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	A Systematic Methodology for Defining Coarse-Grained Sites in Large Biomolecules. Biophysical Journal, 2008, 95, 5073-5083.	0.5	153
2	Molecular Dynamics Simulations of Peptides and Proteins with Amplified Collective Motions. Biophysical Journal, 2003, 84, 3583-3593.	0.5	114
3	Structural Insights into SraP-Mediated Staphylococcus aureus Adhesion to Host Cells. PLoS Pathogens, 2014, 10, e1004169.	4.7	85
4	Defining Coarse-Grained Representations of Large Biomolecules and Biomolecular Complexes from Elastic Network Models. Biophysical Journal, 2009, 97, 2327-2337.	0.5	82
5	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
6	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
7	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
8	Structural basis for receptor recognition and pore formation of a zebrafish aerolysinâ€like protein. EMBO Reports, 2016, 17, 235-248.	4.5	53
9	Highly Promiscuous Flavonoid 3-O-Glycosyltransferase from Scutellaria baicalensis. Organic Letters, 2019, 21, 2241-2245.	4.6	50
10	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
11	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
12	Structural Determinants for the Strict Monomethylation Activity by Trypanosoma brucei Protein Arginine Methyltransferase 7. Structure, 2014, 22, 756-768.	3.3	43
13	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
14	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
15	Mitosis-specific acetylation tunes Ran effector binding for chromosome segregation. Journal of Molecular Cell Biology, 2018, 10, 18-32.	3.3	32
16	Crystal structure of human BS69 Bromo-ZnF-PWWP reveals its role in H3K36me3 nucleosome binding. Cell Research, 2014, 24, 890-893.	12.0	29
17	Structural insights into HetRâ^'PatS interaction involved in cyanobacterial pattern formation. Scientific Reports, 2015, 5, 16470.	3.3	29
18	Dynamic crotonylation of EB1 by TIP60 ensures accurate spindle positioning in mitosis. Nature Chemical Biology, 2021, 17, 1314-1323.	8.0	29

#	Article	IF	Citations
19	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
20	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
21	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
22	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
23	Crystal Structure of Arginine Methyltransferase 6 from Trypanosoma brucei. PLoS ONE, 2014, 9, e87267.	2.5	21
24	Characterization of Protein Flexibility Using Small-Angle X-Ray Scattering and Amplified Collective Motion Simulations. Biophysical Journal, 2014, 107, 956-964.	0.5	20
25	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
26	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
27	SAXS-Oriented Ensemble Refinement of Flexible Biomolecules. Biophysical Journal, 2017, 112, 1295-1301.	0.5	17
28	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
29	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
30	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
31	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
32	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
33	Coarse-Graining Protein Structures With Local Multivariate Features from Molecular Dynamics. Journal of Physical Chemistry B, 2008, 112, 14026-14035.	2.6	13
34	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
35	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
36	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

#	Article	IF	Citations
37	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
38	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
39	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
40	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
41	Systematic Methods for Defining Coarse-Grained Maps in Large Biomolecules. Advances in Experimental Medicine and Biology, 2015, 827, 33-48.	1.6	6
42	Biochemical characterization of G64W mutant of acidic beta-crystallin 4. Experimental Eye Research, 2019, 186, 107712.	2.6	5
43	Structural modeling of proteins by integrating small-angle x-ray scattering data. Chinese Physics B, 2015, 24, 126101.	1.4	3
44	Conformational Selection in Ligand Recognition by the First Tudor Domain of PHF20L1. Journal of Physical Chemistry Letters, 2020, 11, 7932-7938.	4.6	3
45	Fragment-Based Discovery of AF9 YEATS Domain Inhibitors. International Journal of Molecular Sciences, 2022, 23, 3893.	4.1	3
46	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
47	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
48	Halophilic to mesophilic adaptation of ubiquitinâ€like proteins. FEBS Letters, 2021, 595, 521-531.	2.8	1
49	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
50	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