

# Qiang Zhou

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

10,370  
citations

147566

31  
h-index

189595

50  
g-index

58  
all docs

58  
docs citations

58  
times ranked

19218  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2. <i>Science</i> , 2020, 367, 1444-1448.	6.0	4,319
2	A neutralizing human antibody binds to the N-terminal domain of the Spike protein of SARS-CoV-2. <i>Science</i> , 2020, 369, 650-655.	6.0	1,292
3	Structure of the voltage-gated calcium channel Cav1.1 at 3.6Å resolution. <i>Nature</i> , 2016, 537, 191-196.	13.7	398
4	AXL is a candidate receptor for SARS-CoV-2 that promotes infection of pulmonary and bronchial epithelial cells. <i>Cell Research</i> , 2021, 31, 126-140.	5.7	356
5	Structure of a eukaryotic voltage-gated sodium channel at near-atomic resolution. <i>Science</i> , 2017, 355, .	6.0	351
6	Structure of the human voltage-gated sodium channel Na <sup>v</sup> 1.4 in complex with $\beta$ 1. <i>Science</i> , 2018, 362, .	6.0	333
7	Structural and biochemical basis for induced self-propagation of NLRC4. <i>Science</i> , 2015, 350, 399-404.	6.0	282
8	Structure of the Nav1.4- $\beta$ 1 Complex from Electric Eel. <i>Cell</i> , 2017, 170, 470-482.e11.	13.5	272
9	Structural Insights into the Niemann-Pick C1 (NPC1)-Mediated Cholesterol Transfer and Ebola Infection. <i>Cell</i> , 2016, 165, 1467-1478.	13.5	266
10	Recognition of the amyloid precursor protein by human $\beta$ -secretase. <i>Science</i> , 2019, 363, .	6.0	229
11	Structure of the human LAT1-4F2hc heteromeric amino acid transporter complex. <i>Nature</i> , 2019, 568, 127-130.	13.7	217
12	Structural basis for the modulation of voltage-gated sodium channels by animal toxins. <i>Science</i> , 2018, 362, .	6.0	200
13	Structural basis of Notch recognition by human $\beta$ -secretase. <i>Nature</i> , 2019, 565, 192-197.	13.7	194
14	Structural basis for the recognition of Sonic Hedgehog by human Patched1. <i>Science</i> , 2018, 361, .	6.0	168
15	SARS-CoV-2 exacerbates proinflammatory responses in myeloid cells through C-type lectin receptors and Tweety family member 2. <i>Immunity</i> , 2021, 54, 1304-1319.e9.	6.6	115
16	Modulation of cardiac ryanodine receptor 2 by calmodulin. <i>Nature</i> , 2019, 572, 347-351.	13.7	110
17	The cryo-EM structure of the SF3b spliceosome complex bound to a splicing modulator reveals a pre-mRNA substrate competitive mechanism of action. <i>Genes and Development</i> , 2018, 32, 309-320.	2.7	89
18	Structural basis for the different states of the spike protein of SARS-CoV-2 in complex with ACE2. <i>Cell Research</i> , 2021, 31, 717-719.	5.7	77

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19	Engineered trimeric ACE2 binds viral spike protein and locks it in a "Three-up" conformation to potently inhibit SARS-CoV-2 infection. <i>Cell Research</i> , 2021, 31, 98-100.	5.7	76
20	Structure of the human plasma membrane Ca <sup>2+</sup> -ATPase 1 in complex with its obligatory subunit neuroplastin. <i>Nature Communications</i> , 2018, 9, 3623.	5.8	71
21	Neutralization mechanism of a human antibody with pan-coronavirus reactivity including SARS-CoV-2. <i>Nature Microbiology</i> , 2022, 7, 1063-1074.	5.9	63
22	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
23	ACE2-targeting monoclonal antibody as potent and broad-spectrum coronavirus blocker. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 315.	7.1	53
24	Molecular architecture of the luminal ring of the <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2020, 30, 532-540.	5.7	51
25	Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex by cryo-electron microscopy single particle analysis. <i>Cell Research</i> , 2020, 30, 520-531.	5.7	51
26	Structural mechanism of phospholipids translocation by MlaFEDB complex. <i>Cell Research</i> , 2020, 30, 1127-1135.	5.7	49
27	The structure of erastin-bound xCT <sup>4F2hc</sup> complex reveals molecular mechanisms underlying erastin-induced ferroptosis. <i>Cell Research</i> , 2022, 32, 687-690.	5.7	48
28	Structural and Functional Characterization of Ryanodine Receptor-Natratin Toxin Interaction. <i>Biophysical Journal</i> , 2008, 95, 4289-4299.	0.2	46
29	A structure of human Scap bound to Insig-2 suggests how their interaction is regulated by sterols. <i>Science</i> , 2021, 371, .	6.0	44
30	Structure of the cytoplasmic ring of the <i>Xenopus laevis</i> nuclear pore complex. <i>Science</i> , 2022, 376, .	6.0	44
31	Cryo-EM structure of SNAP-SNARE assembly in 20S particle. <i>Cell Research</i> , 2015, 25, 551-560.	5.7	42
32	Mechanism of substrate transport and inhibition of the human LAT1-4F2hc amino acid transporter. <i>Cell Discovery</i> , 2021, 7, 16.	3.1	40
33	Cryo-EM structures of the full-length human KCC2 and KCC3 cation-chloride cotransporters. <i>Cell Research</i> , 2021, 31, 482-484.	5.7	31
34	Cryo-EM structure of the human heteromeric amino acid transporter b <sup>0,+</sup> AT-rBAT. <i>Science Advances</i> , 2020, 6, eaay6379.	4.7	27
35	Mechanistic insights into the SNARE complex disassembly. <i>Science Advances</i> , 2019, 5, eaau8164.	4.7	25
36	Cryo-EM structures of <i>Acinetobacter baumannii</i> glycerophospholipid transporter. <i>Cell Discovery</i> , 2020, 6, 86.	3.1	23

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37	Novel sarbecovirus bispecific neutralizing antibodies with exceptional breadth and potency against currently circulating SARS-CoV-2 variants and sarbecoviruses. <i>Cell Discovery</i> , 2022, 8, 36.	3.1	22
38	Cryo-EM structure of human Wntless in complex with Wnt3a. <i>Nature Communications</i> , 2021, 12, 4541.	5.8	20
39	Structural biology in the fight against COVID-19. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 2-7.	3.6	20
40	Cryo-EM structure of the nuclear ring from <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2022, 32, 349-358.	5.7	19
41	Broad ultra-potent neutralization of SARS-CoV-2 variants by monoclonal antibodies specific to the tip of RBD. <i>Cell Discovery</i> , 2022, 8, 16.	3.1	18
42	Cryo-EM structure of the inner ring from the <i>Xenopus laevis</i> nuclear pore complex. <i>Cell Research</i> , 2022, 32, 451-460.	5.7	15
43	Broadly neutralizing antibodies against Omicron-included SARS-CoV-2 variants induced by vaccination. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 139.	7.1	14
44	Structural insight into the substrate recognition and transport mechanism of the human LAT2 $\alpha$ 4F2hc complex. <i>Cell Discovery</i> , 2020, 6, 82.	3.1	13
45	ACE2, BOAT1, and SARS-CoV-2 spike protein: Structural and functional implications. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102388.	2.6	10
46	Cryo-EM structures of recombinant human sodium-potassium pump determined in three different states. <i>Nature Communications</i> , 2022, 13, .	5.8	10
47	Particle segmentation algorithm for flexible single particle reconstruction. <i>Biophysics Reports</i> , 2017, 3, 43-55.	0.2	9
48	Structural Characterization of the Complex of SecB and Metallothionein-Labeled proOmpA by Cryo-Electron Microscopy. <i>PLoS ONE</i> , 2012, 7, e47015.	1.1	6
49	Cryo-EM structure of L-fucokinase/GDP-fucose pyrophosphorylase (FKP) in <i>Bacteroides fragilis</i> . <i>Protein and Cell</i> , 2019, 10, 365-369.	4.8	6