

Exploring one-state downhill protein folding in single m

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Citation Report

#	ARTICLE	IF	CITATIONS
1	From A to B: A ride in the free energy surfaces of protein G domains suggests how new folds arise. <i>Journal of Chemical Physics</i> , 2012, 136, 185101.	1.2	14
2	Configuration-Dependent Diffusion Dynamics of Downhill and Two-State Protein Folding. <i>Journal of Physical Chemistry B</i> , 2012, 116, 5152-5159.	1.2	23
3	Equilibrium Unfolding of the PDZ Domain of β 2-Syntrophin. <i>Biophysical Journal</i> , 2012, 102, 2835-2844.	0.2	6
4	Downhill Protein Folding Modules as Scaffolds for Broad-Range Ultrafast Biosensors. <i>Journal of the American Chemical Society</i> , 2012, 134, 8010-8013.	6.6	18
5	Gradual Disorder of the Native State on a Slow Two-State Folding Protein Monitored by Single-Molecule Fluorescence Spectroscopy and NMR. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13120-13131.	1.2	22
6	FRET between a donor and an acceptor covalently bound to human serum albumin in native and non-native states. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 16286.	1.3	34
7	Don't waste good methods on bad buffers and ambiguous data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E331-E332.	3.3	6
8	Exploring the top of the protein folding funnel by experiment. <i>Current Opinion in Structural Biology</i> , 2013, 23, 30-35.	2.6	17
9	Differential scanning calorimetry as a tool for protein folding and stability. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 100-109.	1.4	289
10	Single-molecule spectroscopy of protein folding dynamics—expanding scope and timescales. <i>Current Opinion in Structural Biology</i> , 2013, 23, 36-47.	2.6	252
11	Reply to Huang et al.: Slow proton exchange can duplicate the number of species observed in single-molecule experiments of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1242-3.	3.3	5
12	Reply to Campos and Muñoz: Why phosphate is a bad buffer for guanidinium chloride titrations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1244-5.	3.3	4
13	Slow Proton Transfer Coupled to Unfolding Explains the Puzzling Results of Single-Molecule Experiments on BBL, a Paradigmatic Downhill Folding Protein. <i>PLoS ONE</i> , 2013, 8, e78044.	1.1	6
14	Precursory signatures of protein folding/unfolding: From time series correlation analysis to atomistic mechanisms. <i>Journal of Chemical Physics</i> , 2014, 140, 204905.	1.2	3
15	Effect of ethanol-water mixture on the structure and dynamics of lysozyme: A fluorescence correlation spectroscopy study. <i>Journal of Chemical Physics</i> , 2014, 140, 115105.	1.2	34
16	Isomerization and Temperature-Induced Dynamics of a Photoswitchable β -Hairpin. <i>Chemistry - A European Journal</i> , 2014, 20, 694-703.	1.7	23
17	Shedding light on protein folding landscapes by single-molecule fluorescence. <i>Chemical Society Reviews</i> , 2014, 43, 1172-1188.	18.7	72
18	Thermodynamics of Downhill Folding: Multi-Probe Analysis of PDD, a Protein that Folds Over a Marginal Free Energy Barrier. <i>Journal of Physical Chemistry B</i> , 2014, 118, 8982-8994.	1.2	34

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19	Kinetics of Fast Changing Intramolecular Distance Distributions Obtained by Combined Analysis of FRET Efficiency Kinetics and Time-Resolved FRET Equilibrium Measurements. <i>Biophysical Journal</i> , 2014, 106, 667-676.	0.2	13
20	An Adequate Account of Excluded Volume Is Necessary To Infer Compactness and Asphericity of Disordered Proteins by Förster Resonance Energy Transfer. <i>Journal of Physical Chemistry B</i> , 2015, 119, 15191-15202.	1.2	44
21	β -Structure within the Denatured State of the Helical Protein Domain BBL. <i>Journal of Molecular Biology</i> , 2015, 427, 3166-3176.	2.0	6
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23	A Method for Extracting the Free Energy Surface and Conformational Dynamics of Fast-Folding Proteins from Single Molecule Photon Trajectories. <i>Journal of Physical Chemistry B</i> , 2015, 119, 7944-7956.	1.2	19
24	Globular Protein Folding In Vitro and In Vivo. <i>Annual Review of Biophysics</i> , 2016, 45, 233-251.	4.5	82
25	Meandering Down the Energy Landscape of Protein Folding: Are We There Yet?. <i>Biophysical Journal</i> , 2016, 110, 1924-1932.	0.2	16
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27	How cooperative are protein folding and unfolding transitions?. <i>Protein Science</i> , 2016, 25, 1924-1941.	3.1	70
28	Computational scrutiny of the effect of N-terminal proline and residue stereochemistry in the nucleation of β -helix fold. <i>RSC Advances</i> , 2016, 6, 74162-74176.	1.7	12
29	Single-Molecule Fluorescence Studies of Fast Protein Folding. <i>Methods in Enzymology</i> , 2016, 581, 417-459.	0.4	9
30	Limited cooperativity in protein folding. <i>Current Opinion in Structural Biology</i> , 2016, 36, 58-66.	2.6	59
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34	Conformational Heterogeneity and FRET Data Interpretation for Dimensions of Unfolded Proteins. <i>Biophysical Journal</i> , 2017, 113, 1012-1024.	0.2	61
35	pH-Dependent cooperativity and existence of a dry molten globule in the folding of a miniprotein BBL. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 3523-3530.	1.3	10
36	Protein folding transition path times from single molecule FRET. <i>Current Opinion in Structural Biology</i> , 2018, 48, 30-39.	2.6	97

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37	Diffusion-limited association of disordered protein by non-native electrostatic interactions. <i>Nature Communications</i> , 2018, 9, 4707.	5.8	45
38	Modeling of Multicolor Single-Molecule Förster Resonance Energy-Transfer Experiments on Protein Folding. <i>Journal of Physical Chemistry B</i> , 2018, 122, 10678-10685.	1.2	2
39	Dissecting the Conformational Dynamics-Modulated Enzyme Catalysis with Single-Molecule FRET. <i>Journal of Physical Chemistry B</i> , 2018, 122, 6179-6187.	1.2	6
40	Structural dynamics of membrane-protein folding from single-molecule FRET. <i>Current Opinion in Structural Biology</i> , 2019, 58, 124-137.	2.6	23
41	Diverse Folding Pathways of HIV-1 Protease Monomer on a Rugged Energy Landscape. <i>Biophysical Journal</i> , 2019, 117, 1456-1466.	0.2	5
42	How the dyes affect folding of small proteins in single-molecule FRET experiments: A simulation study. <i>Biophysical Chemistry</i> , 2019, 254, 106243.	1.5	1
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45	A Disordered Loop Mediates Heterogeneous Unfolding of an Ordered Protein by Altering the Native Ensemble. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 6749-6756.	2.1	2
46	Lessons about Protein Folding and Binding from Archetypal Folds. <i>Accounts of Chemical Research</i> , 2020, 53, 2180-2188.	7.6	9
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48	Small-Angle X-ray Scattering Signatures of Conformational Heterogeneity and Homogeneity of Disordered Protein Ensembles. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6451-6478.	1.2	19
49	Protein Folding, Energy Landscapes and Downhill Protein Folding Scenarios. , 2018, , 1-19.		2
52	Molten globule-like transition state of protein barnase measured with calorimetric force spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112382119.	3.3	18
53	Extraction of kinetics from equilibrium distributions of states using the Metropolis Monte Carlo method. <i>Physical Review E</i> , 2022, 105, 034407.	0.8	0