Wenwei Zheng

List of Publications by Year
in descending order

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47	4,070	201674	233421
papers	citations	27 h-index	45 g-index

55	55	55	3358
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Diffusion of a disordered protein on its folded ligand. Biophysical Journal, 2022, 121, 200a.	0.5	2
2	Using a sequence-specific coarse-grained model for studying protein liquidâ€“liquid phase separation. Methods in Enzymology, 2021, 646, 1-17.	1.0	27
3	Salt-Dependent Conformational Changes of Intrinsically Disordered Proteins. Journal of Physical Chemistry Letters, 2021, 12, 6684-6691.	4.6	32
4	Quantitative NMR Study of Insulin-Degrading Enzyme Using Amyloid-Î² and HIV-1 p6 Elucidates Its Chaperone Activity. Biochemistry, 2021, 60, 2519-2523.	2.5	8
5	Diffusion of a disordered protein on its folded ligand. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	28
6	Sequence dependent phase separation of protein-polynucleotide mixtures elucidated using molecular simulations. Nucleic Acids Research, 2020, 48, 12593-12603.	14.5	83
7	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. Journal of Physical Chemistry B, 2020, 124, 11671-11679.	2.6	127
8	Hydropathy Patterning Complements Charge Patterning to Describe Conformational Preferences of Disordered Proteins. Journal of Physical Chemistry Letters, 2020, 11, 3408-3415.	4.6	70
9	Impact of Hydrophobic Patterning on Conformational Ensemble of Disordered Proteins. Biophysical Journal, 2020, 118, 214a.	0.5	0
10	Single-molecule fluorescence studies of IDPs and IDRs. , 2019, , 93-136.		0
11	Temperature-Controlled Liquidâ€“Liquid Phase Separation of Disordered Proteins. ACS Central Science, 2019, 5, 821-830.	11.3	199
12	Simulation methods for liquidâ€“liquid phase separation of disordered proteins. Current Opinion in Chemical Engineering, 2019, 23, 92-98.	7.8	89
13	Evolution of All-Atom Protein Force Fields to Improve Local and Global Properties. Journal of Physical Chemistry Letters, 2019, 10, 2227-2234.	4.6	65
14	A High-Throughput Approach to Phase Separation of Disordered Proteins. Biophysical Journal, 2019, 116, 350a.	0.5	1
15	Polymer effects modulate binding affinities in disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19506-19512.	7.1	63
16	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. Structure, 2019, 27, 229-240.e4.	3.3	39
17	Inferring properties of disordered chains from FRET transfer efficiencies. Journal of Chemical Physics, 2018, 148, 123329.	3.0	84
18	An Extended Guinier Analysis for Intrinsically Disordered Proteins. Journal of Molecular Biology, 2018, 430, 2540-2553.	4.2	64

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19	Accurate Transfer Efficiencies, Distance Distributions, and Ensembles of Unfolded and Intrinsically Disordered Proteins From Single-Molecule FRET. Methods in Enzymology, 2018, 611, 287-325.	1.0	46
20	Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. Journal of Physical Chemistry B, 2018, 122, 11478-11487.	2.6	19
21	Relation between single-molecule properties and phase behavior of intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9929-9934.	7.1	283
22	Coarse-Grained Simulations of Intrinsically Disordered Proteins in the Context of Liquid-Liquid Phase Separation. Biophysical Journal, 2018, 114, 431a-432a.	0.5	1
23	Comment on â€œInnovative scattering analysis shows that hydrophobic disordered proteins are expanded in waterâ€. Science, 2018, 361, .	12.6	36
24	Sequence determinants of protein phase behavior from a coarse-grained model. PLoS Computational Biology, 2018, 14, e1005941.	3.2	427
25	Phosphorylation of the <scp>FUS</scp> lowâ€complexity domain disrupts phase separation, aggregation, and toxicity. EMBO Journal, 2017, 36, 2951-2967.	7.8	544
26	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. Journal of the American Chemical Society, 2016, 138, 11702-11713.	13.7	121
27	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. Journal of the American Chemical Society, 2016, 138, 11714-11726.	13.7	171
28	Modulation of Folding Internal Friction by Local and Global Barrier Heights. Journal of Physical Chemistry Letters, 2016, 7, 1028-1034.	4.6	15
29	Empirical Optimization of Interactions between Proteins and Chemical Denaturants in Molecular Simulations. Journal of Chemical Theory and Computation, 2015, 11, 5543-5553.	5.3	23
30	Reduction of All-Atom Protein Folding Dynamics to One-Dimensional Diffusion. Journal of Physical Chemistry B, 2015, 119, 15247-15255.	2.6	31
31	Dependence of Internal Friction on Folding Mechanism. Journal of the American Chemical Society, 2015, 137, 3283-3290.	13.7	41
32	Optimized Force Fields for Simulations of Intrinsically Disordered Proteins. Biophysical Journal, 2015, 108, 227a.	0.5	0
33	A comparative analysis of clustering algorithms: O2 migration in truncated hemoglobin I from transition networks. Journal of Chemical Physics, 2015, 142, 025103.	3.0	10
34	Multiscale Approach to the Determination of the Photoactive Yellow Protein Signaling State Ensemble. PLoS Computational Biology, 2014, 10, e1003797.	3.2	5
35	Balanced Proteinâ€“Water Interactions Improve Properties of Disordered Proteins and Non-Specific Protein Association. Journal of Chemical Theory and Computation, 2014, 10, 5113-5124.	5.3	564
36	A tripodal peptide ligand for asymmetric Rh(<scp>ii</scp>) catalysis highlights unique features of on-bead catalyst development. Chemical Science, 2014, 5, 1401-1407.	7.4	40

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37	Discovering Mountain Passes via Torchlight: Methods for the Definition of Reaction Coordinates and Pathways in Complex Macromolecular Reactions. Annual Review of Physical Chemistry, 2013, 64, 295-316.	10.8	177
38	Rapid Exploration of Configuration Space with Diffusion-Map-Directed Molecular Dynamics. Journal of Physical Chemistry B, 2013, 117, 12769-12776.	2.6	71
39	Molecular recognition of DNA by ligands: Roughness and complexity of the free energy profile. Journal of Chemical Physics, 2013, 139, 145102.	3.0	20
40	Multiscale characterization of macromolecular dynamics. , 2013, , .		0
41	Delineation of Folding Pathways of a Î²-Sheet Miniprotein. Journal of Physical Chemistry B, 2011, 115, 13065-13074.	2.6	41
42	Determination of reaction coordinates via locally scaled diffusion map. Journal of Chemical Physics, 2011, 134, 124116.	3.0	212
43	Polymer reversal rate calculated via locally scaled diffusion map. Journal of Chemical Physics, 2011, 134, 144109.	3.0	44
44	The intrinsic load-resisting capacity of kinesin. Physical Biology, 2009, 6, 036002.	1.8	23
45	From molecular shuttles to directed procession of nanorings. Chemical Physics, 2008, 352, 235-240.	1.9	7
46	Modeling Motility of the Kinesin Dimer from Molecular Properties of Individual Monomers^{â€}. Biochemistry, 2008, 47, 4733-4742.	2.5	25
47	Kinesin Is an Evolutionarily Fine-Tuned Molecular Ratchet-and-Pawl Device of Decisively Locked Direction. Biophysical Journal, 2007, 93, 3363-3372.	0.5	51