The Native Ensemble and Folding of a Protein Molten-G Downhill Folding

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Citation Report

#	Article	IF	Citations
1	A Preformed Binding Interface in the Unbound Ensemble of an Intrinsically Disordered Protein: Evidence from Molecular Simulations. PLoS Computational Biology, 2012, 8, e1002605.	1.5	104
2	Simulation of the polypeptide chain folding process using the â€œfuzzy oil dropâ€•model. , 2012, , 123-140.		2
3	Is a Malleable Protein Necessarily Highly Dynamic? The Hydrophobic Core of the Nuclear Coactivator Binding Domain Is Well Ordered. Biophysical Journal, 2012, 102, 1627-1635.	0.2	22
4	Effect of Surfactant Hydrophobicity on the Pathway for Unfolding of Ubiquitin. Journal of the American Chemical Society, 2012, 134, 18739-18745.	6.6	19
5	Predictions from an Ising-like Statistical Mechanical Model on the Dynamic and Thermodynamic Effects of Protein Surface Electrostatics. Journal of Chemical Theory and Computation, 2012, 8, 4646-4656.	2.3	54
6	Modulation of an IDP binding mechanism and rates by helix propensity and non-native interactions: association of HIF1Î± with CBP. Molecular BioSystems, 2012, 8, 256-267.	2.9	83
7	Side-Chain Interactions Form Late and Cooperatively in the Binding Reaction between Disordered Peptides and PDZ Domains. Journal of the American Chemical Society, 2012, 134, 599-605.	6.6	41
8	Towards the physical basis of how intrinsic disorder mediates protein function. Archives of Biochemistry and Biophysics, 2012, 524, 123-131.	1.4	74
9	Defining the Nature of Thermal Intermediate in 3 State Folding Proteins: Apoflavodoxin, a Study Case. PLoS Computational Biology, 2012, 8, e1002647.	1.5	14
10	Structural and Dynamical Insights into the Molten-Globule Form of Ovalbumin. Journal of Physical Chemistry B, 2012, 116, 520-531.	1.2	40
11	Modulation of the Intrinsic Helix Propensity of an Intrinsically Disordered Protein Reveals Long-Range Helixâ€“Helix Interactions. Journal of the American Chemical Society, 2013, 135, 10155-10163.	6.6	44
12	The Conformational Landscape of an Intrinsically Disordered DNA-Binding Domain of a Transcription Regulator. Journal of Physical Chemistry B, 2013, 117, 13842-13850.	1.2	27
13	Coarseâ€grained models of protein folding as detailed tools to connect with experiments. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2013, 3, 504-514.	6.2	11
14	A Folded Excited State of Ligand-Free Nuclear Coactivator Binding Domain (NCBD) Underlies Plasticity in Ligand Recognition. Biochemistry, 2013, 52, 1686-1693.	1.2	39
15	A Disorder-Induced Domino-Like Destabilization Mechanism Governs the Folding and Functional Dynamics of the Repeat Protein IIºBÎ±. PLoS Computational Biology, 2013, 9, e1003403.	1.5	25
16	Multiscaled exploration of coupled folding and binding of an intrinsically disordered molecular recognition element in measles virus nucleoprotein. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3743-52.	3.3	102
17	Insights into the binding of intrinsically disordered proteins from molecular dynamics simulation. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2014, 4, 182-198.	6.2	56
18	Discriminating binding mechanisms of an intrinsically disordered protein via a multi-state coarse-grained model. Journal of Chemical Physics, 2014, 140, 175102.	1.2	46

#	Article	IF	Citations
19	A theoretical view of protein dynamics. Chemical Society Reviews, 2014, 43, 5051-5066.	18.7	111
20	Conformational Selection and Functional Dynamics of Calmodulin: A ¹⁹F Nuclear Magnetic Resonance Study. Biochemistry, 2014, 53, 5727-5736.	1.2	27
21	Long Molecular Dynamics Simulations of Intrinsically Disordered Proteins Reveal Preformed Structural Elements for Target Binding. , 2014, , 260-283.		0
23	The RING Domain of the Scaffold Protein Ste5 Adopts a Molten Globular Character with High Thermal and Chemical Stability. Angewandte Chemie - International Edition, 2014, 53, 1320-1323.	7.2	6
24	Molecular dynamics simulations: advances and applications. Advances and Applications in Bioinformatics and Chemistry, 2015, 8, 37.	1.6	409
25	Decoding Structural Properties of a Partially Unfolded Protein Substrate: En Route to Chaperone Binding. PLoS Computational Biology, 2015, 11, e1004496.	1.5	12
26	Bridging Experiments and Native-Centric Simulations of a Downhill Folding Protein. Journal of Physical Chemistry B, 2015, 119, 14925-14933.	1.2	7
27	Imprints of function on the folding landscape: functional role for an intermediate in a conserved eukaryotic binding protein. Physical Chemistry Chemical Physics, 2015, 17, 11042-11052.	1.3	17
28	Are Protein Folding Intermediates the Evolutionary Consequence of Functional Constraints?. Journal of Physical Chemistry B, 2015, 119, 1323-1333.	1.2	22
29	Quantifying Protein Disorder through Measures of Excess Conformational Entropy. Journal of Physical Chemistry B, 2016, 120, 4341-4350.	1.2	36
30	When fast is better: protein folding fundamentals and mechanisms from ultrafast approaches. Biochemical Journal, 2016, 473, 2545-2559.	1.7	69
31	How cooperative are protein folding and unfolding transitions?. Protein Science, 2016, 25, 1924-1941.	3.1	70
32	Activation Barrier-Limited Folding and Conformational Sampling of a Dynamic Protein Domain. Biochemistry, 2016, 55, 5289-5295.	1.2	14
33	Role of Intrinsic Protein Disorder in the Function and Interactions of the Transcriptional Coactivators CREB-binding Protein (CBP) and p300. Journal of Biological Chemistry, 2016, 291, 6714-6722.	1.6	251
34	Limited cooperativity in protein folding. Current Opinion in Structural Biology, 2016, 36, 58-66.	2.6	59
35	Using the folding landscapes of proteins to understand protein function. Current Opinion in Structural Biology, 2016, 36, 67-74.	2.6	35
36	Single-Molecule Fluorescence Spectroscopy of the Folding of a Repeat Protein. Springer Theses, 2016, , .	0.0	1
37	Tuning the Continuum of Structural States in the Native Ensemble of a Regulatory Protein. Journal of Physical Chemistry Letters, 2017, 8, 1683-1687.	2.1	9

#	Article	IF	Citations
38	Graded Structural Polymorphism in a Bacterial Thermosensor Protein. Journal of the American Chemical Society, 2017, 139, 792-802.	6.6	28
39	Roles of conformational disorder and downhill folding in modulating proteinâ€“DNA recognition. Physical Chemistry Chemical Physics, 2017, 19, 28527-28539.	1.3	21
40	Protein plasticity driven by disorder and collapse governs the heterogeneous binding of CytR to DNA. Nucleic Acids Research, 2018, 46, 4044-4053.	6.5	19
41	Protein Folding Cooperativity and Thermodynamic Barriers of the Simplest Î²-Sheet Fold: A Survey of WW Domains. Journal of Physical Chemistry B, 2018, 122, 11058-11071.	1.2	11
42	Entropic Control of an Excited Folded-Like Conformation in a Disordered Protein Ensemble. Journal of Molecular Biology, 2018, 430, 2688-2694.	2.0	14
43	Glutton: a tool for generating structural ensembles of partly disordered proteins from chemical shifts. Bioinformatics, 2019, 35, 1234-1236.	1.8	4
44	The influence of intrinsic folding mechanism of an unfolded protein on the coupled foldingâ€binding process during target recognition. Proteins: Structure, Function and Bioinformatics, 2019, 87, 265-275.	1.5	2
45	Insights from molecular dynamics simulations and steered molecular dynamics simulations to exploit new trends of the interaction between HIF-1Î± and p300. Journal of Biomolecular Structure and Dynamics, 2020, 38, 1-12.	2.0	70
46	Performance of CHARMM36m with modified water model in simulating intrinsically disordered proteins: a case study. Biophysics Reports, 2020, 6, 80-87.	0.2	10
47	Investigating the Conformational Ensembles of Intrinsically Disordered Proteins with a Simple Physics-Based Model. Journal of Physical Chemistry B, 2020, 124, 4097-4113.	1.2	11
48	Advances in targeting â€˜undruggableâ€™ transcription factors with small molecules. Nature Reviews Drug Discovery, 2021, 20, 669-688.	21.5	152
49	The Differential Response of Proteins to Macromolecular Crowding. PLoS Computational Biology, 2016, 12, e1005040.	1.5	44
53	A modular approach to map out the conformational landscapes of unbound intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	7
54	A look at the face of the molten globule: Structural model of the <scp>Helicobacter pylori</scp> apoflavodoxin ensemble at acidic <scp>pH</scp>. Protein Science, 2022, 31, .	3.1	3
55	Targeting androgen receptor phase separation to overcome antiandrogen resistance. Nature Chemical Biology, 2022, 18, 1341-1350.	3.9	48
56	Markov State Models of Molecular Simulations to Study Protein Folding and Dynamics. , 2023, , 147-164.		1