# Wenwei Zheng

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6990346/publications.pdf

Version: 2024-02-01

| 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 | 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 |
| 2 | Phosphorylation of the <scp>FUS</scp> lowâ€complexity domain disrupts phase separation, aggregation, and toxicity. EMBO Journal, 2017, 36, 2951-2967. | 7.8 | 544 |
| 3 | Sequence determinants of protein phase behavior from a coarse-grained model. PLoS Computational Biology, 2018, 14, e1005941. | 3.2 | 427 |
| 4 | 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 |
| 5 | Determination of reaction coordinates via locally scaled diffusion map. Journal of Chemical Physics, 2011, 134, 124116. | 3.0 | 212 |
| 6 | Temperature-Controlled Liquidâ€“Liquid Phase Separation of Disordered Proteins. ACS Central Science, 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. Annual Review of Physical Chemistry, 2013, 64, 295-316. | 10.8 | 177 |
| 8 | 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 |
| 9 | Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. Journal of Physical Chemistry B, 2020, 124, 11671-11679. | 2.6 | 127 |
| 10 | 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 |
| 11 | Simulation methods for liquidâ€“liquid phase separation of disordered proteins. Current Opinion in Chemical Engineering, 2019, 23, 92-98. | 7.8 | 89 |
| 12 | Inferring properties of disordered chains from FRET transfer efficiencies. Journal of Chemical Physics, 2018, 148, 123329. | 3.0 | 84 |
| 13 | Sequence dependent phase separation of protein-polynucleotide mixtures elucidated using molecular simulations. Nucleic Acids Research, 2020, 48, 12593-12603. | 14.5 | 83 |
| 14 | Rapid Exploration of Configuration Space with Diffusion-Map-Directed Molecular Dynamics. Journal of Physical Chemistry B, 2013, 117, 12769-12776. | 2.6 | 71 |
| 15 | Hydropathy Patterning Complements Charge Patterning to Describe Conformational Preferences of Disordered Proteins. Journal of Physical Chemistry Letters, 2020, 11, 3408-3415. | 4.6 | 70 |
| 16 | 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 |
| 17 | An Extended Guinier Analysis for Intrinsically Disordered Proteins. Journal of Molecular Biology, 2018, 430, 2540-2553. | 4.2 | 64 |
| 18 | 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 |

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|---|---|---|---|
| 19 | Kinesin Is an Evolutionarily Fine-Tuned Molecular Ratchet-and-Pawl Device of Decisively Locked Direction. Biophysical Journal, 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. Methods in Enzymology, 2018, 611, 287-325. | 1.0 | 46 |
| 21 | Polymer reversal rate calculated via locally scaled diffusion map. Journal of Chemical Physics, 2011, 134, 144109. | 3.0 | 44 |
| 22 | Delineation of Folding Pathways of a Î²-Sheet Miniprotein. Journal of Physical Chemistry B, 2011, 115, 13065-13074. | 2.6 | 41 |
| 23 | Dependence of Internal Friction on Folding Mechanism. Journal of the American Chemical Society, 2015, 137, 3283-3290. | 13.7 | 41 |
| 24 | 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 |
| 25 | A Metastable Contact and Structural Disorder in the Estrogen Receptor Transactivation Domain. Structure, 2019, 27, 229-240.e4. | 3.3 | 39 |
| 26 | Comment on â€œInnovative scattering analysis shows that hydrophobic disordered proteins are expanded in waterâ€. Science, 2018, 361, . | 12.6 | 36 |
| 27 | Salt-Dependent Conformational Changes of Intrinsically Disordered Proteins. Journal of Physical Chemistry Letters, 2021, 12, 6684-6691. | 4.6 | 32 |
| 28 | Reduction of All-Atom Protein Folding Dynamics to One-Dimensional Diffusion. Journal of Physical Chemistry B, 2015, 119, 15247-15255. | 2.6 | 31 |
| 29 | 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 |
| 30 | Using a sequence-specific coarse-grained model for studying protein liquidâ€“liquid phase separation. Methods in Enzymology, 2021, 646, 1-17. | 1.0 | 27 |
| 31 | Modeling Motility of the Kinesin Dimer from Molecular Properties of Individual Monomers<sup>â€</sup>. Biochemistry, 2008, 47, 4733-4742. | 2.5 | 25 |
| 32 | The intrinsic load-resisting capacity of kinesin. Physical Biology, 2009, 6, 036002. | 1.8 | 23 |
| 33 | 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 |
| 34 | Molecular recognition of DNA by ligands: Roughness and complexity of the free energy profile. Journal of Chemical Physics, 2013, 139, 145102. | 3.0 | 20 |
| 35 | Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. Journal of Physical Chemistry B, 2018, 122, 11478-11487. | 2.6 | 19 |
| 36 | Modulation of Folding Internal Friction by Local and Global Barrier Heights. Journal of Physical Chemistry Letters, 2016, 7, 1028-1034. | 4.6 | 15 |

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|---|---|---|---|
| 37 | 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 |
| 38 | 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 |
| 39 | From molecular shuttles to directed procession of nanorings. Chemical Physics, 2008, 352, 235-240. | 1.9 | 7 |
| 40 | Multiscale Approach to the Determination of the Photoactive Yellow Protein Signaling State Ensemble. PLoS Computational Biology, 2014, 10, e1003797. | 3.2 | 5 |
| 41 | Diffusion of a disordered protein on its folded ligand. Biophysical Journal, 2022, 121, 200a. | 0.5 | 2 |
| 42 | Coarse-Grained Simulations of Intrinsically Disordered Proteins in the Context of Liquid-Liquid Phase Separation. Biophysical Journal, 2018, 114, 431a-432a. | 0.5 | 1 |
| 43 | A High-Throughput Approach to Phase Separation of Disordered Proteins. Biophysical Journal, 2019, 116, 350a. | 0.5 | 1 |
| 44 | Optimized Force Fields for Simulations of Intrinsically Disordered Proteins. Biophysical Journal, 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. Biophysical Journal, 2020, 118, 214a. | 0.5 | 0 |