

Trinh Xuan Hoang

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

1,624
citations

361045

20
h-index

315357

38
g-index

72
all docs

72
docs citations

72
times ranked

1097
citing authors

#	ARTICLE	IF	CITATIONS
1	Geometry and symmetry prescript the free-energy landscape of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7960-7964.	3.3	203
2	Universality Classes in Folding Times of Proteins. Biophysical Journal, 2003, 84, 475-488.	0.2	119
3	Molecular dynamics of folding of secondary structures in Go-type models of proteins. Journal of Chemical Physics, 2000, 112, 6851-6862.	1.2	117
4	Sequencing of folding events in Go-type proteins. Journal of Chemical Physics, 2000, 113, 8319-8328.	1.2	100
5	Thermal effects in stretching of Go-like models of titin and secondary structures. Proteins: Structure, Function and Bioinformatics, 2004, 56, 285-297.	1.5	73
6	Scaling of Folding Properties in Simple Models of Proteins. Physical Review Letters, 1999, 83, 1684-1687.	2.9	67
7	Folding and stretching in a Go-like model of titin. Proteins: Structure, Function and Bioinformatics, 2002, 49, 114-124.	1.5	64
8	Thermal folding and mechanical unfolding pathways of protein secondary structures. Proteins: Structure, Function and Bioinformatics, 2002, 49, 104-113.	1.5	62
9	Unified perspective on proteins: A physics approach. Physical Review E, 2004, 70, 041905.	0.8	61
10	Energy landscapes, supergraphs, and "folding funnels" in spin systems. Physical Review E, 1999, 60, 3219-3226.	0.8	57
11	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.	3.3	48
12	Folding Pathways of Prion and Doppel. Biophysical Journal, 2002, 83, 3533-3541.	0.2	40
13	Elasticity of Semiflexible Polymers with and without Self-Interactions. Macromolecules, 2003, 36, 10095-10102.	2.2	40
14	Structural motifs of biomolecules. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17283-17286.	3.3	31
15	Mechanical properties of the domains of titin in a Go-like model. Journal of Chemical Physics, 2005, 122, 054906.	1.2	27
16	From toroidal to rod-like condensates of semiflexible polymers. Journal of Chemical Physics, 2014, 140, 064902.	1.2	27
17	Theoretical Model for the Structural Relaxation Time in Coamorphous Drugs. Molecular Pharmaceutics, 2019, 16, 2992-2998.	2.3	27
18	First-principles design of nanomachines. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6900-6903.	3.3	25

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19	From polymers to proteins: the effect of side chains and broken symmetry on the formation of secondary structures within a Wang-Landau approach. <i>Soft Matter</i> , 2016, 12, 4783-4793.	1.2	24
20	Surface plasmon resonances of protein-conjugated gold nanoparticles on graphitic substrates. <i>Applied Physics Letters</i> , 2013, 103, .	1.5	23
21	Effective stiffness and formation of secondary structures in a protein-like model. <i>Journal of Chemical Physics</i> , 2016, 145, 084904.	1.2	23
22	Stretching of proteins in the entropic limit. <i>Physical Review E</i> , 2004, 69, 011912.	0.8	20
23	THE RANGE OF THE CONTACT INTERACTIONS AND THE KINETICS OF THE GO MODELS OF PROTEINS. <i>International Journal of Modern Physics C</i> , 2002, 13, 1231-1242.	0.8	19
24	A new interpolation formula for semiflexible polymers. <i>Biophysical Chemistry</i> , 2005, 115, 251-254.	1.5	19
25	Kinetic nonoptimality and vibrational stability of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 20-25.	1.5	18
26	Scaling of folding properties in go models of proteins. , 2000, 26, 273-294.		16
27	Proteins and polymers. <i>Journal of Chemical Physics</i> , 2005, 122, 234910.	1.2	15
28	Transport properties through graphene grain boundaries: strain effects versus lattice symmetry. <i>Nanoscale</i> , 2016, 8, 11658-11673.	2.8	15
29	Geometry of proteins: Hydrogen bonding, sterics, and marginally compact tubes. <i>Physical Review E</i> , 2006, 73, 031921.	0.8	14
30	Symmetry, shape, and order. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 19187-19192.	3.3	14
31	Folding and escape of nascent proteins at ribosomal exit tunnel. <i>Journal of Chemical Physics</i> , 2016, 144, 095102.	1.2	14
32	Protein escape at the ribosomal exit tunnel: Effects of native interactions, tunnel length, and macromolecular crowding. <i>Journal of Chemical Physics</i> , 2018, 149, 045102.	1.2	14
33	Assembly of protein tertiary structures from secondary structures using optimized potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 52, 155-165.	1.5	13
34	Stretching of homopolymers and contact order. <i>Physical Review E</i> , 2004, 70, 011917.	0.8	13
35	Sequence dependent aggregation of peptides and fibril formation. <i>Journal of Chemical Physics</i> , 2017, 147, 105102.	1.2	13
36	Local symmetry determines the phases of linear chains: a simple model for the self-assembly of peptides. <i>Soft Matter</i> , 2019, 15, 5596-5613.	1.2	13

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37	Coarse grained description of protein folding. <i>Physical Review E</i> , 1998, 58, 3589-3596.	0.8	12
38	The elixir phase of chain molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 176-184.	1.5	11
39	Hydrophobic and electrostatic interactions modulate protein escape at the ribosomal exit tunnel. <i>Biophysical Journal</i> , 2021, 120, 4798-4808.	0.2	10
40	Folding of proteins in Go models with angular interactions. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2003, 330, 195-205.	1.2	9
41	Protein escape at the ribosomal exit tunnel: Effect of the tunnel shape. <i>Journal of Chemical Physics</i> , 2020, 153, 045105.	1.2	9
42	Protein folding and models of dynamics on the lattice. <i>Journal of Chemical Physics</i> , 1998, 109, 9192-9196.	1.2	8
43	Phase diagram of the ground states of DNA condensates. <i>Physical Review E</i> , 2015, 92, 060701.	0.8	8
44	Geometrical model for the native-state folds of proteins. <i>Biophysical Chemistry</i> , 2005, 115, 289-294.	1.5	7
45	Form of Growing Strings. <i>Physical Review Letters</i> , 2005, 95, 098103.	2.9	6
46	Marginal compactness of protein native structures. <i>Journal of Physics Condensed Matter</i> , 2006, 18, S297-S306.	0.7	6
47	Repulsive interactions of a lipid membrane with graphene in composite materials. <i>Journal of Chemical Physics</i> , 2013, 139, 184703.	1.2	6
48	The pH-dependent electrostatic interaction of a metal nanoparticle with the MS2 virus-like particles. <i>Chemical Physics Letters</i> , 2019, 730, 84-88.	1.2	6
49	Prediction of protein secondary structures from conformational biases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 558-565.	1.5	5
50	What determines the structures of native folds of proteins?. <i>Journal of Physics Condensed Matter</i> , 2005, 17, S1515-S1522.	0.7	5
51	Inference of the solvation energy parameters of amino acids using maximum entropy approach. <i>Journal of Chemical Physics</i> , 2008, 129, 035102.	1.2	4
52	Protein Sequence and Structure: Is One More Fundamental than the Other?. <i>Journal of Statistical Physics</i> , 2012, 148, 637-646.	0.5	4
53	Proteins – a celebration of consilience. <i>International Journal of Modern Physics B</i> , 2022, 36, .	1.0	4
54	Spontaneous dimensional reduction and ground state degeneracy in a simple chain model. <i>Physical Review E</i> , 2021, 104, L012101.	0.8	3

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55	Spin analogues of proteins: scaling of 'folding' properties. Journal of Physics A, 2000, 33, 3977-3987.	1.6	2
56	Sequence repeats and protein structure. Physical Review E, 2012, 86, 050901.	0.8	2
57	Effects of inter-organism interactions in biofouling on microtopographic surfaces. Biofouling, 2019, 35, 684-695.	0.8	2
58	Marginally compact phase and ordered ground states in a model polymer with side spheres. Physical Review E, 2021, 104, L012501.	0.8	2
59	Aggregation of peptides in the tube model with correlated sidechain orientations. Journal of Physics: Conference Series, 2015, 627, 012028.	0.3	1
60	Effects of macromolecular crowding on protein folding. Journal of Physics: Conference Series, 2015, 627, 012027.	0.3	1
61	Cascaded plasmon resonant field enhancement in protein-conjugated gold nanoparticles: Role of protein shell. Journal of Science: Advanced Materials and Devices, 2016, 1, 61-64.	1.5	1
62	Protein escape at an atomistic model of the ribosomal exit tunnel. Journal of Physics: Conference Series, 2020, 1506, 012022.	0.3	1
63	Effects of ribosomal exit tunnel on protein's cotranslational folding. Communications in Physics, 2013, 23, 219.	0.0	1
64	Shapes of hydrophobic thick membranes. Europhysics Letters, 2012, 98, 56006.	0.7	0
65	Aggregation of Zoospores on Sharklet Microtopographic Surfaces. Communications in Physics, 0, 31, .	0.0	0
66	Symmetry and Folded Structures of Biomolecules. IFMBE Proceedings, 2013, , 372-375.	0.2	0
67	Folding of proteins in presculpted free energy landscape. Communications in Physics, 2014, 23, 313.	0.0	0
68	Additive Effects of Macromolecular Crowding and Confinement on Protein Stability. Communications in Physics, 2018, 28, 351.	0.0	0
69	Sampling the Folding Transition State Ensemble in a Tube-like Model of Protein. Communications in Physics, 2019, 29, 129.	0.0	0
70	Effects of macromolecular crowding on folding of small globular proteins. Communications in Physics, 2022, 32, .	0.0	0