Xuejun Cai Zhang

List of Publications by Year
in descending order

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58	2,033	279798	265206
papers	citations	23 h-index	42 g-index

60	60	60	3507
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural basis for lipopolysaccharide insertion in the bacterial outer membrane. Nature, 2014, 511, 108-111.	27.8	221
2	Structure of the YajR transporter suggests a transport mechanism based on the conserved motif A. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14664-14669.	7.1	174
3	Substrate-bound structure of the E. coli multidrug resistance transporter MdfA. Cell Research, 2015, 25, 1060-1073.	12.0	149
4	Structure of the APPL1 BAR-PH domain and characterization of its interaction with Rab5. EMBO Journal, 2007, 26, 3484-3493.	7.8	119
5	Energy coupling mechanisms of <scp>MFS</scp> transporters. Protein Science, 2015, 24, 1560-1579.	7.6	101
6	Structure of the nonameric bacterial amyloid secretion channel. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5439-44.	7.1	87
7	<scp>BH</scp> 3â€inâ€groove dimerization initiates and helix 9 dimerization expands Bax pore assembly in membranes. EMBO Journal, 2016, 35, 208-236.	7.8	81
8	Crystal structure of E. coli lipoprotein diacylglyceryl transferase. Nature Communications, 2016, 7, 10198.	12.8	81
9	Molecular mechanism of substrate recognition and transport by the AtSWEET13 sugar transporter. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10089-10094.	7.1	75
10	Crystal Structure of the E.Âcoli Peptide Transporter YbgH. Structure, 2014, 22, 1152-1160.	3.3	66
11	After Embedding in Membranes Antiapoptotic Bcl-XL Protein Binds Both Bcl-2 Homology Region 3 and Helix 1 of Proapoptotic Bax Protein to Inhibit Apoptotic Mitochondrial Permeabilization. Journal of Biological Chemistry, 2014, 289, 11873-11896.	3.4	61
12	Structural basis for signal recognition and transduction by platelet-activating-factor receptor. Nature Structural and Molecular Biology, 2018, 25, 488-495.	8.2	58
13	Crystal structure of lipid phosphatase Escherichia coli phosphatidylglycerophosphate phosphatase B. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7636-7640.	7.1	52
14	Structure and mechanism of the human NHE1-CHP1 complex. Nature Communications, 2021, 12, 3474.	12.8	45
15	Structural basis for modulation of human NaV1.3 by clinical drug and selective antagonist. Nature Communications, 2022, 13, 1286.	12.8	36
16	Closed-state inactivation and pore-blocker modulation mechanisms of human CaV2.2. Cell Reports, 2021, 37, 109931.	6.4	35
17	Crystal structure of 1,3Gal43A, an exo-Î²-1,3-galactanase from Clostridium thermocellum. Journal of Structural Biology, 2012, 180, 447-457.	2.8	32
18	Crystal structure of E. coli apolipoprotein N-acyl transferase. Nature Communications, 2017, 8, 15948.	12.8	31

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19	Proton transfer-mediated GPCR activation. Protein and Cell, 2015, 6, 12-17.	11.0	28
20	Structure of YidC from Thermotoga maritima and its implications for YidCâ€mediated membrane protein insertion. FASEB Journal, 2018, 32, 2411-2421.	0.5	28
21	An efficient strategy for high throughput screening of recombinant integral membrane protein expression and stability. Protein Expression and Purification, 2011, 78, 6-13.	1.3	27
22	Crystal structures of NAC domains of human nascent polypeptide-associated complex (NAC) and its Î±NAC subunit. Protein and Cell, 2010, 1, 406-416.	11.0	26
23	GPCR activation: protonation and membrane potential. Protein and Cell, 2013, 4, 747-760.	11.0	26
24	From membrane tension to channel gating: A principal energy transfer mechanism for mechanosensitive channels. Protein Science, 2016, 25, 1954-1964.	7.6	25
25	Single-molecule fluorescence studies on the conformational change of the ABC transporter MsbA. Biophysics Reports, 2018, 4, 153-165.	0.8	25
26	Crystal structure of the hexamer of human heat shock factor binding protein 1. Proteins: Structure, Function and Bioinformatics, 2009, 75, 1-11.	2.6	24
27	Thermodynamics of voltage-gated ion channels. Biophysics Reports, 2018, 4, 300-319.	0.8	22
28	<scp>Cryoâ€</scp>electron microscopy structure of human <scp>ABCB6</scp> transporter. Protein Science, 2020, 29, 2363-2374.	7.6	22
29	Kainate receptor modulation by NETO2. Nature, 2021, 599, 325-329.	27.8	20
30	Thermodynamics of ABC transporters. Protein and Cell, 2016, 7, 17-27.	11.0	19
31	Crystal structure of dopamine receptor D4 bound to the subtype selective ligand, L745870. ELife, 2019, 8, .	6.0	19
32	Interplay between the electrostatic membrane potential and conformational changes in membrane proteins. Protein Science, 2019, 28, 502-512.	7.6	18
33	Energy coupling mechanisms of AcrB-like RND transporters. Biophysics Reports, 2017, 3, 73-84.	0.8	15
34	Why is dimerization essential for class-C GPCR function? New insights from mGluR1 crystal structure analysis. Protein and Cell, 2014, 5, 492-495.	11.0	14
35	Crystal Structure of TetR Family Repressor AlkX from Dietzia sp. Strain DQ12-45-1b Implicated in Biodegradation of n -Alkanes. Applied and Environmental Microbiology, 2017, 83, .	3.1	12
36	Thermodynamic secrets of multidrug resistance: A new take on transport mechanisms of secondary active antiporters. Protein Science, 2018, 27, 595-613.	7.6	11

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37	smFRET Probing Reveals Substrate-Dependent Conformational Dynamics of E.Âcoli Multidrug MdfA. Biophysical Journal, 2019, 116, 2296-2303.	0.5	11
38	Cryoâ€electron microscopy structure of <scp>CLHM1</scp> ion channel from <scp>Caenorhabditis elegans</scp>. Protein Science, 2020, 29, 1803-1815.	7.6	11
39	Structure of human glycosylphosphatidylinositol transamidase. Nature Structural and Molecular Biology, 2022, 29, 203-209.	8.2	11
40	Structural basis of autoinhibition of the human NHE3-CHP1 complex. Science Advances, 2022, 8, .	10.3	11
41	How does a Î²-barrel integral membrane protein insert into the membrane?. Protein and Cell, 2016, 7, 471-477.	11.0	10
42	Uniporter substrate binding and transport: reformulating mechanistic questions. Biophysics Reports, 2016, 2, 45-54.	0.8	10
43	Thermodynamic aspects of ATP hydrolysis of actomyosin complex. Biophysics Reports, 2016, 2, 87-94.	0.8	10
44	P-type ATPases use a domain-association mechanism to couple ATP hydrolysis to conformational change. Biophysics Reports, 2019, 5, 167-175.	0.8	9
45	Atomic resolution structure of the E. coli YajR transporter YAM domain. Biochemical and Biophysical Research Communications, 2014, 450, 929-935.	2.1	8
46	Proton transfer during class-A GPCR activation: do the CWxP motif and the membrane potential act in concert?. Biophysics Reports, 2018, 4, 115-122.	0.8	8
47	Structure of theDietziaMrp complex reveals molecular mechanism of this giant bacterial sodium proton pump. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 31166-31176.	7.1	8
48	Structural dynamics of GiÎ± protein revealed by single molecule FRET. Biochemical and Biophysical Research Communications, 2017, 491, 603-608.	2.1	7
49	Crystal structure and biochemical studies of Brucella melitensis 5â€²-methylthioadenosine/S-adenosylhomocysteine nucleosidase. Biochemical and Biophysical Research Communications, 2014, 446, 965-970.	2.1	6
50	Energy-coupling mechanism of the multidrug resistance transporter AcrB: Evidence for membrane potential-driving hypothesis through mutagenic analysis. Protein and Cell, 2017, 8, 623-627.	11.0	6
51	Towards understanding the mechanisms of proton pumps in Complex-I of the respiratory chain. Biophysics Reports, 2019, 5, 219-234.	0.8	5
52	Thermodynamics of GPCR activation. Biophysics Reports, 2015, 1, 115-119.	0.8	4
53	How does the chemical potential of the substrate drive a uniporter?. Protein Science, 2016, 25, 933-937.	7.6	4
54	Structural basis for distinct quality control mechanisms of GABA _B receptor during evolution. FASEB Journal, 2020, 34, 16348-16363.	0.5	4

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55	How does transmembrane electrochemical potential drive the rotation of Fo motor in an ATP synthase?. Protein and Cell, 2015, 6, 784-791.	11.0	3
56	Crystal structure of cyclic nucleotide-binding-like protein from Brucella abortus. Biochemical and Biophysical Research Communications, 2015, 468, 647-652.	2.1	1
57	Energy coupling mechanism of FO in a rotary ATP synthase: a model update. Biophysics Reports, 2019, 5, 61-64.	0.8	1
58	Cysteine-based crosslinking approach for characterization of oligomeric pore-forming proteins in the mitochondrial membranes. Methods in Enzymology, 2021, 649, 371-396.	1.0	0