

Xuejun Cai Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/825987/publications.pdf>

Version: 2024-02-01

58
papers

2,033
citations

279798

23
h-index

265206

42
g-index

60
all docs

60
docs citations

60
times ranked

3507
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of human glycosylphosphatidylinositol transamidase. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 203-209.	8.2	11
2	Structural basis for modulation of human NaV1.3 by clinical drug and selective antagonist. <i>Nature Communications</i> , 2022, 13, 1286.	12.8	36
3	Structural basis of autoinhibition of the human NHE3-CHP1 complex. <i>Science Advances</i> , 2022, 8, .	10.3	11
4	Cysteine-based crosslinking approach for characterization of oligomeric pore-forming proteins in the mitochondrial membranes. <i>Methods in Enzymology</i> , 2021, 649, 371-396.	1.0	0
5	Structure and mechanism of the human NHE1-CHP1 complex. <i>Nature Communications</i> , 2021, 12, 3474.	12.8	45
6	Kainate receptor modulation by NETO2. <i>Nature</i> , 2021, 599, 325-329.	27.8	20
7	Closed-state inactivation and pore-blocker modulation mechanisms of human CaV2.2. <i>Cell Reports</i> , 2021, 37, 109931.	6.4	35
8	Cryo-electron microscopy structure of human ABCB6 transporter. <i>Protein Science</i> , 2020, 29, 2363-2374.	7.6	22
9	Structure of the <i>Dietzia</i> Mrp complex reveals molecular mechanism of this giant bacterial sodium proton pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31166-31176.	7.1	8
10	Structural basis for distinct quality control mechanisms of GABA _B receptor during evolution. <i>FASEB Journal</i> , 2020, 34, 16348-16363.	0.5	4
11	Cryo-electron microscopy structure of CLHM1 ion channel from <i>Caenorhabditis elegans</i> . <i>Protein Science</i> , 2020, 29, 1803-1815.	7.6	11
12	Interplay between the electrostatic membrane potential and conformational changes in membrane proteins. <i>Protein Science</i> , 2019, 28, 502-512.	7.6	18
13	P-type ATPases use a domain-association mechanism to couple ATP hydrolysis to conformational change. <i>Biophysics Reports</i> , 2019, 5, 167-175.	0.8	9
14	Towards understanding the mechanisms of proton pumps in Complex-I of the respiratory chain. <i>Biophysics Reports</i> , 2019, 5, 219-234.	0.8	5
15	Energy coupling mechanism of FO in a rotary ATP synthase: a model update. <i>Biophysics Reports</i> , 2019, 5, 61-64.	0.8	1
16	smFRET Probing Reveals Substrate-Dependent Conformational Dynamics of <i>E. coli</i> Multidrug MdfA. <i>Biophysical Journal</i> , 2019, 116, 2296-2303.	0.5	11
17	Crystal structure of dopamine receptor D4 bound to the subtype selective ligand, L745870. <i>ELife</i> , 2019, 8, .	6.0	19
18	Structure of YidC from <i>Thermotoga maritima</i> and its implications for YidC-mediated membrane protein insertion. <i>FASEB Journal</i> , 2018, 32, 2411-2421.	0.5	28

#	ARTICLE	IF	CITATIONS
19	Thermodynamic secrets of multidrug resistance: A new take on transport mechanisms of secondary active antiporters. <i>Protein Science</i> , 2018, 27, 595-613.	7.6	11
20	Thermodynamics of voltage-gated ion channels. <i>Biophysics Reports</i> , 2018, 4, 300-319.	0.8	22
21	Proton transfer during class-A GPCR activation: do the CWxP motif and the membrane potential act in concert?. <i>Biophysics Reports</i> , 2018, 4, 115-122.	0.8	8
22	Single-molecule fluorescence studies on the conformational change of the ABC transporter MsbA. <i>Biophysics Reports</i> , 2018, 4, 153-165.	0.8	25
23	Structural basis for signal recognition and transduction by platelet-activating-factor receptor. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 488-495.	8.2	58
24	Energy-coupling mechanism of the multidrug resistance transporter AcrB: Evidence for membrane potential-driving hypothesis through mutagenic analysis. <i>Protein and Cell</i> , 2017, 8, 623-627.	11.0	6
25	Molecular mechanism of substrate recognition and transport by the AtSWEET13 sugar transporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10089-10094.	7.1	75
26	Structural dynamics of Gii± protein revealed by single molecule FRET. <i>Biochemical and Biophysical Research Communications</i> , 2017, 491, 603-608.	2.1	7
27	Crystal Structure of TetR Family Repressor AlkX from <i>Dietzia</i> sp. Strain DQ12-45-1b Implicated in Biodegradation of <i>n</i> -Alkanes. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	12
28	Energy coupling mechanisms of AcrB-like RND transporters. <i>Biophysics Reports</i> , 2017, 3, 73-84.	0.8	15
29	Crystal structure of <i>E. coli</i> apolipoprotein N-acyl transferase. <i>Nature Communications</i> , 2017, 8, 15948.	12.8	31
30	How does the chemical potential of the substrate drive a uniporter?. <i>Protein Science</i> , 2016, 25, 933-937.	7.6	4
31	How does a β^2 -barrel integral membrane protein insert into the membrane?. <i>Protein and Cell</i> , 2016, 7, 471-477.	11.0	10
32	From membrane tension to channel gating: A principal energy transfer mechanism for mechanosensitive channels. <i>Protein Science</i> , 2016, 25, 1954-1964.	7.6	25
33	α -Groove dimerization initiates and helix 9 dimerization expands Bax pore assembly in membranes. <i>EMBO Journal</i> , 2016, 35, 208-236.	7.8	81
34	Uniporter substrate binding and transport: reformulating mechanistic questions. <i>Biophysics Reports</i> , 2016, 2, 45-54.	0.8	10
35	Thermodynamic aspects of ATP hydrolysis of actomyosin complex. <i>Biophysics Reports</i> , 2016, 2, 87-94.	0.8	10
36	Crystal structure of <i>E. coli</i> lipoprotein diacylglycerol transferase. <i>Nature Communications</i> , 2016, 7, 10198.	12.8	81

#	ARTICLE	IF	CITATIONS
37	Thermodynamics of ABC transporters. <i>Protein and Cell</i> , 2016, 7, 17-27.	11.0	19
38	Thermodynamics of GPCR activation. <i>Biophysics Reports</i> , 2015, 1, 115-119.	0.8	4
39	How does transmembrane electrochemical potential drive the rotation of Fo motor in an ATP synthase?. <i>Protein and Cell</i> , 2015, 6, 784-791.	11.0	3
40	Energy coupling mechanisms of <i>MFS</i> transporters. <i>Protein Science</i> , 2015, 24, 1560-1579.	7.6	101
41	Crystal structure of cyclic nucleotide-binding-like protein from <i>Brucella abortus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2015, 468, 647-652.	2.1	1
42	Proton transfer-mediated GPCR activation. <i>Protein and Cell</i> , 2015, 6, 12-17.	11.0	28
43	Substrate-bound structure of the <i>E. coli</i> multidrug resistance transporter MdfA. <i>Cell Research</i> , 2015, 25, 1060-1073.	12.0	149
44	Crystal structure of lipid phosphatase <i>Escherichia coli</i> phosphatidylglycerophosphate phosphatase B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7636-7640.	7.1	52
45	Structure of the nonameric bacterial amyloid secretion channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5439-44.	7.1	87
46	Crystal structure and biochemical studies of <i>Brucella melitensis</i> 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 446, 965-970.	2.1	6
47	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. <i>Journal of Biological Chemistry</i> , 2014, 289, 11873-11896.	3.4	61
48	Atomic resolution structure of the <i>E. coli</i> YajR transporter YAM domain. <i>Biochemical and Biophysical Research Communications</i> , 2014, 450, 929-935.	2.1	8
49	Crystal Structure of the <i>E. coli</i> Peptide Transporter YbgH. <i>Structure</i> , 2014, 22, 1152-1160.	3.3	66
50	Why is dimerization essential for class-C GPCR function? New insights from mGluR1 crystal structure analysis. <i>Protein and Cell</i> , 2014, 5, 492-495.	11.0	14
51	Structural basis for lipopolysaccharide insertion in the bacterial outer membrane. <i>Nature</i> , 2014, 511, 108-111.	27.8	221
52	GPCR activation: protonation and membrane potential. <i>Protein and Cell</i> , 2013, 4, 747-760.	11.0	26
53	Structure of the YajR transporter suggests a transport mechanism based on the conserved motif A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14664-14669.	7.1	174
54	Crystal structure of 1,3Gal43A, an exo- β -1,3-galactanase from <i>Clostridium thermocellum</i> . <i>Journal of Structural Biology</i> , 2012, 180, 447-457.	2.8	32

#	ARTICLE	IF	CITATIONS
55	An efficient strategy for high throughput screening of recombinant integral membrane protein expression and stability. <i>Protein Expression and Purification</i> , 2011, 78, 6-13.	1.3	27
56	Crystal structures of NAC domains of human nascent polypeptide-associated complex (NAC) and its $\hat{I}\pm$ NAC subunit. <i>Protein and Cell</i> , 2010, 1, 406-416.	11.0	26
57	Crystal structure of the hexamer of human heat shock factor binding protein 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 1-11.	2.6	24
58	Structure of the APPL1 BAR-PH domain and characterization of its interaction with Rab5. <i>EMBO Journal</i> , 2007, 26, 3484-3493.	7.8	119