Zhi-yong Zhang

List of Publications by Year
in descending order

50 papers	1,439 citations	361413 20 h-index	345221 36 g-index
50 all docs	50 docs citations	50 times ranked	2013 citing authors

#	Article	IF	Citations
1	The O2-ZmGRAS11 transcriptional regulatory network orchestrates the coordination of endosperm cell expansion and grain filling inÂmaize. Molecular Plant, 2022, 15, 468-487.	8.3	25
2	Fragment-Based Discovery of AF9 YEATS Domain Inhibitors. International Journal of Molecular Sciences, 2022, 23, 3893.	4.1	3
3	Structural insights into the activation of autoinhibited human lipid flippase ATP8B1 upon substrate binding. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2118656119.	7.1	15
4	Halophilic to mesophilic adaptation of ubiquitinâ€like proteins. FEBS Letters, 2021, 595, 521-531.	2.8	1
5	Integrating an Enhanced Sampling Method and Small-Angle X-Ray Scattering to Study Intrinsically Disordered Proteins. Frontiers in Molecular Biosciences, 2021, 8, 621128.	3.5	2
6	Ligand binding and release investigated by contact-guided iterative multiple independent molecular dynamics simulations. Chinese Journal of Chemical Physics, 2021, 34, 334-342.	1.3	0
7	Choice of force fields and water models for sampling solution conformations of bacteriophage T4 lysozyme. Chinese Journal of Chemical Physics, 2021, 34, 487-496.	1.3	0
8	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. Nature Chemical Biology, 2021, 17, 1314-1323.	8.0	29
9	Molecular mechanism of histone variant H2A.B on stability and assembly of nucleosome and chromatin structures. Epigenetics and Chromatin, 2020, 13, 28.	3.9	12
10	Conformational Selection in Ligand Recognition by the First Tudor Domain of PHF20L1. Journal of Physical Chemistry Letters, 2020, 11, 7932-7938.	4.6	3
11	Functional Characterization and Structural Basis of an Efficient Di-C-glycosyltransferase from Glycyrrhiza glabra. Journal of the American Chemical Society, 2020, 142, 3506-3512.	13.7	76
12	Structural insights into repression of the Pneumococcal fatty acid synthesis pathway by repressor FabT and coâ€repressor acylâ€ACP. FEBS Letters, 2019, 593, 2730-2741.	2.8	20
13	Biochemical characterization of G64W mutant of acidic beta-crystallin 4. Experimental Eye Research, 2019, 186, 107712.	2.6	5
14	Highly Promiscuous Flavonoid 3-O-Glycosyltransferase from Scutellaria baicalensis. Organic Letters, 2019, 21, 2241-2245.	4.6	50
15	Backmapping from Multiresolution Coarse-Grained Models to Atomic Structures of Large Biomolecules by Restrained Molecular Dynamics Simulations Using Bayesian Inference. Journal of Chemical Theory and Computation, 2019, 15, 3344-3353.	5.3	41
16	Structural insight into the unique ds<scp>DNA</scp> binding topology of the human <scp>ORC</scp>2 wing helix domain. FEBS Journal, 2019, 286, 2726-2736.	4.7	2
17	Aurora-A mediated phosphorylation of LDHB promotes glycolysis and tumor progression by relieving the substrate-inhibition effect. Nature Communications, 2019, 10, 5566.	12.8	66
18	Electrostatic interactions determine entrance/release order of substrates in the catalytic cycle of adenylate kinase. Proteins: Structure, Function and Bioinformatics, 2019, 87, 337-347.	2.6	7

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19	Coordinating carbon and nitrogen metabolic signaling through the cyanobacterial global repressor NdhR. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 403-408.	7.1	65
20	Mitosis-specific acetylation tunes Ran effector binding for chromosome segregation. Journal of Molecular Cell Biology, 2018, 10, 18-32.	3.3	32
21	Dynamic Nature of CTCF Tandem 11 Zinc Fingers in Multivalent Recognition of DNA As Revealed by NMR Spectroscopy. Journal of Physical Chemistry Letters, 2018, 9, 4020-4028.	4.6	18
22	SAXS-Oriented Ensemble Refinement of Flexible Biomolecules. Biophysical Journal, 2017, 112, 1295-1301.	0.5	17
23	Insights into the Structure of Dimeric RNA Helicase CsdA and Indispensable Role of Its C-Terminal Regions. Structure, 2017, 25, 1795-1808.e5.	3.3	23
24	Structural and dynamic properties of the C-terminal region of the Escherichia coli RNA chaperone Hfq: integrative experimental and computational studies. Physical Chemistry Chemical Physics, 2017, 19, 21152-21164.	2.8	15
25	Unraveling low-resolution structural data of large biomolecules by constructing atomic models with experiment-targeted parallel cascade selection simulations. Scientific Reports, 2016, 6, 29360.	3.3	7
26	Structural basis for receptor recognition and pore formation of a zebrafish aerolysinâ€like protein. EMBO Reports, 2016, 17, 235-248.	4.5	53
27	pH dependence of ligand-induced human epidermal growth factor receptor activation investigated by molecular dynamics simulations. Journal of Molecular Modeling, 2016, 22, 131.	1.8	7
28	Large Conformational Changes of Insertion 3 in Human Glycyl-tRNA Synthetase (hGlyRS) during Catalysis. Journal of Biological Chemistry, 2016, 291, 5740-5752.	3.4	14
29	Structural modeling of proteins by integrating small-angle x-ray scattering data. Chinese Physics B, 2015, 24, 126101.	1.4	3
30	Structural insights into HetRâ^'PatS interaction involved in cyanobacterial pattern formation. Scientific Reports, 2015, 5, 16470.	3.3	29
31	Systematic Methods for Defining Coarse-Grained Maps in Large Biomolecules. Advances in Experimental Medicine and Biology, 2015, 827, 33-48.	1.6	6
32	Determining structural ensembles of flexible multi-domain proteins using small-angle X-ray scattering and molecular dynamics simulations. Protein and Cell, 2015, 6, 619-623.	11.0	9
33	Crystal and EM Structures of Human Phosphoribosyl Pyrophosphate Synthase I (PRS1) Provide Novel Insights into the Disease-Associated Mutations. PLoS ONE, 2015, 10, e0120304.	2.5	14
34	Crystal Structure of Arginine Methyltransferase 6 from Trypanosoma brucei. PLoS ONE, 2014, 9, e87267.	2.5	21
35	Structural Insights into SraP-Mediated Staphylococcus aureus Adhesion to Host Cells. PLoS Pathogens, 2014, 10, e1004169.	4.7	85
36	Crystal structure of human BS69 Bromo-ZnF-PWWP reveals its role in H3K36me3 nucleosome binding. Cell Research, 2014, 24, 890-893.	12.0	29

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37	Characterization of Protein Flexibility Using Small-Angle X-Ray Scattering and Amplified Collective Motion Simulations. Biophysical Journal, 2014, 107, 956-964.	0.5	20
38	Crystal structure of tripleâ€BRCTâ€domain of ECT2 and insights into the binding characteristics to CYKâ€4. FEBS Letters, 2014, 588, 2911-2920.	2.8	22
39	Simulating Large-Scale Conformational Changes of Proteins by Accelerating Collective Motions Obtained from Principal Component Analysis. Journal of Chemical Theory and Computation, 2014, 10, 3449-3458.	5.3	26
40	Structural Determinants for the Strict Monomethylation Activity by Trypanosoma brucei Protein Arginine Methyltransferase 7. Structure, 2014, 22, 756-768.	3.3	43
41	Structural investigation of the interaction between the tandem SH3 domains of c-Cbl-associated protein and vinculin. Journal of Structural Biology, 2014, 187, 194-205.	2.8	11
42	Polymorphism of the Epidermal Growth Factor Receptor Extracellular Ligand Binding Domain: The Dimer Interface Depends on Domain Stabilization. Biochemistry, 2011, 50, 2144-2156.	2.5	14
43	Key Intermolecular Interactions in the E. coli 70S Ribosome Revealed by Coarse-Grained Analysis. Journal of the American Chemical Society, 2011, 133, 16828-16838.	13.7	38
44	Coarse-Grained Representations of Large Biomolecular Complexes from Low-Resolution Structural Data. Journal of Chemical Theory and Computation, 2010, 6, 2990-3002.	5.3	44
45	Defining Coarse-Grained Representations of Large Biomolecules and Biomolecular Complexes from Elastic Network Models. Biophysical Journal, 2009, 97, 2327-2337.	0.5	82
46	A Systematic Methodology for Defining Coarse-Grained Sites in Large Biomolecules. Biophysical Journal, 2008, 95, 5073-5083.	0.5	153
47	Coarse-Graining Protein Structures With Local Multivariate Features from Molecular Dynamics. Journal of Physical Chemistry B, 2008, 112, 14026-14035.	2.6	13
48	Entropic Folding Pathway of Human Epidermal Growth Factor Explored by Disulfide Scrambling and Amplified Collective Motion Simulationsâ€,â€¡. Biochemistry, 2006, 45, 15269-15278.	2.5	10
49	Molecular Dynamics Simulations of Peptides and Proteins with Amplified Collective Motions. Biophysical Journal, 2003, 84, 3583-3593.	0.5	114
50	Efficiently explore the energy landscape of proteins in molecular dynamics simulations by amplifying collective motions. Journal of Chemical Physics, 2003, 119, 4005-4017.	3.0	45