entry. <i>Virology</i> , <b>2014</b> , 471-473, 49-53	3.6	32
4	Potent neutralization of MERS-CoV by human neutralizing monoclonal antibodies to the viral spike glycoprotein. <i>Science Translational Medicine</i> , <b>2014</b> , 6, 234ra59	17.5	165
3	Structure of MERS-CoV spike receptor-binding domain complexed with human receptor DPP4. <i>Cell Research</i> , <b>2013</b> , 23, 986-93	24.7	459
2	Receptor binding and proteolysis do not induce large conformational changes in the SARS-CoV spike		1
1	A combination of RBD and NTD neutralizing antibodies limits the generation of SARS-CoV-2 spike neutralization-escape mutants		2