

Michael T Woodside

List of Publications by Year in descending order

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62
papers

4,713
citations

126708

33
h-index

118652

62
g-index

71
all docs

71
docs citations

71
times ranked

3416
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution, Single-Molecule Measurements of Biomolecular Motion. Annual Review of Biophysics and Biomolecular Structure, 2007, 36, 171-190.	18.3	425
2	Nanomechanical measurements of the sequence-dependent folding landscapes of single nucleic acid hairpins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6190-6195.	3.3	397
3	Direct Observation of Hierarchical Folding in Single Riboswitch Aptamers. Science, 2008, 319, 630-633.	6.0	361
4	Direct Measurement of the Full, Sequence-Dependent Folding Landscape of a Nucleic Acid. Science, 2006, 314, 1001-1004.	6.0	356
5	Direct observation of transition paths during the folding of proteins and nucleic acids. Science, 2016, 352, 239-242.	6.0	204
6	Passive All-Optical Force Clamp for High-Resolution Laser Trapping. Physical Review Letters, 2005, 95, 208102.	2.9	201
7	Reconstructing Folding Energy Landscapes by Single-Molecule Force Spectroscopy. Annual Review of Biophysics, 2014, 43, 19-39.	4.5	200
8	Structural and functional conservation of the programmed ~ 1 ribosomal frameshift signal of SARS coronavirus 2 (SARS-CoV-2). Journal of Biological Chemistry, 2020, 295, 10741-10748.	1.6	163
9	Energy landscape analysis of native folding of the prion protein yields the diffusion constant, transition path time, and rates. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14452-14457.	3.3	140
10	Experimental validation of free-energy-landscape reconstruction from non-equilibrium single-molecule force spectroscopy measurements. Nature Physics, 2011, 7, 631-634.	6.5	138
11	Direct observation of multiple misfolding pathways in a single prion protein molecule. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5283-5288.	3.3	131
12	Programmed ~ 1 frameshifting efficiency correlates with RNA pseudoknot conformational plasticity, not resistance to mechanical unfolding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16167-16172.	3.3	120
13	Single-molecule force spectroscopy of the add adenine riboswitch relates folding to regulatory mechanism. Nucleic Acids Research, 2011, 39, 7677-7687.	6.5	113
14	Transition Path Times for Nucleic Acid Folding Determined from Energy-Landscape Analysis of Single-Molecule Trajectories. Physical Review Letters, 2012, 109, 068102.	2.9	103
15	Probing the structural dynamics of proteins and nucleic acids with optical tweezers. Current Opinion in Structural Biology, 2015, 34, 43-51.	2.6	102
16	Folding and unfolding single RNA molecules under tension. Current Opinion in Chemical Biology, 2008, 12, 640-646.	2.8	92
17	Protein folding trajectories can be described quantitatively by one-dimensional diffusion over measured energy landscapes. Nature Physics, 2016, 12, 700-703.	6.5	86
18	Protein misfolding occurs by slow diffusion across multiple barriers in a rough energy landscape. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8308-8313.	3.3	80

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19	Anti-frameshifting Ligand Reduces the Conformational Plasticity of the SARS Virus Pseudoknot. <i>Journal of the American Chemical Society</i> , 2014, 136, 2196-2199.	6.6	73
20	Diverse Metastable Structures Formed by Small Oligomers of $\hat{\pm}$ -Synuclein Probed by Force Spectroscopy. <i>PLoS ONE</i> , 2014, 9, e86495.	1.1	54
21	Reconstructing folding energy landscapes from splitting probability analysis of single-molecule trajectories. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7183-7188.	3.3	53
22	Partially native intermediates mediate misfolding of SOD1 in single-molecule folding trajectories. <i>Nature Communications</i> , 2017, 8, 1881.	5.8	50
23	Early stages of aggregation of engineered $\hat{\pm}$ -synuclein monomers and oligomers in solution. <i>Scientific Reports</i> , 2019, 9, 1734.	1.6	47
24	Direct measurement of sequence-dependent transition path times and conformational diffusion in DNA duplex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1329-1334.	3.3	46
25	Anti-Frameshifting Ligand Active against SARS Coronavirus-2 Is Resistant to Natural Mutations of the Frameshift-Stimulatory Pseudoknot. <i>Journal of Molecular Biology</i> , 2020, 432, 5843-5847.	2.0	45
26	Programmed $\hat{\pm}$ Ribosomal Frameshifting in coronaviruses: A therapeutic target. <i>Virology</i> , 2021, 554, 75-82.	1.1	45
27	Complex dynamics under tension in a high-efficiency frameshift stimulatory structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19500-19505.	3.3	44
28	Single-Molecule Force Spectroscopy of Rapidly Fluctuating, Marginally Stable Structures in the Intrinsically Disordered Protein $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"} \rangle \langle \text{mml:mi} \rangle \hat{\pm} \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle$ -Synuclein. <i>Physical Review Letters</i> , 2014, 112, 158103.	2.9	43
29	Transition-Path Probability as a Test of Reaction-Coordinate Quality Reveals DNA Hairpin Folding Is a One-Dimensional Diffusive Process. <i>Journal of Physical Chemistry Letters</i> , 2015, 6, 1005-1010.	2.1	43
30	Pharmacological chaperone reshapes the energy landscape for folding and aggregation of the prion protein. <i>Nature Communications</i> , 2016, 7, 12058.	5.8	38
31	Quantifying Instrumental Artifacts in Folding Kinetics Measured by Single-Molecule Force Spectroscopy. <i>Biophysical Journal</i> , 2016, 111, 283-286.	0.2	38
32	Probing microscopic conformational dynamics in folding reactions by measuring transition paths. <i>Current Opinion in Chemical Biology</i> , 2019, 53, 68-74.	2.8	38
33	Modeling the structure of the frameshift-stimulatory pseudoknot in SARS-CoV-2 reveals multiple possible conformers. <i>PLoS Computational Biology</i> , 2021, 17, e1008603.	1.5	38
34	Single-Molecule Force Spectroscopy of Protein Folding. <i>Journal of Molecular Biology</i> , 2021, 433, 167207.	2.0	38
35	High-Precision Single-Molecule Characterization of the Folding of an HIV RNA Hairpin by Atomic Force Microscopy. <i>Nano Letters</i> , 2018, 18, 6318-6325.	4.5	34
36	Measuring the average shape of transition paths during the folding of a single biological molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8125-8130.	3.3	34

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37	Reconstructing Folding Energy Landscape Profiles from Nonequilibrium Pulling Curves with an Inverse Weierstrass Integral Transform. <i>Physical Review Letters</i> , 2014, 113, 238104.	2.9	33
38	Determining Intrachain Diffusion Coefficients for Biopolymer Dynamics from Single-Molecule Force Spectroscopy Measurements. <i>Biophysical Journal</i> , 2014, 107, 1647-1653.	0.2	33
39	Conformational dynamics of the frameshift stimulatory structure in HIV-1. <i>Rna</i> , 2017, 23, 1376-1384.	1.6	30
40	Mechanical strength of RNA knot in Zika virus protects against cellular defenses. <i>Nature Chemical Biology</i> , 2021, 17, 975-981.	3.9	29
41	Structural dynamics of single SARS-CoV-2 pseudoknot molecules reveal topologically distinct conformers. <i>Nature Communications</i> , 2021, 12, 4749.	5.8	29
42	Single-molecule assays for investigating protein misfolding and aggregation. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 7934.	1.3	26
43	Signal- ϵ Pair Correlation Analysis of Single-Molecule Trajectories. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 12643-12646.	7.2	23
44	Probing Position-Dependent Diffusion in Folding Reactions Using Single-Molecule Force Spectroscopy. <i>Biophysical Journal</i> , 2018, 114, 1657-1666.	0.2	23
45	Structural characteristics and membrane interactions of tandem β -synuclein oligomers. <i>Scientific Reports</i> , 2018, 8, 6755.	1.6	23
46	Identifying Inhibitors of β -1 Programmed Ribosomal Frameshifting in a Broad Spectrum of Coronaviruses. <i>Viruses</i> , 2022, 14, 177.	1.5	21
47	Unfolded and intermediate states of PrP play a key role in the mechanism of action of an antiprion chaperone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
48	Conformational Shannon Entropy of mRNA Structures from Force Spectroscopy Measurements Predicts the Efficiency of β -1 Programmed Ribosomal Frameshift Stimulation. <i>Physical Review Letters</i> , 2021, 126, 038102.	2.9	16
49	Comparing the energy landscapes for native folding and aggregation of PrP. <i>Prion</i> , 2016, 10, 207-220.	0.9	15
50	Phthalocyanine tetrasulfonates bind to multiple sites on natively-folded prion protein. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 826-832.	1.1	14
51	Molecular free energy profiles from force spectroscopy experiments by inversion of observed committors. <i>Journal of Chemical Physics</i> , 2019, 151, 154115.	1.2	14
52	Single-molecule approaches to prion protein misfolding. <i>Prion</i> , 2013, 7, 140-146.	0.9	13
53	Internalization of β -synuclein oligomers into SH-SY5Y cells. <i>Biophysical Journal</i> , 2021, 120, 877-885.	0.2	12
54	Integration of light scattering with machine learning for label free cell detection. <i>Biomedical Optics Express</i> , 2021, 12, 3512.	1.5	12

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55	$\hat{\alpha}$ -synuclein dimer structures found from computational simulations. <i>Biochimie</i> , 2015, 116, 133-140.	1.3	11
56	Testing Kinetic Identities Involving Transition-Path Properties Using Single-Molecule Folding Trajectories. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11095-11099.	1.2	11
57	Probing the Basis of $\hat{\alpha}$ -Synuclein Aggregation by Comparing Simulations to Single-Molecule Experiments. <i>Biophysical Journal</i> , 2019, 117, 1125-1135.	0.2	11
58	Phase transitions and structure analysis in wild-type, A30P, E46K, and A53T mutants of $\hat{\alpha}$ -synuclein. <i>European Biophysics Journal</i> , 2016, 45, 355-364.	1.2	10
59	Memory effects in single-molecule force spectroscopy measurements of biomolecular folding. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 24527-24534.	1.3	10
60	Transition-path properties for folding reactions in the limit of small barriers. <i>Journal of Chemical Physics</i> , 2018, 149, 115101.	1.2	9
61	Characterizing the inhibition of $\hat{\alpha}$ -synuclein oligomerization by a pharmacological chaperone that prevents prion formation by the protein PrP. <i>Protein Science</i> , 2019, 28, 1690-1702.	3.1	9
62	Observing the base-by-base search for native structure along transition paths during the folding of single nucleic acid hairpins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	5