

Wenwei Zheng

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

4,070
citations

201658

27
h-index

233409

45
g-index

55
all docs

55
docs citations

55
times ranked

3358
citing authors

#	ARTICLE	IF	CITATIONS
1	Balanced Protein-Water Interactions Improve Properties of Disordered Proteins and Non-Specific Protein Association. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 5113-5124.	5.3	564
2	Phosphorylation of the <scp>FUS</scp> low-complexity domain disrupts phase separation, aggregation, and toxicity. <i>EMBO Journal</i> , 2017, 36, 2951-2967.	7.8	544
3	Sequence determinants of protein phase behavior from a coarse-grained model. <i>PLoS Computational Biology</i> , 2018, 14, e1005941.	3.2	427
4	Relation between single-molecule properties and phase behavior of intrinsically disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9929-9934.	7.1	283
5	Determination of reaction coordinates via locally scaled diffusion map. <i>Journal of Chemical Physics</i> , 2011, 134, 124116.	3.0	212
6	Temperature-Controlled Liquid-Liquid Phase Separation of Disordered Proteins. <i>ACS Central Science</i> , 2019, 5, 821-830.	11.3	199
7	Discovering Mountain Passes via Torchlight: Methods for the Definition of Reaction Coordinates and Pathways in Complex Macromolecular Reactions. <i>Annual Review of Physical Chemistry</i> , 2013, 64, 295-316.	10.8	177
8	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. <i>Journal of the American Chemical Society</i> , 2016, 138, 11714-11726.	13.7	171
9	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. <i>Journal of Physical Chemistry B</i> , 2020, 124, 11671-11679.	2.6	127
10	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. <i>Journal of the American Chemical Society</i> , 2016, 138, 11702-11713.	13.7	121
11	Simulation methods for liquid-liquid phase separation of disordered proteins. <i>Current Opinion in Chemical Engineering</i> , 2019, 23, 92-98.	7.8	89
12	Inferring properties of disordered chains from FRET transfer efficiencies. <i>Journal of Chemical Physics</i> , 2018, 148, 123329.	3.0	84
13	Sequence dependent phase separation of protein-polynucleotide mixtures elucidated using molecular simulations. <i>Nucleic Acids Research</i> , 2020, 48, 12593-12603.	14.5	83
14	Rapid Exploration of Configuration Space with Diffusion-Map-Directed Molecular Dynamics. <i>Journal of Physical Chemistry B</i> , 2013, 117, 12769-12776.	2.6	71
15	Hydropathy Patterning Complements Charge Patterning to Describe Conformational Preferences of Disordered Proteins. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 3408-3415.	4.6	70
16	Evolution of All-Atom Protein Force Fields to Improve Local and Global Properties. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 2227-2234.	4.6	65
17	An Extended Guinier Analysis for Intrinsically Disordered Proteins. <i>Journal of Molecular Biology</i> , 2018, 430, 2540-2553.	4.2	64
18	Polymer effects modulate binding affinities in disordered proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19506-19512.	7.1	63

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19	Kinesin Is an Evolutionarily Fine-Tuned Molecular Ratchet-and-Pawl Device of Decisively Locked Direction. <i>Biophysical Journal</i> , 2007, 93, 3363-3372.	0.5	51
20	Accurate Transfer Efficiencies, Distance Distributions, and Ensembles of Unfolded and Intrinsically Disordered Proteins From Single-Molecule FRET. <i>Methods in Enzymology</i> , 2018, 611, 287-325.	1.0	46
21	Polymer reversal rate calculated via locally scaled diffusion map. <i>Journal of Chemical Physics</i> , 2011, 134, 144109.	3.0	44
22	Delineation of Folding Pathways of a β^2 -Sheet Miniprotein. <i>Journal of Physical Chemistry B</i> , 2011, 115, 13065-13074.	2.6	41
23	Dependence of Internal Friction on Folding Mechanism. <i>Journal of the American Chemical Society</i> , 2015, 137, 3283-3290.	13.7	41
24	A tripodal peptide ligand for asymmetric Rh(<i>II</i>) catalysis highlights unique features of on-bead catalyst development. <i>Chemical Science</i> , 2014, 5, 1401-1407.	7.4	40
25	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. <i>Structure</i> , 2019, 27, 229-240.e4.	3.3	39
26	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , 2018, 361, .	12.6	36
27	Salt-Dependent Conformational Changes of Intrinsically Disordered Proteins. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 6684-6691.	4.6	32
28	Reduction of All-Atom Protein Folding Dynamics to One-Dimensional Diffusion. <i>Journal of Physical Chemistry B</i> , 2015, 119, 15247-15255.	2.6	31
29	Diffusion of a disordered protein on its folded ligand. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	28
30	Using a sequence-specific coarse-grained model for studying protein liquid-liquid phase separation. <i>Methods in Enzymology</i> , 2021, 646, 1-17.	1.0	27
31	Modeling Motility of the Kinesin Dimer from Molecular Properties of Individual Monomers. <i>Biochemistry</i> , 2008, 47, 4733-4742.	2.5	25
32	The intrinsic load-resisting capacity of kinesin. <i>Physical Biology</i> , 2009, 6, 036002.	1.8	23
33	Empirical Optimization of Interactions between Proteins and Chemical Denaturants in Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5543-5553.	5.3	23
34	Molecular recognition of DNA by ligands: Roughness and complexity of the free energy profile. <i>Journal of Chemical Physics</i> , 2013, 139, 145102.	3.0	20
35	Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11478-11487.	2.6	19
36	Modulation of Folding Internal Friction by Local and Global Barrier Heights. <i>Journal of Physical Chemistry Letters</i> , 2016, 7, 1028-1034.	4.6	15

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37	A comparative analysis of clustering algorithms: O ₂ migration in truncated hemoglobin I from transition networks. <i>Journal of Chemical Physics</i> , 2015, 142, 025103.	3.0	10
38	Quantitative NMR Study of Insulin-Degrading Enzyme Using Amyloid- β^2 and HIV-1 p6 Elucidates Its Chaperone Activity. <i>Biochemistry</i> , 2021, 60, 2519-2523.	2.5	8
39	From molecular shuttles to directed procession of nanorings. <i>Chemical Physics</i> , 2008, 352, 235-240.	1.9	7
40	Multiscale Approach to the Determination of the Photoactive Yellow Protein Signaling State Ensemble. <i>PLoS Computational Biology</i> , 2014, 10, e1003797.	3.2	5
41	Diffusion of a disordered protein on its folded ligand. <i>Biophysical Journal</i> , 2022, 121, 200a.	0.5	2
42	Coarse-Grained Simulations of Intrinsically Disordered Proteins in the Context of Liquid-Liquid Phase Separation. <i>Biophysical Journal</i> , 2018, 114, 431a-432a.	0.5	1
43	A High-Throughput Approach to Phase Separation of Disordered Proteins. <i>Biophysical Journal</i> , 2019, 116, 350a.	0.5	1
44	Optimized Force Fields for Simulations of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2015, 108, 227a.	0.5	0
45	Single-molecule fluorescence studies of IDPs and IDRs. , 2019, , 93-136.		0
46	Multiscale characterization of macromolecular dynamics. , 2013, , .		0
47	Impact of Hydrophobic Patterning on Conformational Ensemble of Disordered Proteins. <i>Biophysical Journal</i> , 2020, 118, 214a.	0.5	0