

# Trinh Xuan Hoang

## List of Publications by Year in descending order

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Version: 2024-02-01

70  
papers

1,624  
citations

361296

20  
h-index

315616

38  
g-index

72  
all docs

72  
docs citations

72  
times ranked

1097  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteins – a celebration of consilience. International Journal of Modern Physics B, 2022, 36, .	1.0	4
2	Effects of macromolecular crowding on folding of small globular proteins. Communications in Physics, 2022, 32, .	0.0	0
3	Spontaneous dimensional reduction and ground state degeneracy in a simple chain model. Physical Review E, 2021, 104, L012101.	0.8	3
4	Marginally compact phase and ordered ground states in a model polymer with side spheres. Physical Review E, 2021, 104, L012501.	0.8	2
5	Hydrophobic and electrostatic interactions modulate protein escape at the ribosomal exit tunnel. Biophysical Journal, 2021, 120, 4798-4808.	0.2	10
6	Protein escape at an atomistic model of the ribosomal exit tunnel. Journal of Physics: Conference Series, 2020, 1506, 012022.	0.3	1
7	Protein escape at the ribosomal exit tunnel: Effect of the tunnel shape. Journal of Chemical Physics, 2020, 153, 045105.	1.2	9
8	Effects of inter-organism interactions in biofouling on microtopographic surfaces. Biofouling, 2019, 35, 684-695.	0.8	2
9	Local symmetry determines the phases of linear chains: a simple model for the self-assembly of peptides. Soft Matter, 2019, 15, 5596-5613.	1.2	13
10	The pH-dependent electrostatic interaction of a metal nanoparticle with the MS2 virus-like particles. Chemical Physics Letters, 2019, 730, 84-88.	1.2	6
11	Theoretical Model for the Structural Relaxation Time in Coamorphous Drugs. Molecular Pharmaceutics, 2019, 16, 2992-2998.	2.3	27
12	The elixir phase of chain molecules. Proteins: Structure, Function and Bioinformatics, 2019, 87, 176-184.	1.5	11
13	Sampling the Folding Transition State Ensemble in a Tube-like Model of Protein. Communications in Physics, 2019, 29, 129.	0.0	0
14	Protein escape at the ribosomal exit tunnel: Effects of native interactions, tunnel length, and macromolecular crowding. Journal of Chemical Physics, 2018, 149, 045102.	1.2	14
15	Additive Effects of Macromolecular Crowding and Confinement on Protein Stability. Communications in Physics, 2018, 28, 351.	0.0	0
16	Sequence dependent aggregation of peptides and fibril formation. Journal of Chemical Physics, 2017, 147, 105102.	1.2	13
17	Folding and escape of nascent proteins at ribosomal exit tunnel. Journal of Chemical Physics, 2016, 144, 095102.	1.2	14
18	Effective stiffness and formation of secondary structures in a protein-like model. Journal of Chemical Physics, 2016, 145, 084904.	1.2	23

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19	Cascaded plasmon resonant field enhancement in protein-conjugated gold nanoparticles: Role of protein shell. <i>Journal of Science: Advanced Materials and Devices</i> , 2016, 1, 61-64.	1.5	1
20	Transport properties through graphene grain boundaries: strain effects versus lattice symmetry. <i>Nanoscale</i> , 2016, 8, 11658-11673.	2.8	15
21	From polymers to proteins: the effect of side chains and broken symmetry on the formation of secondary structures within a Wang's Landau approach. <i>Soft Matter</i> , 2016, 12, 4783-4793.	1.2	24
22	Phase diagram of the ground states of DNA condensates. <i>Physical Review E</i> , 2015, 92, 060701.	0.8	8
23	Aggregation of peptides in the tube model with correlated sidechain orientations. <i>Journal of Physics: Conference Series</i> , 2015, 627, 012028.	0.3	1
24	Effects of macromolecular crowding on protein folding. <i>Journal of Physics: Conference Series</i> , 2015, 627, 012027.	0.3	1
25	From toroidal to rod-like condensates of semiflexible polymers. <i>Journal of Chemical Physics</i> , 2014, 140, 064902.	1.2	27
26	Folding of proteins in presculpted free energy landscape. <i>Communications in Physics</i> , 2014, 23, 313.	0.0	0
27	Repulsive interactions of a lipid membrane with graphene in composite materials. <i>Journal of Chemical Physics</i> , 2013, 139, 184703.	1.2	6
28	Surface plasmon resonances of protein-conjugated gold nanoparticles on graphitic substrates. <i>Applied Physics Letters</i> , 2013, 103, .	1.5	23
29	Effects of ribosomal exit tunnel on protein's cotranslational folding. <i>Communications in Physics</i> , 2013, 23, 219.	0.0	1
30	Symmetry and Folded Structures of Biomolecules. <i>IFMBE Proceedings</i> , 2013, , 372-375.	0.2	0
31	Shapes of hydrophobic thick membranes. <i>Europhysics Letters</i> , 2012, 98, 56006.	0.7	0
32	Sequence repeats and protein structure. <i>Physical Review E</i> , 2012, 86, 050901.	0.8	2
33	Protein Sequence and Structure: Is One More Fundamental than the Other?. <i>Journal of Statistical Physics</i> , 2012, 148, 637-646.	0.5	4
34	First-principles design of nanomachines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6900-6903.	3.3	25
35	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
36	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

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37	Structural motifs of biomolecules. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17283-17286.	3.3	31
38	Marginal compactness of protein native structures. Journal of Physics Condensed Matter, 2006, 18, S297-S306.	0.7	6
39	Geometry of proteins: Hydrogen bonding, sterics, and marginally compact tubes. Physical Review E, 2006, 73, 031921.	0.8	14
40	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
41	Geometrical model for the native-state folds of proteins. Biophysical Chemistry, 2005, 115, 289-294.	1.5	7
42	A new interpolation formula for semiflexible polymers. Biophysical Chemistry, 2005, 115, 251-254.	1.5	19
43	What determines the structures of native folds of proteins?. Journal of Physics Condensed Matter, 2005, 17, S1515-S1522.	0.7	5
44	Mechanical properties of the domains of titin in a Go-like model. Journal of Chemical Physics, 2005, 122, 054906.	1.2	27
45	Form of Growing Strings. Physical Review Letters, 2005, 95, 098103.	2.9	6
46	Proteins and polymers. Journal of Chemical Physics, 2005, 122, 234910.	1.2	15
47	Stretching of proteins in the entropic limit. Physical Review E, 2004, 69, 011912.	0.8	20
48	Stretching of homopolymers and contact order. Physical Review E, 2004, 70, 011917.	0.8	13
49	Unified perspective on proteins: A physics approach. Physical Review E, 2004, 70, 041905.	0.8	61
50	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
51	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
52	Folding of proteins in Go models with angular interactions. Physica A: Statistical Mechanics and Its Applications, 2003, 330, 195-205.	1.2	9
53	Assembly of protein tertiary structures from secondary structures using optimized potentials. Proteins: Structure, Function and Bioinformatics, 2003, 52, 155-165.	1.5	13
54	Elasticity of Semiflexible Polymers with and without Self-Interactions. Macromolecules, 2003, 36, 10095-10102.	2.2	40

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55	Universality Classes in Folding Times of Proteins. Biophysical Journal, 2003, 84, 475-488.	0.2	119
56	THE RANGE OF THE CONTACT INTERACTIONS AND THE KINETICS OF THE GO MODELS OF PROTEINS. International Journal of Modern Physics C, 2002, 13, 1231-1242.	0.8	19
57	Folding Pathways of Prion and Doppel. Biophysical Journal, 2002, 83, 3533-3541.	0.2	40
58	Folding and stretching in a Go-like model of titin. Proteins: Structure, Function and Bioinformatics, 2002, 49, 114-124.	1.5	64
59	Prediction of protein secondary structures from conformational biases. Proteins: Structure, Function and Bioinformatics, 2002, 48, 558-565.	1.5	5
60	Thermal folding and mechanical unfolding pathways of protein secondary structures. Proteins: Structure, Function and Bioinformatics, 2002, 49, 104-113.	1.5	62
61	Kinetic nonoptimality and vibrational stability of proteins. Proteins: Structure, Function and Bioinformatics, 2001, 44, 20-25.	1.5	18
62	Scaling of folding properties in go models of proteins. , 2000, 26, 273-294.		16
63	Spin analogues of proteins: scaling of 'folding' properties. Journal of Physics A, 2000, 33, 3977-3987.	1.6	2
64	Molecular dynamics of folding of secondary structures in Go-type models of proteins. Journal of Chemical Physics, 2000, 112, 6851-6862.	1.2	117
65	Sequencing of folding events in Go-type proteins. Journal of Chemical Physics, 2000, 113, 8319-8328.	1.2	100
66	Scaling of Folding Properties in Simple Models of Proteins. Physical Review Letters, 1999, 83, 1684-1687.	2.9	67
67	Energy landscapes, supergraphs, and 'folding funnels' in spin systems. Physical Review E, 1999, 60, 3219-3226.	0.8	57
68	Protein folding and models of dynamics on the lattice. Journal of Chemical Physics, 1998, 109, 9192-9196.	1.2	8
69	Coarse grained description of protein folding. Physical Review E, 1998, 58, 3589-3596.	0.8	12
70	Aggregation of Zoospores on Sharklet Microtopographic Surfaces. Communications in Physics, 0, 31, .	0.0	0