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	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
2	Finite-size shifts in simulated protein droplet phase diagrams. Journal of Chemical Physics, 2021, 154, 235101.	3.0	9
3	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
4	Finite-size scaling analysis of protein droplet formation. Physical Review E, 2020, 101, 022413.	2.1	12
5	Stability and Local Unfolding of SOD1 in the Presence of Protein Crowders. Journal of Physical Chemistry B, 2019, 123, 1920-1930.	2.6	20
6	Peptide Folding in Cellular Environments: A Monte Carlo andÂMarkov Modeling Approach. Springer Series on Bio- and Neurosystems, 2019, , 453-466.	0.2	0
7	Markov modeling of peptide folding in the presence of protein crowders. Journal of Chemical Physics, 2018, 148, 055101.	3.0	6
8	Fitting a function to time-dependent ensemble averaged data. Scientific Reports, 2018, 8, 6984.	3.3	9
9	Protein folding/unfolding in the presence of interacting macromolecular crowders. European Physical Journal: Special Topics, 2017, 226, 627-638.	2.6	6
10	Peptide folding in the presence of interacting protein crowders. Journal of Chemical Physics, 2016, 144, 175105.	3.0	15
11	Equilibrium simulation of trp-cage in the presence of protein crowders. Journal of Chemical Physics, 2015, 143, 175102.	3.0	25
12	Thermodynamics of amyloid formation and the role of intersheet interactions. Journal of Chemical Physics, 2015, 143, 105104.	3.0	10
13	Conformational and aggregation properties of the 1â€“93 fragment of apolipoprotein Aâ€I. Protein Science, 2014, 23, 1559-1571.	7.6	16
14	Hybrid Monte Carlo with non-uniform step size. Journal of Chemical Physics, 2014, 140, 044105.	3.0	3
15	All-Atom Monte Carlo Simulations of Protein Folding and Aggregation. Springer Series in Bio-/neuroinformatics, 2014, , 433-444.	0.1	2
16	Robust Estimation of Diffusion-Optimized Ensembles for Enhanced Sampling. Journal of Chemical Theory and Computation, 2014, 10, 543-553.	5.3	12
17	Aggregate Geometry in Amyloid Fibril Nucleation. Physical Review Letters, 2013, 110, 058101.	7.8	50
18	Mechanical Resistance in Unstructured Proteins. Biophysical Journal, 2013, 104, 2725-2732.	0.5	15

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19	Local Unfolding and Aggregation Mechanisms of SOD1: A Monte Carlo Exploration. Journal of Physical Chemistry B, 2013, 117, 9194-9202.	2.6	20
20	Monte Carlo Studies of Protein Aggregation. Physics Procedia, 2012, 34, 49-54.	1.2	1
21	Distinct phases of free Î±â€synucleinâ€"A Monte Carlo study. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2169-2177.	2.6	38
22	Mutation-induced fold switching among lattice proteins. Journal of Chemical Physics, 2011, 135, 195101.	3.0	31
23	Effective All-Atom Potentials for Proteins. , 2011, , 111-126.		0
24	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
25	Accelerating atomic-level protein simulations by flat-histogram techniques. Journal of Chemical Physics, 2011, 135, 125102.	3.0	12
26	Microscopic Mechanism of Specific Peptide Adhesion to Semiconductor Substrates. Angewandte Chemie - International Edition, 2010, 49, 9530-9533.	13.8	47
27	Protein folding, aggregation and unfolding in Monte Carlo simulations. Physics Procedia, 2010, 7, 68-71.	1.2	1
28	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
29	Unfolding times for proteins in a force clamp. Physical Review E, 2010, 81, 010902.	2.1	16
30	An effective all-atom potential for proteins. PMC Biophysics, 2009, 2, 2.	2.3	63
31	Changing the Mechanical Unfolding Pathway of FnIII10 by Tuning the Pulling Strength. Biophysical Journal, 2009, 96, 429-441.	0.5	42
32	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
33	Formation and Growth of Oligomers: A Monte Carlo Study of an Amyloid Tau Fragment. PLoS Computational Biology, 2008, 4, e1000238.	3.2	104
34	Protein Folding, Unfolding and Aggregation Studied Using an All-Atom Model with~a~Simplified Interaction Potential. , 2008, , 269-291.		0
35	Differences in Solution Behavior among Four Semiconductor-Binding Peptides. Journal of Physical Chemistry B, 2007, 111, 4355-4360.	2.6	11
36	Thermal versus mechanical unfolding of ubiquitin. Proteins: Structure, Function and Bioinformatics, 2006, 65, 759-766.	2.6	28

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37	PROFASI: A Monte Carlo simulation package for protein folding and aggregation. Journal of Computational Chemistry, 2006, 27, 1548-1555.	3.3	104
38	Peptide folding and aggregation studied using a simplified atomic model. Journal of Physics Condensed Matter, 2005, 17, S1553-S1564.	1.8	5
39	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
40	Folding Thermodynamics of Peptides. Biophysical Journal, 2005, 88, 1560-1569.	0.5	82
41	Coupled foldingâ€“binding versus docking: A lattice model study. Journal of Chemical Physics, 2004, 120, 3983-3989.	3.0	22
42	Folding thermodynamics of three Î²-sheet peptides: A model study. Proteins: Structure, Function and Bioinformatics, 2004, 56, 110-116.	2.6	25
43	Oligomerization of Amyloid AÎ²16â€“22 Peptides Using Hydrogen Bonds and Hydrophobicity Forces. Biophysical Journal, 2004, 87, 3657-3664.	0.5	130
44	Sequence-based study of two related proteins with different folding behaviors. Proteins: Structure, Function and Bioinformatics, 2003, 54, 8-12.	2.6	3
45	Two-State Folding over a Weak Free-Energy Barrier. Biophysical Journal, 2003, 85, 1457-1465.	0.5	13
46	Thermodynamics of Îµ- and Îµ-Structure Formation in Proteins. Biophysical Journal, 2003, 85, 1466-1473.	0.5	62
47	Folding of a small helical protein using hydrogen bonds and hydrophobicity forces. Proteins: Structure, Function and Bioinformatics, 2002, 47, 99-105.	2.6	73
48	Enumerating Designing Sequences in the HP Model. Journal of Biological Physics, 2002, 28, 1-15.	1.5	79
49	Monte Carlo update for chain molecules: Biased Gaussian steps in torsional space. Journal of Chemical Physics, 2001, 114, 8154-8158.	3.0	102
50	Hydrogen bonds, hydrophobicity forces and the character of the collapse transition. Journal of Biological Physics, 2001, 27, 169-179.	1.5	20
51	Sequence Design in Coarse-Grained Protein Models. Progress of Theoretical Physics Supplement, 2000, 138, 273-281.	0.1	0
52	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
53	On Hydrophobicity Correlations in Protein Chains. Biophysical Journal, 2000, 79, 2252-2258.	0.5	51
54	Monte Carlo study of the phase structure of compact polymer chains. Journal of Chemical Physics, 1999, 110, 12256-12262.	3.0	48

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55	Design of sequences with good folding properties in coarse-grained protein models. Structure, 1999, 7, 347-360.	3.3	25
56	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
57	Monte Carlo procedure for protein design. Physical Review E, 1998, 58, R5249-R5252.	2.1	23
58	Simulations of toy proteins. , 1998, , 143-154.		0
59	Binary assignments of amino acids from pattern conservation. Protein Engineering, Design and Selection, 1997, 10, 1013-1017.	2.1	0
60	Identification of amino acid sequences with good folding properties in an off-lattice model. Physical Review E, 1997, 55, 860-867.	2.1	53
61	Local interactions and protein folding: A three-dimensional off-lattice approach. Journal of Chemical Physics, 1997, 107, 273-282.	3.0	102
62	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
63	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
64	Sequence dependence of self-interacting random chains. Journal of Physics A, 1995, 28, 2121-2132.	1.6	9
65	Scaling in Steiner random surfaces. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1994, 325, 45-50.	4.1	13
66	The theory of dynamical random surfaces with extrinsic curvature. Nuclear Physics B, 1993, 393, 571-600.	2.5	76
67	Finite-size scaling at phase coexistence. Nuclear Physics B, 1993, 409, 663-683.	2.5	5
68	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
69	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
70	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
71	Measuring the string tension in random surface models with extrinsic curvature. Computer Physics Communications, 1992, 70, 59-68.	7.5	3
72	The heavy quark potential in SU(2) gauge theory at high temperature. Nuclear Physics B, 1991, 363, 34-64.	2.5	39

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73	Dynamics near a first-order phase transition with the Metropolis and Swendsen-Wang algorithms. Nuclear Physics B, 1991, 358, 231-248.	2.5	23
74	Hadronic correlation functions in the QCD plasma phase. Physical Review Letters, 1991, 67, 302-305.	7.8	88
75	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
76	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
77	Comment on â€˜â€˜Finite-size effects at temperature-driven first-order transitionsâ€™â€™. Physical Review B, 1990, 42, 6743-6744.	3.2	25
78	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
79	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
80	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
81	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
82	Compact three-dimensional U(1) gauge theory reexamined. Physical Review D, 1987, 36, 3804-3808.	4.7	7
83	The effective string andSU(2) lattice MC data. Zeitschrift FÃ¼r Physik C-Particles and Fields, 1987, 36, 629-637.	1.5	5
84	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
85	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
86	Mixed-Symmetry Interacting-Boson-Model States in the NucleiBa140,Ce142, andNd144withN=84. Physical Review Letters, 1984, 53, 2469-2472.	7.8	169