PatrÃ-cia F N FaÃ-sca

List of Publications by Year
in descending order

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40	781	471061	552369
papers	citations	17	26
		h-index	g-index

45	45	45	563
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Knotted proteins: A tangled tale of Structural Biology. Computational and Structural Biotechnology Journal, 2015, 13, 459-468.	1.9	70
2	The folding of knotted proteins: insights from lattice simulations. Physical Biology, 2010, 7, 016009.	0.8	46
3	Identification of a Conserved Aggregation-Prone Intermediate State in the Folding Pathways of Spc-SH3 Amyloidogenic Variants. Journal of Molecular Biology, 2012, 422, 705-722.	2.0	43
4	Nonâ€native interactions play an effective role in protein folding dynamics. Protein Science, 2010, 19, 2196-2209.	3.1	42
5	Effects of knot type in the folding of topologically complex lattice proteins. Journal of Chemical Physics, 2014, 141, 025101.	1.2	41
6	Effects of Knots on Protein Folding Properties. PLoS ONE, 2013, 8, e74755.	1.1	39
7	A Simulated Intermediate State for Folding and Aggregation Provides Insights into Î”N6 Î²2-Microglobulin Amyloidogenic Behavior. PLoS Computational Biology, 2014, 10, e1003606.	1.5	34
8	Robustness of atomistic GÅ•models in predicting native-like folding intermediates. Journal of Chemical Physics, 2012, 137, 085102.	1.2	30
9	Steric confinement and enhanced local flexibility assist knotting in simple models of protein folding. Physical Chemistry Chemical Physics, 2016, 18, 26391-26403.	1.3	30
10	Thermodynamic control and dynamical regimes in protein folding. Journal of Chemical Physics, 2002, 116, 7231-7237.	1.2	26
11	Cooperativity and the origins of rapid, single-exponential kinetics in protein folding. Protein Science, 2006, 15, 1608-1618.	3.1	25
12	Why Do Protein Folding Rates Correlate with Metrics of Native Topology?. PLoS ONE, 2012, 7, e35599.	1.1	24
13	Structural and energetic determinants of co-translational folding. Journal of Chemical Physics, 2013, 138, 215101.	1.2	24
14	The nucleation mechanism of protein folding: a survey of computer simulation studies. Journal of Physics Condensed Matter, 2009, 21, 373102.	0.7	23
15	How Difficult Is It to Fold a Knotted Protein? In Silico Insights from Surface-Tethered Folding Experiments. PLoS ONE, 2012, 7, e52343.	1.1	21
16	Topological complexity, contact order, and protein folding rates. Journal of Chemical Physics, 2002, 117, 8587-8591.	1.2	19
17	Identifying critical residues in protein folding: Insights from Ï•-value and Pfold analysis. Journal of Chemical Physics, 2008, 129, 095108.	1.2	19
18	Hydrophobic confinement modulates thermal stability and assists knotting in the folding of tangled proteins. Physical Chemistry Chemical Physics, 2019, 21, 11764-11775.	1.3	18

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19	Assessing the Effect of Loop Mutations in the Folding Space of Î²2-Microglobulin with Molecular Dynamics Simulations. International Journal of Molecular Sciences, 2013, 14, 17256-17278.	1.8	17
20	Interplay between native topology and non-native interactions in the folding of tethered proteins. Physical Biology, 2013, 10, 016002.	0.8	17
21	A tale of two tails: The importance of unstructured termini in the aggregation pathway of Î²2â€microglobulin. Proteins: Structure, Function and Bioinformatics, 2017, 85, 2045-2057.	1.5	17
22	Native geometry and the dynamics of protein folding. Biophysical Chemistry, 2005, 115, 169-175.	1.5	14
23	The protein folding transition state: Insights from kinetics and thermodynamics. Journal of Chemical Physics, 2010, 133, 125102.	1.2	14
24	How determinant is N-terminal to C-terminal coupling for protein folding?. Physical Chemistry Chemical Physics, 2015, 17, 3512-3524.	1.3	14
25	The GÅ•model revisited: Native structure and the geometric coupling between local and long-range contacts. Proteins: Structure, Function and Bioinformatics, 2005, 60, 712-722.	1.5	13
26	Calcium binding to gatekeeper residues flanking aggregation-prone segments underlies non-fibrillar amyloid traits in superoxide dismutase 1 (SOD1). Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 118-126.	1.1	13
27	Thermal unfolding simulations of NBD1 domain variants reveal structural motifs associated with the impaired folding of F508del-CFTR. Molecular BioSystems, 2016, 12, 2834-2848.	2.9	13
28	Pathways to folding, nucleation events, and native geometry. Journal of Chemical Physics, 2007, 127, 145106.	1.2	11
29	The Early Phase of Î²2m Aggregation: An Integrative Computational Study Framed on the D76N Mutant and the Î”N6 Variant. Biomolecules, 2019, 9, 366.	1.8	11
30	The Early Phase of Î²2-Microglobulin Aggregation: Perspectives From Molecular Simulations. Frontiers in Molecular Biosciences, 2020, 7, 578433.	1.6	10
31	Protein Folding: An Introduction. Springer Briefs in Molecular Science, 2019, , 1-63.	0.1	8
32	A Specific Set of Heterogeneous Native Interactions Yields Efficient Knotting in Protein Folding. Journal of Physical Chemistry B, 2021, 125, 7359-7367.	1.2	6
33	Nucleation phenomena in protein folding: the modulating role of protein sequence. Journal of Physics Condensed Matter, 2007, 19, 285212.	0.7	5
34	Conformational States and Protein Stability from a Proteomic Perspective. Current Proteomics, 2007, 4, 44-52.	0.1	4
35	The folding space of protein Î²2-microglobulin is modulated by a single disulfide bridge. Physical Biology, 2021, 18, 056001.	0.8	4
36	Melnikov method for parabolic orbits. Nonlinear Differential Equations and Applications, 2003, 10, 119-131.	0.4	3

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37	On the relation between native geometry and conformational plasticity. Biophysical Chemistry, 2008, 138, 99-106.	1.5	3
38	Predicting stable binding modes from simulated dimers of the D76N mutant of <mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si14.svg"><mml:mrow><mml:mi>Î²</mml:mi></mml:mrow></mml:math>2-microglobulin. Computational and Structural Biotechnology Journal, 2021, 19, 5160-5169.	1.9	2
39	Folding of small proteins: a matter of geometry?. Molecular Physics, 2005, 103, 2903-2910.	0.8	1
40	Interview with Mike Kosterlitz. Europhysics News, 2019, 50, 12-14.	0.1	0