

# Krishna Neupane

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7719578/publications.pdf>

Version: 2024-02-01

24  
papers

1,631  
citations

361413

20  
h-index

610901

24  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1413  
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct observation of transition paths during the folding of proteins and nucleic acids. <i>Science</i> , 2016, 352, 239-242.	12.6	204
2	Structural and functional conservation of the programmed $\sim 1$ ribosomal frameshift signal of SARS coronavirus 2 (SARS-CoV-2). <i>Journal of Biological Chemistry</i> , 2020, 295, 10741-10748.	3.4	163
3	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.	7.1	140
4	Experimental validation of free-energy-landscape reconstruction from non-equilibrium single-molecule force spectroscopy measurements. <i>Nature Physics</i> , 2011, 7, 631-634.	16.7	138
5	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.	7.1	131
6	Single-molecule force spectroscopy of the add adenine riboswitch relates folding to regulatory mechanism. <i>Nucleic Acids Research</i> , 2011, 39, 7677-7687.	14.5	113
7	Transition Path Times for Nucleic Acid Folding Determined from Energy-Landscape Analysis of Single-Molecule Trajectories. <i>Physical Review Letters</i> , 2012, 109, 068102.	7.8	103
8	Protein folding trajectories can be described quantitatively by one-dimensional diffusion over measured energy landscapes. <i>Nature Physics</i> , 2016, 12, 700-703.	16.7	86
9	Diverse Metastable Structures Formed by Small Oligomers of $\Delta$ -Synuclein Probed by Force Spectroscopy. <i>PLoS ONE</i> , 2014, 9, e86495.	2.5	54
10	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.	7.1	46
11	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.	4.2	45
12	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.	7.1	44
13	Single-Molecule Force Spectroscopy of Rapidly Fluctuating, Marginally Stable Structures in the Intrinsically Disordered Protein $\Delta$ -Synuclein. <i>Physical Review Letters</i> , 2014, 112, 158103.	7.8	43
14	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.	4.6	43
15	Measuring the Local Velocity along Transition Paths during the Folding of Single Biological Molecules. <i>Physical Review Letters</i> , 2018, 121, 018102.	7.8	41
16	Pharmacological chaperone reshapes the energy landscape for folding and aggregation of the prion protein. <i>Nature Communications</i> , 2016, 7, 12058.	12.8	38
17	Quantifying Instrumental Artifacts in Folding Kinetics Measured by Single-Molecule Force Spectroscopy. <i>Biophysical Journal</i> , 2016, 111, 283-286.	0.5	38
18	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.	7.1	34

#	ARTICLE	IF	CITATIONS
19	Structural dynamics of single SARS-CoV-2 pseudoknot molecules reveal topologically distinct conformers. <i>Nature Communications</i> , 2021, 12, 4749.	12.8	29
20	Single-molecule assays for investigating protein misfolding and aggregation. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 7934.	2.8	26
21	Identifying Inhibitors of $\sim 1$ Programmed Ribosomal Frameshifting in a Broad Spectrum of Coronaviruses. <i>Viruses</i> , 2022, 14, 177.	3.3	21
22	Testing Kinetic Identities Involving Transition-Path Properties Using Single-Molecule Folding Trajectories. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11095-11099.	2.6	11
23	Transition-path properties for folding reactions in the limit of small barriers. <i>Journal of Chemical Physics</i> , 2018, 149, 115101.	3.0	9
24	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, .	7.1	5