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List of Publications by Year in descending order

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62 papers	2,483 citations	304743 22 h-index	206112 48 g-index
65 all docs	65 docs citations	65 times ranked	2801 citing authors

#	Article	IF	Citations
1	Statistical potentials from the Gaussian scaling behaviour of chain fragments buried within protein globules. PLoS ONE, 2022, 17, e0254969.	2.5	0
2	Folding Rate Optimization Promotes Frustrated Interactions in Entangled Protein Structures. International Journal of Molecular Sciences, 2020, 21, 213.	4.1	6
3	Sequence and structural patterns detected in entangled proteins reveal the importance of co-translational folding. Scientific Reports, 2019, 9, 8426.	3.3	30
4	Vibrational entropy estimation can improve binding affinity prediction for nonâ€obligatory protein complexes. Proteins: Structure, Function and Bioinformatics, 2018, 86, 393-404.	2.6	7
5	Signature of Pareto optimization in the Escherichia coli proteome. Scientific Reports, 2018, 8, 9141.	3.3	8
6	Bubble-bound state of triple-stranded DNA: Efimov physics in DNA with repulsion. Journal of Statistical Mechanics: Theory and Experiment, 2017, 2017, 073203.	2.3	6
7	Exploring the correlation between the folding rates of proteins and the entanglement of their native states. Journal of Physics A: Mathematical and Theoretical, 2017, 50, 504001.	2.1	44
8	Bacterial bioluminescence onset and quenching: a dynamical model for aquorum sensing-mediated property. Royal Society Open Science, 2017, 4, 171586.	2.4	9
9	Linking in domain-swapped protein dimers. Scientific Reports, 2016, 6, 33872.	3.3	33
10	Modeling quorum sensing trade-offs between bacterial cell density and system extension from open boundaries. Scientific Reports, 2016, 6, 39142.	3.3	20
11	Efimov-Like Behaviour in Low-Dimensional Polymer Models. Journal of Low Temperature Physics, 2016, 185, 102-121.	1.4	1
12	An Efficient Algorithm to Perform Local Concerted Movements of a Chain Molecule. PLoS ONE, 2015, 10, e0118342.	2.5	14
13	Native fold and docking pose discrimination by the same residueâ€based scoring function. Proteins: Structure, Function and Bioinformatics, 2015, 83, 621-630.	2.6	17
14	Quorum vs. diffusion sensing: a quantitative analysis of the relevance of absorbing or reflecting boundaries. FEMS Microbiology Letters, 2014, 352, 198-203.	1.8	39
15	Melting behavior and different bound states in three-stranded DNA models. Physical Review E, 2014, 89, 012121.	2.1	8
16	PASTA 2.0: an improved server for protein aggregation prediction. Nucleic Acids Research, 2014, 42, W301-W307.	14.5	349
17	BACHSCORE. A tool for evaluating efficiently and reliably the quality of large sets of protein structures. Computer Physics Communications, 2013, 184, 2860-2865.	7.5	20
18	A simple and efficient statistical potential for scoring ensembles of protein structures. Scientific Reports, 2012, 2, .	3.3	48

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19	Sequence repeats and protein structure. Physical Review E, 2012, 86, 050901.	2.1	2
20	Protein Sequence and Structure: Is One More Fundamental than the Other?. Journal of Statistical Physics, 2012, 148, 637-646.	1.2	4
21	Exploring by Enhanced Sampling Techniques: The Proteinâ€™s Conformational Space Beyond the PDB. Biophysical Journal, 2011, 100, 209a.	0.5	0
22	Fibril elongation mechanisms of HETâ€s prionâ€forming domain: Topological evidence for growth polarity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3067-3081.	2.6	8
23	Different pulling modes in DNA overstretching: A theoretical analysis. Physical Review E, 2010, 81, 051926.	2.1	14
24	Exploring the Universe of Protein Structures beyond the Protein Data Bank. PLoS Computational Biology, 2010, 6, e1000957.	3.2	62
25	When a DNA triple helix melts: an analogue of the Efimov state. New Journal of Physics, 2010, 12, 083057.	2.9	16
26	Simplified Exactly Solvable Model for<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" display="inline"><mml:mi>Î²</mml:mi></mml:math>-Amyloid Aggregation. Physical Review Letters, 2010, 105, 108102.	7.8	15
27	Amyloidogenic Potential of Transthyretin Variants. Journal of Biological Chemistry, 2009, 284, 25832-25841.	3.4	44
28	REPETITA: detection and discrimination of the periodicity of protein solenoid repeats by discrete Fourier transform. Bioinformatics, 2009, 25, i289-i295.	4.1	57
29	Consequences of relative cellular positioning on quorum sensing and bacterial cell-to-cell communication. FEMS Microbiology Letters, 2009, 292, 149-161.	1.8	59
30	A Condensation-Ordering Mechanism in Nanoparticle-Catalyzed Peptide Aggregation. PLoS Computational Biology, 2009, 5, e1000458.	3.2	90
31	Phase diagrams for DNA denaturation under stretching forces. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, L04001.	2.3	11
32	Inference of the solvation energy parameters of amino acids using maximum entropy approach. Journal of Chemical Physics, 2008, 129, 035102.	3.0	4
33	Maximum Entropy Approach for Deducing Amino Acid Interactions in Proteins. Physical Review Letters, 2008, 100, 078102.	7.8	34
34	Emergence of secondary motifs in tubelike polymers in a solvent. Physical Review E, 2008, 77, 061804.	2.1	11
35	Aggregation of natively folded proteins: a theoretical approach. Journal of Physics Condensed Matter, 2007, 19, 285221.	1.8	5
36	The PASTA server for protein aggregation prediction. Protein Engineering, Design and Selection, 2007, 20, 521-523.	2.1	217

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37	Symmetry, shape, and order. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19187-19192.	7.1	14
38	Structural motifs of biomolecules. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17283-17286.	7.1	31
39	Minireview: The compact phase in polymers and proteins. Physica A: Statistical Mechanics and Its Applications, 2007, 384, 122-127.	2.6	4
40	Simple solvation potential for coarse-grained models of proteins. Proteins: Structure, Function and Bioinformatics, 2007, 67, 285-292.	2.6	4
41	Marginal compactness of protein native structures. Journal of Physics Condensed Matter, 2006, 18, S297-S306.	1.8	6
42	Insight into the Structure of Amyloid Fibrils from the Analysis of Globular Proteins. PLoS Computational Biology, 2006, 2, e170.	3.2	180
43	Geometry of proteins: Hydrogen bonding, sterics, and marginally compact tubes. Physical Review E, 2006, 73, 031921.	2.1	14
44	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6883-6888.	7.1	48
45	Geometrical model for the native-state folds of proteins. Biophysical Chemistry, 2005, 115, 289-294.	2.8	7
46	Physics of thick polymers. Journal of Polymer Science, Part B: Polymer Physics, 2005, 43, 650-679.	2.1	21
47	What determines the structures of native folds of proteins?. Journal of Physics Condensed Matter, 2005, 17, S1515-S1522.	1.8	5
48	Design of amino acid sequences to fold into CÎ±-model proteins. Journal of Chemical Physics, 2005, 123, 054904.	3.0	4
49	Continuum model for polymers with finite thickness. Journal of Physics A, 2005, 38, L277-L283.	1.6	16
50	Unified perspective on proteins: A physics approach. Physical Review E, 2004, 70, 041905.	2.1	61
51	Geometry and symmetry presculpt the free-energy landscape of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7960-7964.	7.1	203
52	A new perspective on analysis of helix-helix packing preferences in globular proteins. Proteins: Structure, Function and Bioinformatics, 2004, 55, 1014-1022.	2.6	16
53	Compact phases of polymers with hydrogen bonding. Physical Review E, 2003, 67, 021805.	2.1	8
54	Tubes near the edge of compactness and folded protein structures *. Journal of Physics Condensed Matter, 2003, 15, S1787-S1796.	1.8	8

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55	Geometry of Compact Tubes and Protein Structures. Complexus, 2003, 1, 4-13.	0.6	22
56	Geometry and physics of proteins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 315-322.	2.6	69
57	Phase diagram of force-induced DNA unzipping in exactly solvable models. Physical Review E, 2001, 64, 031901.	2.1	92
58	Optimal shapes of compact strings. Nature, 2000, 406, 287-290.	27.8	270
59	A variational approach to the localization transition of heteropolymers at interfaces. Europhysics Letters, 1999, 46, 301-306.	2.0	19
60	Heteropolymers in a solvent at an interface. Journal of Physics A, 1999, 32, L275-L280.	1.6	20
61	Swollen-collapsed transition in random hetero-polymers. European Physical Journal B, 1998, 6, 63-73.	1.5	13
62	Universality for interacting oriented self-avoiding walk: A transfer matrix calculation. Physical Review E, 1997, 56, 131-143.	2.1	14