

# 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	Identifying Inhibitors of $\hat{\sim}1$ Programmed Ribosomal Frameshifting in a Broad Spectrum of Coronaviruses. <i>Viruses</i> , 2022, 14, 177.	1.5	21
2	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
3	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
4	Programmed $\hat{\sim}1$ Ribosomal Frameshifting in coronaviruses: A therapeutic target. <i>Virology</i> , 2021, 554, 75-82.	1.1	45
5	Internalization of $\hat{\pm}$ -synuclein oligomers into SH-SY5Y cells. <i>Biophysical Journal</i> , 2021, 120, 877-885.	0.2	12
6	Integration of light scattering with machine learning for label free cell detection. <i>Biomedical Optics Express</i> , 2021, 12, 3512.	1.5	12
7	Mechanical strength of RNA knot in Zika virus protects against cellular defenses. <i>Nature Chemical Biology</i> , 2021, 17, 975-981.	3.9	29
8	Structural dynamics of single SARS-CoV-2 pseudoknot molecules reveal topologically distinct conformers. <i>Nature Communications</i> , 2021, 12, 4749.	5.8	29
9	Single-Molecule Force Spectroscopy of Protein Folding. <i>Journal of Molecular Biology</i> , 2021, 433, 167207.	2.0	38
10	Conformational Shannon Entropy of mRNA Structures from Force Spectroscopy Measurements Predicts the Efficiency of $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"} \langle \text{mml:mo form="prefix"} \rangle \hat{\sim} \langle \text{mml:mo} \rangle \langle \text{mml:mn} \rangle 1 \langle \text{mml:mn} \rangle \langle \text{mml:math} \rangle$ Programmed Ribosomal Frameshift Stimulation. <i>Physical Review Letters</i> , 2021, 126, 038102.	2.9	16
11	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
12	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
13	Structural and functional conservation of the programmed $\hat{\sim}1$ ribosomal frameshift signal of SARS coronavirus 2 (SARS-CoV-2). <i>Journal of Biological Chemistry</i> , 2020, 295, 10741-10748.	1.6	163
14	Characterizing the inhibition of $\hat{\pm}$ -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
15	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
16	Probing the Basis of $\hat{\pm}$ -Synuclein Aggregation by Comparing Simulations to Single-Molecule Experiments. <i>Biophysical Journal</i> , 2019, 117, 1125-1135.	0.2	11
17	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
18	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

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19	Measuring the average shape of transition paths during the folding of a single biological molecule. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8125-8130.	3.3	34
20	Early stages of aggregation of engineered $\hat{I}\pm$ -synuclein monomers and oligomers in solution. Scientific Reports, 2019, 9, 1734.	1.6	47
21	Memory effects in single-molecule force spectroscopy measurements of biomolecular folding. Physical Chemistry Chemical Physics, 2019, 21, 24527-24534.	1.3	10
22	Probing Position-Dependent Diffusion in Folding Reactions Using Single-Molecule Force Spectroscopy. Biophysical Journal, 2018, 114, 1657-1666.	0.2	23
23	Structural characteristics and membrane interactions of tandem $\hat{I}\pm$ -synuclein oligomers. Scientific Reports, 2018, 8, 6755.	1.6	23
24	Transition-path properties for folding reactions in the limit of small barriers. Journal of Chemical Physics, 2018, 149, 115101.	1.2	9
25	High-Precision Single-Molecule Characterization of the Folding of an HIV RNA Hairpin by Atomic Force Microscopy. Nano Letters, 2018, 18, 6318-6325.	4.5	34
26	Testing Kinetic Identities Involving Transition-Path Properties Using Single-Molecule Folding Trajectories. Journal of Physical Chemistry B, 2018, 122, 11095-11099.	1.2	11
27	Direct measurement of sequence-dependent transition path times and conformational diffusion in DNA duplex formation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1329-1334.	3.3	46
28	Conformational dynamics of the frameshift stimulatory structure in HIV-1. Rna, 2017, 23, 1376-1384.	1.6	30
29	Partially native intermediates mediate misfolding of SOD1 in single-molecule folding trajectories. Nature Communications, 2017, 8, 1881.	5.8	50
30	Comparing the energy landscapes for native folding and aggregation of PrP. Prion, 2016, 10, 207-220.	0.9	15
31	Direct observation of transition paths during the folding of proteins and nucleic acids. Science, 2016, 352, 239-242.	6.0	204
32	Pharmacological chaperone reshapes the energy landscape for folding and aggregation of the prion protein. Nature Communications, 2016, 7, 12058.	5.8	38
33	Quantifying Instrumental Artifacts in Folding Kinetics Measured by Single-Molecule Force Spectroscopy. Biophysical Journal, 2016, 111, 283-286.	0.2	38
34	Protein folding trajectories can be described quantitatively by one-dimensional diffusion over measured energy landscapes. Nature Physics, 2016, 12, 700-703.	6.5	86
35	Phase transitions and structure analysis in wild-type, A30P, E46K, and A53T mutants of $\hat{I}\pm$ -synuclein. European Biophysics Journal, 2016, 45, 355-364.	1.2	10
36	Reconstructing folding energy landscapes from splitting probability analysis of single-molecule trajectories. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7183-7188.	3.3	53

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37	Probing the structural dynamics of proteins and nucleic acids with optical tweezers. <i>Current Opinion in Structural Biology</i> , 2015, 34, 43-51.	2.6	102
38	$\hat{I}\pm$ -synuclein dimer structures found from computational simulations. <i>Biochimie</i> , 2015, 116, 133-140.	1.3	11
39	Protein misfolding occurs by slow diffusion across multiple barriers in a rough energy landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8308-8313.	3.3	80
40	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
41	Diverse Metastable Structures Formed by Small Oligomers of $\hat{I}\pm$ -Synuclein Probed by Force Spectroscopy. <i>PLoS ONE</i> , 2014, 9, e86495.	1.1	54
42	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
43	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
44	Single-Molecule Force Spectroscopy of Rapidly Fluctuating, Marginally Stable Structures in the Intrinsically Disordered Protein $\hat{I}\pm$ -Synuclein. <i>Physical Review Letters</i> , 2014, 112, 158103.	2.9	43
45	Reconstructing Folding Energy Landscapes by Single-Molecule Force Spectroscopy. <i>Annual Review of Biophysics</i> , 2014, 43, 19-39.	4.5	200
46	Determining Intrachain Diffusion Coefficients for Biopolymer Dynamics from Single-Molecule Force Spectroscopy Measurements. <i>Biophysical Journal</i> , 2014, 107, 1647-1653.	0.2	33
47	Single-molecule assays for investigating protein misfolding and aggregation. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 7934.	1.3	26
48	Single-molecule approaches to prion protein misfolding. <i>Prion</i> , 2013, 7, 140-146.	0.9	13
49	Transition Path Times for Nucleic Acid Folding Determined from Energy-Landscape Analysis of Single-Molecule Trajectories. <i>Physical Review Letters</i> , 2012, 109, 068102.	2.9	103
50	Energy landscape analysis of native folding of the prion protein yields the diffusion constant, transition path time, and rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14452-14457.	3.3	140
51	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
52	Programmed $\hat{I}\pm$ frameshifting efficiency correlates with RNA pseudoknot conformational plasticity, not resistance to mechanical unfolding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16167-16172.	3.3	120
53	Direct observation of multiple misfolding pathways in a single prion protein molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5283-5288.	3.3	131
54	Experimental validation of free-energy-landscape reconstruction from non-equilibrium single-molecule force spectroscopy measurements. <i>Nature Physics</i> , 2011, 7, 631-634.	6.5	138

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55	Signal-Pair Correlation Analysis of Single-Molecule Trajectories. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 12643-12646.	7.2	23
56	Single-molecule force spectroscopy of the add adenine riboswitch relates folding to regulatory mechanism. <i>Nucleic Acids Research</i> , 2011, 39, 7677-7687.	6.5	113
57	Folding and unfolding single RNA molecules under tension. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 640-646.	2.8	92
58	Direct Observation of Hierarchical Folding in Single Riboswitch Aptamers. <i>Science</i> , 2008, 319, 630-633.	6.0	361
59	High-Resolution, Single-Molecule Measurements of Biomolecular Motion. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007, 36, 171-190.	18.3	425
60	Nanomechanical measurements of the sequence-dependent folding landscapes of single nucleic acid hairpins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6190-6195.	3.3	397
61	Direct Measurement of the Full, Sequence-Dependent Folding Landscape of a Nucleic Acid. <i>Science</i> , 2006, 314, 1001-1004.	6.0	356
62	Passive All-Optical Force Clamp for High-Resolution Laser Trapping. <i>Physical Review Letters</i> , 2005, 95, 208102.	2.9	201