

Yuanyuan Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

6,408
citations

516215

16
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676716

22
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28
all docs

28
docs citations

28
times ranked

14154
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	TFPI is a colonic crypt receptor for TcdB from hypervirulent clade 2 <i>C.Âdifficile</i> . <i>Cell</i> , 2022, 185, 980-994.e15.	13.5	30
3	The structure of erastin-bound xCTâ€“4F2hc complexÂreveals molecular mechanisms underlying erastin-induced ferroptosis. <i>Cell Research</i> , 2022, 32, 687-690.	5.7	48
4	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
5	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
6	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
7	Structural and functional analysis of an inter-Spike bivalent neutralizing antibody against SARS-CoV-2 variants. <i>IScience</i> , 2022, 25, 104431.	1.9	3
8	Engineered trimeric ACE2 binds viral spike protein and locks it in â€œThree-upâ€–conformation to potently inhibit SARS-CoV-2 infection. <i>Cell Research</i> , 2021, 31, 98-100.	5.7	76
9	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
10	Functional analyses of epidemic <i>Clostridioides difficile</i> toxin B variants reveal their divergence in utilizing receptors and inducing pathology. <i>PLoS Pathogens</i> , 2021, 17, e1009197.	2.1	23
11	Mechanism of substrate transport and inhibition of the human LAT1-4F2hc amino acid transporter. <i>Cell Discovery</i> , 2021, 7, 16.	3.1	40
12	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
13	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
14	Cryo-EM structure of human Wntless in complex with Wnt3a. <i>Nature Communications</i> , 2021, 12, 4541.	5.8	20
15	ACE2-targeting monoclonal antibody as potent and broad-spectrum coronavirus blocker. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 315.	7.1	53
16	Structural mechanism of phospholipids translocation by MlaFEDB complex. <i>Cell Research</i> , 2020, 30, 1127-1135.	5.7	49
17	Structural insights into the gating mechanism of human SLC26A9 mediated by its C-terminal sequence. <i>Cell Discovery</i> , 2020, 6, 55.	3.1	43
18	Cryo-EM structures of <i>Acinetobacter baumannii</i> glycerophospholipid transporter. <i>Cell Discovery</i> , 2020, 6, 86.	3.1	23

#	ARTICLE	IF	CITATIONS
19	A neutralizing human antibody binds to the N-terminal domain of the Spike protein of SARS-CoV-2. Science, 2020, 369, 650-655.	6.0	1,292
20	Clinical Significance of the Correlation between Changes in the Major Intestinal Bacteria Species and COVID-19 Severity. Engineering, 2020, 6, 1178-1184.	3.2	116
21	Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2. Science, 2020, 367, 1444-1448.	6.0	4,319