Kai-En Chen

List of Publications by Year
in descending order

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19 papers	1,634 citations	687363 13 h-index	752698 20 g-index
23 all docs	23 docs citations	23 times ranked	3888 citing authors

#	Article	IF	Citations
1	Towards a generic prototyping approach for therapeutically-relevant peptides and proteins in a cell-free translation system. Nature Communications, 2022, 13, 260.	12.8	5
2	SNX27â€“Retromer directly binds ESCPE-1 to transfer cargo proteins during endosomal recycling. PLoS Biology, 2022, 20, e3001601.	5.6	24
3	Community-Wide Experimental Evaluation of the PROSS Stability-Design Method. Journal of Molecular Biology, 2021, 433, 166964.	4.2	42
4	Structural basis for the binding of the cancer targeting scorpion toxin, ClTx, to the vascular endothelia growth factor receptor neuropilin-1. Current Research in Structural Biology, 2021, 3, 179-186.	2.2	3
5	De novo macrocyclic peptides for inhibiting, stabilizing, and probing the function of the retromer endosomal trafficking complex. Science Advances, 2021, 7, eabg4007.	10.3	11
6	Neuropilin-1 is a host factor for SARS-CoV-2 infection. Science, 2020, 370, 861-865.	12.6	1,015
7	Drosophila Snazarus Regulates a Lipid Droplet Population at Plasma Membrane-Droplet Contacts in Adipocytes. Developmental Cell, 2019, 50, 557-572.e5.	7.0	72
8	Towards a molecular understanding of endosomal trafficking by Retromer and Retriever. Traffic, 2019, 20, 465-478.	2.7	134
9	Classification of the human phox homology (PX) domains based on their phosphoinositide binding specificities. Nature Communications, 2019, 10, 1528.	12.8	101
10	Molecular Basis for Membrane Recruitment by the PX and C2 Domains of Class II Phosphoinositide 3-Kinase-C2Î±. Structure, 2018, 26, 1612-1625.e4.	3.3	25
11	Structural insights into the architecture and membrane interactions of the conserved COMMD proteins. ELife, 2018, 7, .	6.0	28
12	Substrate Specificity and Plasticity of FERM-Containing Protein Tyrosine Phosphatases. Structure, 2015, 23, 653-664.	3.3	20
13	Reciprocal allosteric regulation of p38Î³ and PTPN3 involves a PDZ domainâ€“modulated complex formation. Science Signaling, 2014, 7, ra98.	3.6	25
14	Backbone resonance assignments of the monomeric DUF59 domain of human Fam96a. Biomolecular NMR Assignments, 2013, 7, 117-120.	0.8	8
15	The structure of the caspase recruitment domain of BinCARD reveals that all three cysteines can be oxidized. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 774-784.	2.5	13
16	Low-resolution solution structures of Munc18:Syntaxin protein complexes indicate an open binding mode driven by the Syntaxin N-peptide. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9816-9821.	7.1	59
17	The 1.2â€…Ã… resolution crystal structure of TcpG, theVibrio choleraeDsbA disulfide-forming protein required for pilus and cholera-toxin production. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1290-1302.	2.5	20
18	The mammalian DUF59 protein Fam96a forms two distinct types of domain-swapped dimer. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 637-648.	2.5	22

#	Article	IF	Citations
19	Interaction between Plate Make and Protein in Protein Crystallisation Screening. PLoS ONE, 2009, 4, e7851.	2.5	2