Yan Zhao

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4477709/publications.pdf

Version: 2024-02-01

29	1,781	18	29
papers	citations	h-index	g-index
32	32	32	2835
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.	13.7	221
2	Structure of the Cardiac Sodium Channel. Cell, 2020, 180, 122-134.e10.	13.5	217
3	Substrate-bound structure of the E. coli multidrug resistance transporter MdfA. Cell Research, 2015, 25, 1060-1073.	5.7	149
4	Architecture and subunit arrangement of native AMPA receptors elucidated by cryo-EM. Science, 2019, 364, 355-362.	6.0	134
5	Activation and Desensitization Mechanism of AMPA Receptor-TARP Complex by Cryo-EM. Cell, 2017, 170, 1234-1246.e14.	13.5	111
6	Energy coupling mechanisms of <scp>MFS</scp> transporters. Protein Science, 2015, 24, 1560-1579.	3.1	101
7	Architecture of fully occupied GluA2 AMPA receptor–TARP complex elucidated by cryo-EM. Nature, 2016, 536, 108-111.	13.7	100
8	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.	3.3	87
9	Homeostatic Control of Innate Lung Inflammation by Vici Syndrome Gene Epg5 and Additional Autophagy Genes Promotes Influenza Pathogenesis. Cell Host and Microbe, 2016, 19, 102-113.	5.1	83
10	Crystal structure of E. coli lipoprotein diacylglyceryl transferase. Nature Communications, 2016, 7, 10198.	5.8	81
11	Crystal Structure of the E.Âcoli Peptide Transporter YbgH. Structure, 2014, 22, 1152-1160.	1.6	66
12	Dapper1 promotes autophagy by enhancing the Beclin1-Vps34-Atg14L complex formation. Cell Research, 2014, 24, 912-924.	5.7	57
13	Crystal structure of lipid phosphatase <i>Escherichia coli</i> phosphatidylglycerophosphate phosphatase B. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7636-7640.	3.3	52
14	Structure and mechanism of the human NHE1-CHP1 complex. Nature Communications, 2021, 12, 3474.	5.8	45
15	Structural basis for modulation of human NaV1.3 by clinical drug and selective antagonist. Nature Communications, 2022, 13, 1286.	5.8	36
16	Closed-state inactivation and pore-blocker modulation mechanisms of human CaV2.2. Cell Reports, 2021, 37, 109931.	2.9	35
17	Structure of YidC from <i>Thermotoga maritima</i> and its implications for YidCâ€mediated membrane protein insertion. FASEB Journal, 2018, 32, 2411-2421.	0.2	28
18	Structure, gating, and pharmacology of human CaV3.3 channel. Nature Communications, 2022, 13, 2084.	5.8	22

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19	SLC-30A9 is required for Zn $<$ sup $>$ 2+ $<$ /sup $>$ homeostasis, Zn $<$ sup $>$ 2+ $<$ /sup $>$ mobilization, and mitochondrial health. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	21
20	TMEM120A contains a specific coenzyme A-binding site and might not mediate poking- or stretch-induced channel activities in cells. ELife, $2021,10,10$	2.8	20
21	Kainate receptor modulation by NETO2. Nature, 2021, 599, 325-329.	13.7	20
22	Thermodynamics of ABC transporters. Protein and Cell, 2016, 7, 17-27.	4.8	19
23	Etoposide-induced protein 2.4 functions as a regulator of the calcium ATPase and protects pancreatic \hat{l}^2 -cell survival. Journal of Biological Chemistry, 2018, 293, 10128-10140.	1.6	18
24	Structural basis of ligand binding modes of human EAAT2. Nature Communications, 2022, 13, .	5.8	12
25	Structure of human glycosylphosphatidylinositol transamidase. Nature Structural and Molecular Biology, 2022, 29, 203-209.	3.6	11
26	Structural basis of autoinhibition of the human NHE3-CHP1 complex. Science Advances, 2022, 8, .	4.7	11
27	Atomic resolution structure of the E. coli YajR transporter YAM domain. Biochemical and Biophysical Research Communications, 2014, 450, 929-935.	1.0	8
28	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.	3.3	8
29	Crystal structure and biochemical studies of Brucella melitensis 5′-methylthioadenosine/S-adenosylhomocysteine nucleosidase. Biochemical and Biophysical Research Communications, 2014, 446, 965-970.	1.0	6