Minglei Zhao

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Artificial intelligence advances for de novo molecular structure modeling in cryoâ€electron microscopy. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1542.	6.2	15
2	Structural basis for the mechanisms of human presequence protease conformational switch and substrate recognition. Nature Communications, 2022, 13, 1833.	5.8	4
3	A novel membrane complex is required for docking and regulated exocytosis of lysosome-related organelles in Tetrahymena thermophila. PLoS Genetics, 2022, 18, e1010194.	1.5	6
4	Selective regulation of human TRAAK channels by biologically active phospholipids. Nature Chemical Biology, 2021, 17, 89-95.	3.9	24
5	Seesaw conformations of Npl4 in the human p97 complex and the inhibitory mechanism of a disulfiram derivative. Nature Communications, 2021, 12, 121.	5.8	49
6	Molecular assemblies of the catalytic domain of SOS with KRas and oncogenic mutants. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
7	Structural analysis of Mycobacterium tuberculosis M13 metalloprotease Zmp1 open states. Structure, 2021, 29, 709-720.e3.	1.6	3
8	Mechanistic insight into substrate processing and allosteric inhibition of human p97. Nature Structural and Molecular Biology, 2021, 28, 614-625.	3.6	56
9	K29-linked ubiquitin signaling regulates proteotoxic stress response and cell cycle. Nature Chemical Biology, 2021, 17, 896-905.	3.9	40
10	Structural insights into Ubr1-mediated N-degron polyubiquitination. Nature, 2021, 600, 334-338.	13.7	54
11	Structural basis for adhesion G protein-coupled receptor Gpr126 function. Nature Communications, 2020, 11, 194.	5.8	45
12	Alternative splicing controls teneurin-latrophilin interaction and synapse specificity by a shape-shifting mechanism. Nature Communications, 2020, 11, 2140.	5.8	36
13	Structural basis for reversible amyloids of hnRNPA1 elucidates their role in stress granule assembly. Nature Communications, 2019, 10, 2006.	5.8	157
14	Atomic structures of FUS LC domain segments reveal bases for reversible amyloid fibril formation. Nature Structural and Molecular Biology, 2018, 25, 341-346.	3.6	185
15	Stem cell heterogeneity drives the parasitic life cycle of Schistosoma mansoni. ELife, 2018, 7, .	2.8	70
16	NSF-mediated disassembly of on- and off-pathway SNARE complexes and inhibition by complexin. ELife, 2018, 7, .	2.8	34
17	Structural principles of SNARE complex recognition by the AAA+ protein NSF. ELife, 2018, 7, .	2.8	67
18	SNAREâ€Reconstituted Liposomes as Controllable Zeptoliter Nanoreactors for Macromolecules. Advanced Biology, 2017, 1, e1600018.	3.0	11

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19	A Proteoliposome Method for Assessing Nanotoxicity on Synaptic Fusion and Membrane Integrity. Small Methods, 2017, 1, 1700207.	4.6	10
20	Molecular Mechanisms of Synaptic Vesicle Priming by Munc13 and Munc18. Neuron, 2017, 95, 591-607.e10.	3.8	185
21	The primed SNARE–complexin–synaptotagmin complex for neuronal exocytosis. Nature, 2017, 548, 420-425.	13.7	229
22	N-terminal domain of complexin independently activates calcium-triggered fusion. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4698-E4707.	3.3	44
23	Ketones block amyloid entry and improve cognition in an Alzheimer's model. Neurobiology of Aging, 2016, 39, 25-37.	1.5	107
24	Recent Advances in Deciphering the Structure and Molecular Mechanism of the AAA+ ATPase N-Ethylmaleimide-Sensitive Factor (NSF). Journal of Molecular Biology, 2016, 428, 1912-1926.	2.0	47
25	Complexin induces a conformational change at the membrane-proximal C-terminal end of the SNARE complex. ELife, 2016, 5, .	2.8	36
26	Advances in X-ray free electron laser (XFEL) diffraction data processing applied to the crystal structure of the synaptotagmin-1 / SNARE complex. ELife, 2016, 5, .	2.8	28
27	ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes. Nature, 2015, 520, 563-566.	13.7	460
28	Mechanistic insights into the recycling machine of the SNARE complex. Nature, 2015, 518, 61-67.	13.7	216
29	<i>Data Exploration Toolkit</i> for serial diffraction experiments. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 352-356.	2.5	28
30	Architecture of the synaptotagmin–SNARE machinery for neuronal exocytosis. Nature, 2015, 525, 62-67.	13.7	268
31	Complexin-1 Enhances the On-Rate of Vesicle Docking via Simultaneous SNARE and Membrane Interactions. Journal of the American Chemical Society, 2013, 135, 15274-15277.	6.6	49
32	Studying proteinâ€reconstituted proteoliposome fusion with content indicators in vitro. BioEssays, 2013, 35, 658-665.	1.2	24
33	Structure-based discovery of fiber-binding compounds that reduce the cytotoxicity of amyloid beta. ELife, 2013, 2, e00857.	2.8	94
34	Out-of-register β-sheets suggest a pathway to toxic amyloid aggregates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20913-20918.	3.3	184
35	Amyloid β-sheet mimics that antagonize protein aggregation and reduce amyloid toxicity. Nature Chemistry, 2012, 4, 927-933.	6.6	213
36	Atomic View of a Toxic Amyloid Small Oligomer. Science, 2012, 335, 1228-1231.	6.0	518

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37	Direct visualization of the interaction between pilin and exopolysaccharides of Myxococcus xanthus with eGFP-fused PilA protein. FEMS Microbiology Letters, 2012, 326, 23-30.	0.7	21
38	Molecular basis for amyloid-β polymorphism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16938-16943.	3.3	383
39	Structures of segments of αâ€synuclein fused to maltoseâ€binding protein suggest intermediate states during amyloid formation. Protein Science, 2011, 20, 996-1004.	3.1	32
40	An approach to crystallizing proteins by metalâ€mediated synthetic symmetrization. Protein Science, 2011, 20, 1876-1890.	3.1	63
41	High-Resolution Functional Profiling of a Gammaherpesvirus <i>RTA</i> Locus in the Context of the Viral Genome. Journal of Virology, 2009, 83, 1811-1822.	1.5	6
42	The activation of lytic replication of Epstein-Barr virus by baculovirus-mediated gene transduction. Archives of Virology, 2006, 151, 2047-2053.	0.9	9