Wenwei Zheng

List of Publications by Year in Descending Order

45 papers	2,652 citations	26 h-index	51 g-index
55 ext. papers	3,393 ext. citations	6.7 avg, IF	5.64 L-index

#	Paper	IF	Citations
45	Salt-Dependent Conformational Changes of Intrinsically Disordered Proteins. *Journal of Physical Chemistry Letters*, **2021**, 12, 6684-6691	6.4	7
44	Using a sequence-specific coarse-grained model for studying protein liquid-liquid phase separation. *Methods in Enzymology*, **2021**, 646, 1-17	1.7	7
43	Quantitative NMR Study of Insulin-Degrading Enzyme Using Amyloid- and HIV-1 p6 Elucidates Its Chaperone Activity. *Biochemistry*, **2021**, 60, 2519-2523	3.2	2
42	Diffusion of a disordered protein on its folded ligand. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	6
41	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. *Journal of Physical Chemistry B*, **2020**, 124, 11671-11679	3.4	32
40	Hydropathy Patterning Complements Charge Patterning to Describe Conformational Preferences of Disordered Proteins. *Journal of Physical Chemistry Letters*, **2020**, 11, 3408-3415	6.4	34
39	Sequence dependent phase separation of protein-polynucleotide mixtures elucidated using molecular simulations. *Nucleic Acids Research*, **2020**, 48, 12593-12603	20.1	34
38	Temperature-Controlled Liquid-Liquid Phase Separation of Disordered Proteins. *ACS Central Science*, **2019**, 5, 821-830	16.8	108
37	Simulation methods for liquid-liquid phase separation of disordered proteins. *Current Opinion in Chemical Engineering*, **2019**, 23, 92-98	5.4	47
36	Evolution of All-Atom Protein Force Fields to Improve Local and Global Properties. *Journal of Physical Chemistry Letters*, **2019**, 10, 2227-2234	6.4	39
35	Single-molecule fluorescence studies of IDPs and IDRs **2019**, 93-136		
34	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	11.5	29
33	A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. *Structure*, **2019**, 27, 229-240.e4	5.2	31
32	Inferring properties of disordered chains from FRET transfer efficiencies. *Journal of Chemical Physics*, **2018**, 148, 123329	3.9	63
31	An Extended Guinier Analysis for Intrinsically Disordered Proteins. *Journal of Molecular Biology*, **2018**, 430, 2540-2553	6.5	48
30	Sequence determinants of protein phase behavior from a coarse-grained model. *PLoS Computational Biology*, **2018**, 14, e1005941	5	209
29	Accurate Transfer Efficiencies, Distance Distributions, and Ensembles of Unfolded and Intrinsically Disordered Proteins From Single-Molecule FRET. *Methods in Enzymology*, **2018**, 611, 287-325	1.7	28

28	Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. *Journal of Physical Chemistry B*, **2018**, 122, 11478-11487	3.4	14
27	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	11.5	149
26	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". *Science*, **2018**, 361,	33.3	30
25	Phosphorylation of the FUS low-complexity domain disrupts phase separation, aggregation, and toxicity. *EMBO Journal*, **2017**, 36, 2951-2967	13	365
24	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. *Journal of the American Chemical Society*, **2016**, 138, 11702-13	16.4	91
23	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. *Journal of the American Chemical Society*, **2016**, 138, 11714-26	16.4	127
22	Modulation of Folding Internal Friction by Local and Global Barrier Heights. *Journal of Physical Chemistry Letters*, **2016**, 7, 1028-34	6.4	12
21	Dependence of internal friction on folding mechanism. *Journal of the American Chemical Society*, **2015**, 137, 3283-90	16.4	35
20	A comparative analysis of clustering algorithms: O2 migration in truncated hemoglobin I from transition networks. *Journal of Chemical Physics*, **2015**, 142, 025103	3.9	9
19	Empirical Optimization of Interactions between Proteins and Chemical Denaturants in Molecular Simulations. *Journal of Chemical Theory and Computation*, **2015**, 11, 5543-53	6.4	20
18	Reduction of All-Atom Protein Folding Dynamics to One-Dimensional Diffusion. *Journal of Physical Chemistry B*, **2015**, 119, 15247-55	3.4	26
17	Balanced Protein-Water Interactions Improve Properties of Disordered Proteins and Non-Specific Protein Association. *Journal of Chemical Theory and Computation*, **2014**, 10, 5113-5124	6.4	409
16	A tripodal peptide ligand for asymmetric Rh(II) catalysis highlights unique features of on-bead catalyst development. *Chemical Science*, **2014**, 5, 1401-1407	9.4	33
15	Multiscale approach to the determination of the photoactive yellow protein signaling state ensemble. *PLoS Computational Biology*, **2014**, 10, e1003797	5	4
14	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	15.7	147
13	Rapid exploration of configuration space with diffusion-map-directed molecular dynamics. *Journal of Physical Chemistry B*, **2013**, 117, 12769-76	3.4	57
12	Molecular recognition of DNA by ligands: roughness and complexity of the free energy profile. *Journal of Chemical Physics*, **2013**, 139, 145102	3.9	16
11	Delineation of folding pathways of a β-sheet miniprotein. *Journal of Physical Chemistry B*, **2011**, 115, 13065-74	3.4	39

10	Determination of reaction coordinates via locally scaled diffusion map. *Journal of Chemical Physics*, **2011**, 134, 124116	3.9	180
9	Polymer reversal rate calculated via locally scaled diffusion map. *Journal of Chemical Physics*, **2011**, 134, 144109	3.9	39
8	The intrinsic load-resisting capacity of kinesin. *Physical Biology*, **2009**, 6, 036002	3	20
7	Modeling motility of the kinesin dimer from molecular properties of individual monomers. *Biochemistry*, **2008**, 47, 4733-42	3.2	21
6	From molecular shuttles to directed procession of nanorings. *Chemical Physics*, **2008**, 352, 235-240	2.3	7
5	Kinesin is an evolutionarily fine-tuned molecular ratchet-and-pawl device of decisively locked direction. *Biophysical Journal*, **2007**, 93, 3363-72	2.9	48
4	Hydropathy patterning complements charge patterning to describe conformational preferences of disordered proteins		2
3	Sequence dependent co-phase separation of RNA-protein mixtures elucidated using molecular simulations		2
2	Molecular details of protein condensates probed by microsecond-long atomistic simulations		5
1	Diffusion of the disordered E-cadherin tail on β-catenin		2