## Krishna Neupane

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Identifying Inhibitors of â^'1 Programmed Ribosomal Frameshifting in a Broad Spectrum of Coronaviruses. Viruses, 2022, 14, 177.	3.3	21
2	Structural dynamics of single SARS-CoV-2 pseudoknot molecules reveal topologically distinct conformers. Nature Communications, 2021, 12, 4749.	12.8	29
3	Observing the base-by-base search for native structure along transition paths during the folding of single nucleic acid hairpins. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	5
4	Anti-Frameshifting Ligand Active against SARS Coronavirus-2 Is Resistant to Natural Mutations of the Frameshift-Stimulatory Pseudoknot. Journal of Molecular Biology, 2020, 432, 5843-5847.	4.2	45
5	Structural and functional conservation of the programmed â^'1 ribosomal frameshift signal of SARS coronavirus 2 (SARS-CoV-2). Journal of Biological Chemistry, 2020, 295, 10741-10748.	3.4	163
6	Complex dynamics under tension in a high-efficiency frameshift stimulatory structure. Proceedings of the United States of America, 2019, 116, 19500-19505.	7.1	44
7	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.	7.1	34
8	Transition-path properties for folding reactions in the limit of small barriers. Journal of Chemical Physics, 2018, 149, 115101.	3.0	9
9	Measuring the Local Velocity along Transition Paths during the Folding of Single Biological Molecules. Physical Review Letters, 2018, 121, 018102.	7.8	41
10	Testing Kinetic Identities Involving Transition-Path Properties Using Single-Molecule Folding Trajectories. Journal of Physical Chemistry B, 2018, 122, 11095-11099.	2.6	11
11	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.	7.1	46
12	Direct observation of transition paths during the folding of proteins and nucleic acids. Science, 2016, 352, 239-242.	12.6	204
13	Pharmacological chaperone reshapes the energy landscape for folding and aggregation of the prion protein. Nature Communications, 2016, 7, 12058.	12.8	38
14	Quantifying Instrumental Artifacts in Folding Kinetics Measured by Single-Molecule Force Spectroscopy. Biophysical Journal, 2016, 111, 283-286.	0.5	38
15	Protein folding trajectories can be described quantitatively by one-dimensional diffusion over measured energyAlandscapes. Nature Physics, 2016, 12, 700-703.	16.7	86
16	Transition-Path Probability as a Test of Reaction-Coordinate Quality Reveals DNA Hairpin Folding Is a One-Dimensional Diffusive Process. Journal of Physical Chemistry Letters, 2015, 6, 1005-1010.	4.6	43
17	Diverse Metastable Structures Formed by Small Oligomers of α-Synuclein Probed by Force Spectroscopy. PLoS ONE, 2014, 9, e86495.	2.5	54
18	Single-Molecule Force Spectroscopy of Rapidly Fluctuating, Marginally Stable Structures in the Intrinsically Disordered Protein <mml:math <br="" xmlns:mml="http://www.w3.org/1998/Math/MathML">display="inline"&gt;<mml:mi>î±</mml:mi></mml:math> -Synuclein. Physical Review Letters, 2014, 112, 158103.	7.8	43

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19	Single-molecule assays for investigating protein misfolding and aggregation. Physical Chemistry Chemical Physics, 2013, 15, 7934.	2.8	26
20	Transition Path Times for Nucleic Acid Folding Determined from Energy-Landscape Analysis of Single-Molecule Trajectories. Physical Review Letters, 2012, 109, 068102.	7.8	103
21	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.	7.1	140
22	Direct observation of multiple misfolding pathways in a single prion protein molecule. Proceedings of the United States of America, 2012, 109, 5283-5288.	7.1	131
23	Experimental validation of free-energy-landscape reconstruction from non-equilibrium single-molecule force spectroscopy measurements. Nature Physics, 2011, 7, 631-634.	16.7	138
24	Single-molecule force spectroscopy of the add adenine riboswitch relates folding to regulatory mechanism. Nucleic Acids Research, 2011, 39, 7677-7687.	14.5	113