Anders IrbÃ¤ck

List of Publications by Year
in descending order

86 papers	2,901 citations	147801 31 h-index	175258 52 g-index
91 all docs	91 docs citations	91 times ranked	1745 citing authors

#	Article	IF	Citations
1	Mixed-Symmetry Interacting-Boson-Model States in the NucleiBa140,Ce142, andNd144withN=84. Physical Review Letters, 1984, 53, 2469-2472.	7.8	169
2	Oligomerization of Amyloid AÎ²16â€“22 Peptides Using Hydrogen Bonds and Hydrophobicity Forces. Biophysical Journal, 2004, 87, 3657-3664.	0.5	130
3	Studies of an offâ€lattice model for protein folding: Sequence dependence and improved sampling at finite temperature. Journal of Chemical Physics, 1995, 103, 10298-10305.	3.0	113
4	PROFASI: A Monte Carlo simulation package for protein folding and aggregation. Journal of Computational Chemistry, 2006, 27, 1548-1555.	3.3	104
5	Formation and Growth of Oligomers: A Monte Carlo Study of an Amyloid Tau Fragment. PLoS Computational Biology, 2008, 4, e1000238.	3.2	104
6	Local interactions and protein folding: A three-dimensional off-lattice approach. Journal of Chemical Physics, 1997, 107, 273-282.	3.0	102
7	Monte Carlo update for chain molecules: Biased Gaussian steps in torsional space. Journal of Chemical Physics, 2001, 114, 8154-8158.	3.0	102
8	Three-helix-bundle protein in a Ramachandran model. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 13614-13618.	7.1	94
9	Hadronic correlation functions in the QCD plasma phase. Physical Review Letters, 1991, 67, 302-305.	7.8	88
10	Folding Thermodynamics of Peptides. Biophysical Journal, 2005, 88, 1560-1569.	0.5	82
11	Evidence for nonrandom hydrophobicity structures in protein chains.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 9533-9538.	7.1	79
12	Enumerating Designing Sequences in the HP Model. Journal of Biological Physics, 2002, 28, 1-15.	1.5	79
13	The acceptance probability in the hybrid Monte Carlo method. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1990, 242, 437-443.	4.1	78
14	The theory of dynamical random surfaces with extrinsic curvature. Nuclear Physics B, 1993, 393, 571-600.	2.5	76
15	Folding of a small helical protein using hydrogen bonds and hydrophobicity forces. Proteins: Structure, Function and Bioinformatics, 2002, 47, 99-105.	2.6	73
16	Dissecting the mechanical unfolding of ubiquitin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13427-13432.	7.1	70
17	Flavour degrees of freedom and the transition temperature in QCD. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1990, 241, 567-573.	4.1	63
18	An effective all-atom potential for proteins. PMC Biophysics, 2009, 2, 2.	2.3	63

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19	Thermodynamics of Î±- and Î²-Structure Formation in Proteins. Biophysical Journal, 2003, 85, 1466-1473.	0.5	62
20	Identification of amino acid sequences with good folding properties in an off-lattice model. Physical Review E, 1997, 55, 860-867.	2.1	53
21	Spontaneous Î²â€barrel formation: An allâ€atom Monte Carlo study of AÎ²_{16â€“22} oligomerization. Proteins: Structure, Function and Bioinformatics, 2008, 71, 207-214.	2.6	52
22	On Hydrophobicity Correlations in Protein Chains. Biophysical Journal, 2000, 79, 2252-2258.	0.5	51
23	Monte Carlo Study of the Formation and Conformational Properties of Dimers of AÎ²42 Variants. Journal of Molecular Biology, 2011, 410, 357-367.	4.2	50
24	Aggregate Geometry in Amyloid Fibril Nucleation. Physical Review Letters, 2013, 110, 058101.	7.8	50
25	Monte Carlo study of the phase structure of compact polymer chains. Journal of Chemical Physics, 1999, 110, 12256-12262.	3.0	48
26	Microscopic Mechanism of Specific Peptide Adhesion to Semiconductor Substrates. Angewandte Chemie - International Edition, 2010, 49, 9530-9533.	13.8	47
27	Comparing the folding freeâ€energy landscapes of AÎ²42 variants with different aggregation properties. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2600-2608.	2.6	45
28	Changing the Mechanical Unfolding Pathway of FnIII10 by Tuning the Pulling Strength. Biophysical Journal, 2009, 96, 429-441.	0.5	42
29	Critical properties of the dynamical random surface with extrinsic curvature. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1992, 275, 295-303.	4.1	41
30	The heavy quark potential in SU(2) gauge theory at high temperature. Nuclear Physics B, 1991, 363, 34-64.	2.5	39
31	Distinct phases of free Î±â€synucleinâ€”A Monte Carlo study. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2169-2177.	2.6	38
32	Mutation-induced fold switching among lattice proteins. Journal of Chemical Physics, 2011, 135, 195101.	3.0	31
33	Local interactions and protein folding: A model study on the square and triangular lattices. Journal of Chemical Physics, 1998, 108, 2245-2250.	3.0	28
34	Thermal versus mechanical unfolding of ubiquitin. Proteins: Structure, Function and Bioinformatics, 2006, 65, 759-766.	2.6	28
35	Comment on â€˜â€˜Finite-size effects at temperature-driven first-order transitionsâ€™â€™. Physical Review B, 1990, 42, 6743-6744.	3.2	25
36	Design of sequences with good folding properties in coarse-grained protein models. Structure, 1999, 7, 347-360.	3.3	25

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37	Folding thermodynamics of three Î²-sheet peptides: A model study. Proteins: Structure, Function and Bioinformatics, 2004, 56, 110-116.	2.6	25
38	Equilibrium simulation of trp-cage in the presence of protein crowders. Journal of Chemical Physics, 2015, 143, 175102.	3.0	25
39	Dynamics near a first-order phase transition with the Metropolis and Swendsen-Wang algorithms. Nuclear Physics B, 1991, 358, 231-248.	2.5	23
40	Monte Carlo procedure for protein design. Physical Review E, 1998, 58, R5249-R5252.	2.1	23
41	Coupled foldingâ€“binding versus docking: A lattice model study. Journal of Chemical Physics, 2004, 120, 3983-3989.	3.0	22
42	Hydrogen bonds, hydrophobicity forces and the character of the collapse transition. Journal of Biological Physics, 2001, 27, 169-179.	1.5	20
43	Local Unfolding and Aggregation Mechanisms of SOD1: A Monte Carlo Exploration. Journal of Physical Chemistry B, 2013, 117, 9194-9202.	2.6	20
44	Stability and Local Unfolding of SOD1 in the Presence of Protein Crowders. Journal of Physical Chemistry B, 2019, 123, 1920-1930.	2.6	20
45	The correlation lengths and the order of the phase transition in three-dimensional Z3 symmetric models. Nuclear Physics B, 1990, 329, 263-284.	2.5	18
46	Numerical evidence for a mass gap in three-dimensional SU(2). Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1986, 174, 99-103.	4.1	16
47	Unfolding times for proteins in a force clamp. Physical Review E, 2010, 81, 010902.	2.1	16
48	Conformational and aggregation properties of the 1â€“93 fragment of apolipoprotein Aâ€. Protein Science, 2014, 23, 1559-1571.	7.6	16
49	Mechanical Resistance in Unstructured Proteins. Biophysical Journal, 2013, 104, 2725-2732.	0.5	15
50	Peptide folding in the presence of interacting protein crowders. Journal of Chemical Physics, 2016, 144, 175105.	3.0	15
51	The finite temperature phase transition in four flavour QCD on an 8Ã—123 lattice. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1989, 232, 491-497.	4.1	13
52	Scaling in Steiner random surfaces. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1994, 325, 45-50.	4.1	13
53	Two-State Folding over a Weak Free-Energy Barrier. Biophysical Journal, 2003, 85, 1457-1465.	0.5	13
54	Physics beyond instantons. Measuring the physical correlation length. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1992, 286, 112-117.	4.1	12

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55	Accelerating atomic-level protein simulations by flat-histogram techniques. Journal of Chemical Physics, 2011, 135, 125102.	3.0	12
56	Robust Estimation of Diffusion-Optimized Ensembles for Enhanced Sampling. Journal of Chemical Theory and Computation, 2014, 10, 543-553.	5.3	12
57	Finite-size scaling analysis of protein droplet formation. Physical Review E, 2020, 101, 022413.	2.1	12
58	Differences in Solution Behavior among Four Semiconductor-Binding Peptides. Journal of Physical Chemistry B, 2007, 111, 4355-4360.	2.6	11
59	Lattice QCD with small number of flavours. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1989, 216, 177-183.	4.1	10
60	Thermodynamics of amyloid formation and the role of intersheet interactions. Journal of Chemical Physics, 2015, 143, 105104.	3.0	10
61	Sequence dependence of self-interacting random chains. Journal of Physics A, 1995, 28, 2121-2132.	1.6	9
62	Fitting a function to time-dependent ensemble averaged data. Scientific Reports, 2018, 8, 6984.	3.3	9
63	Finite-size shifts in simulated protein droplet phase diagrams. Journal of Chemical Physics, 2021, 154, 235101.	3.0	9
64	Compact three-dimensional U(1) gauge theory reexamined. Physical Review D, 1987, 36, 3804-3808.	4.7	7
65	Measurement of Tc in the scaling region of (2+1)-dimensional SU(2) lattice gauge theory. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1986, 175, 187-191.	4.1	6
66	Protein folding/unfolding in the presence of interacting macromolecular crowders. European Physical Journal: Special Topics, 2017, 226, 627-638.	2.6	6
67	Markov modeling of peptide folding in the presence of protein crowders. Journal of Chemical Physics, 2018, 148, 055101.	3.0	6
68	The effective string andSU(2) lattice MC data. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1987, 36, 629-637.	1.5	5
69	Finite-size scaling at phase coexistence. Nuclear Physics B, 1993, 409, 663-683.	2.5	5
70	Peptide folding and aggregation studied using a simplified atomic model. Journal of Physics Condensed Matter, 2005, 17, S1553-S1564.	1.8	5
71	Measuring the string tension in random surface models with extrinsic curvature. Computer Physics Communications, 1992, 70, 59-68.	7.5	3
72	Sequence-based study of two related proteins with different folding behaviors. Proteins: Structure, Function and Bioinformatics, 2003, 54, 8-12.	2.6	3

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73	Hybrid Monte Carlo with non-uniform step size. Journal of Chemical Physics, 2014, 140, 044105.	3.0	3
74	Limitations of field-theory simulation for exploring phase separation: The role of repulsion in a lattice protein model. Journal of Chemical Physics, 2022, 156, 015101.	3.0	3
75	All-Atom Monte Carlo Simulations of Protein Folding and Aggregation. Springer Series in Bio-/neuroinformatics, 2014, , 433-444.	0.1	2
76	Spectral density analysis of the chiral transition in nf=4 finite temperature QCD. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1992, 280, 261-266.	4.1	1
77	Protein folding, aggregation and unfolding in Monte Carlo simulations. Physics Procedia, 2010, 7, 68-71.	1.2	1
78	Monte Carlo Studies of Protein Aggregation. Physics Procedia, 2012, 34, 49-54.	1.2	1
79	A random surface representation of Wilson loops in Z(2) gauge theory. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1988, 211, 129-131.	4.1	0
80	Binary assignments of amino acids from pattern conservation. Protein Engineering, Design and Selection, 1997, 10, 1013-1017.	2.1	0
81	Simulations of toy proteins. , 1998, , 143-154.		0
82	Sequence Design in Coarse-Grained Protein Models. Progress of Theoretical Physics Supplement, 2000, 138, 273-281.	0.1	0
83	Effective All-Atom Potentials for Proteins. , 2011, , 111-126.		0
84	When a foreign gene meets its native counterpart: computational biophysics analysis of two PgiC loci in the grass Festuca ovina. Scientific Reports, 2020, 10, 18752.	3.3	0
85	Peptide Folding in Cellular Environments: A Monte Carlo andÂMarkov Modeling Approach. Springer Series on Bio- and Neurosystems, 2019, , 453-466.	0.2	0
86	Protein Folding, Unfolding and Aggregation Studied Using an All-Atom Model with~a~Simplified Interaction Potential. , 2008, , 269-291.		0