Ulrich H E Hansmann

List of Publications by Year in Descending Order

173 papers	5,730 citations	36 h-index	71 g-index
201 ext. papers	6,143 ext. citations	3.5 avg, IF	6.09 L-index

#	Paper	IF	Citations
173	Interconversion between Serum Amyloid A Native and Fibril Conformations.. *ACS Omega*, **2022**, 7, 12186-12192	3.9	0
172	Small Peptides for Inhibiting Serum Amyloid A Aggregation. *ACS Medicinal Chemistry Letters*, **2021**, 12, 1613-1621	4.3	0
171	Effect of Lauric Acid on the Stability of A Oligomers. *ACS Omega*, **2021**, 6, 5795-5804	3.9	1
170	Presence of a SARS-CoV-2 Protein Enhances Amyloid Formation of Serum Amyloid A. *Journal of Physical Chemistry B*, **2021**, 125, 9155-9167	3.4	9
169	Cleavage, Downregulation, and Aggregation of Serum Amyloid A. *Journal of Physical Chemistry B*, **2020**, 124, 1009-1019	3.4	7
168	Altering the Solubility of the Antibiotic Candidate Nisin-A Computational Study. *ACS Omega*, **2020**, 5, 24854-24863	3.9	3
167	Stability of Human Serum Amyloid A Fibrils. *Journal of Physical Chemistry B*, **2020**, 124, 10708-10717	3.4	4
166	Bifurcated Hydrogen Bonds and the Fold Switching of Lymphotactin. *Journal of Physical Chemistry B*, **2020**, 124, 6555-6564	3.4	4
165	d-Retro Inverso Amylin and the Stability of Amylin Fibrils. *Journal of Chemical Theory and Computation*, **2020**, 16, 5358-5368	6.4	6
164	The effect of retro-inverse D-amino acid A peptides on A fibril formation. *Journal of Chemical Physics*, **2019**, 150, 095101	3.9	4
163	Large fatty acid-derived A42 oligomers form ring-like assemblies. *Journal of Chemical Physics*, **2019**, 150, 075101	3.9	5
162	Pearl-Necklace-Like Local Ordering Drives Polypeptide Collapse. *Macromolecules*, **2019**, 52, 5491-5498	5.5	5
161	Stability of A fibril fragments in the presence of fatty acids. *Protein Science*, **2019**, 28, 1973-1981	6.3	2
160	Enhanced Sampling for Biomolecular Simulations. *Springer Series on Bio- and Neurosystems*, **2019**, 257-280	0.5	0
159	Conversion between parallel and antiparallel sheets in wild-type and Iowa mutant A fibrils. *Journal of Chemical Physics*, **2018**, 148, 045103	3.9	6
158	Mutations Alter RNA-Mediated Conversion of Human Prions. *ACS Omega*, **2018**, 3, 3936-3944	3.9	2
157	Out-of-Register A Assemblies as Models for Neurotoxic Oligomers and Fibrils. *Journal of Chemical Theory and Computation*, **2018**, 14, 1099-1110	6.4	16

156	Multifunnel Landscape of the Fold-Switching Protein RfaH-CTD. *Journal of Physical Chemistry B*, **2018**, 122, 1600-1607	3.4	14
155	Stability of the N-Terminal Helix and Its Role in Amyloid Formation of Serum Amyloid A. *ACS Omega* , **2018**, 3, 16184-16190	3.9	6
154	Molecular dynamics simulations of early steps in RNA-mediated conversion of prions. *Protein Science*, **2017**, 26, 1524-1534	6.3	7
153	Ring-like N-fold Models of A Fibrils. *Scientific Reports*, **2017**, 7, 6588	4.9	21
152	Fibril-Barrel Transitions in Cylindrin Amyloids. *Journal of Chemical Theory and Computation*, **2017**, 13, 3936-3944	6.4	18
151	Stability differences in the NMR ensembles of amyloid Fibrils. *Journal of Theoretical and Computational Chemistry*, **2016**, 15, 1650059	1.8	3
150	Simulating Protein Fold Switching by Replica Exchange with Tunneling. *Journal of Chemical Theory and Computation*, **2016**, 12, 5656-5666	6.4	21
149	Response to "Comment on Replica-exchange-with-tunneling for fast exploration of protein landscapes" J. Chem. Phys. 145, 057101 (2016)]. *Journal of Chemical Physics*, **2016**, 145, 057102	3.9	
148	Binding of ACE-inhibitors to in vitro and patient-derived amyloid-Fibril models. *Journal of Chemical Physics*, **2016**, 144, 015101	3.9	4
147	Stability of a Recently Found Triple-Stranded A 1-42 Fibril Motif. *Journal of Physical Chemistry B*, **2016**, 120, 4548-57	3.4	17
146	Stability of Osaka Mutant and Wild-Type Fibril Models. *Journal of Physical Chemistry B*, **2015**, 119, 13063-70	3.4	16
145	Self-assembly of phenylalanine-based molecules. *Journal of Physical Chemistry A*, **2015**, 119, 1609-15	2.8	50
144	Replica-exchange-with-tunneling for fast exploration of protein landscapes. *Journal of Chemical Physics*, **2015**, 143, 224102	3.9	14
143	All-atom Simulation of Amyloid Aggregates. *Physics Procedia*, **2015**, 68, 61-68		5
142	Effect of single point mutations in a form of systemic amyloidosis. *Protein Science*, **2015**, 24, 1451-62	6.3	7
141	On the lack of polymorphism in A peptide aggregates derived from patient brains. *Protein Science*, **2015**, 24, 923-35	6.3	14
140	Inter-species cross-seeding: stability and assembly of rat-human amylin aggregates. *PLoS ONE*, **2014**, 9, e97051	3.7	24
139	Stability of amyloid oligomers. *Advances in Protein Chemistry and Structural Biology*, **2014**, 96, 113-41	5.3	17

138	Folding and self-assembly of a small heterotetramer. *Journal of Chemical Physics*, **2014**, 140, 105103	3.9	4
137	Stability of Iowa mutant and wild type A peptide aggregates. *Journal of Chemical Physics*, **2014**, 141, 175101	3.9	20
136	Multicanonical Monte Carlo simulations of a de novo designed protein with end-to-end sheet. *Journal of Chemical Physics*, **2014**, 140, 065101	3.9	2
135	Multicanonical Molecular Dynamics Simulations of the N-terminal Domain of Protein L9. *Europhysics Letters*, **2014**, 105, 30008	1.6	4
134	Enhanced Sampling for Biomolecular Simulations. *Springer Series in Bio-/neuroinformatics*, **2014**, 249-267		1
133	Sampling of Protein Folding Transitions: Multicanonical Versus Replica Exchange Molecular Dynamics. *Journal of Chemical Theory and Computation*, **2013**, 9,	6.4	17
132	Mutations and seeding of amylin fibril-like oligomers. *Journal of Physical Chemistry B*, **2013**, 117, 16076-85	3.4	27
131	In silico cross seeding of A and amylin fibril-like oligomers. *ACS Chemical Neuroscience*, **2013**, 4, 1488-500	5.7	53
130	Folding and association of a homotetrameric protein complex in an all-atom Go model. *Physical Review E*, **2013**, 87, 014701	2.4	6
129	The stability of cylindrin barrel amyloid oligomer models-a molecular dynamics study. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 1542-55	4.2	38
128	Side-chain hydrophobicity and the stability of A aggregates. *Protein Science*, **2012**, 21, 1837-48	6.3	37
127	Modeling Structural Flexibility of Proteins with Go-Models. *Journal of Chemical Theory and Computation*, **2012**, 8, 2127-2133	6.4	11
126	Folding simulations of the A and B domains of protein G. *Journal of Physical Chemistry B*, **2012**, 116, 6645-53	3.4	26
125	Folding and self-assembly of a small protein complex. *Journal of Chemical Theory and Computation*, **2012**, 8, 3416-3422	6.4	20
124	Extension of UNRES force field to treat polypeptide chains with D-amino-acid residues. *Journal of Chemical Theory and Computation*, **2012**, 8, 4746-4757	6.4	18
123	Chameleonicity and folding of the C-fragment of TOP7. *Europhysics Letters*, **2012**, 97, 68003	1.6	6
122	Structure and dynamics of amyloid-segmental polymorphisms. *PLoS ONE*, **2012**, 7, e41479	3.7	61
121	Proteins Studied by Computer Simulations. *Lecture Notes in Computer Science*, **2012**, 56-65	0.9	

120	Sampling Protein Energy Landscapes The Quest for Efficient Algorithms **2011**, 209-230		2
119	Velocity scaling for optimizing replica exchange molecular dynamics. *Journal of Chemical Physics*, **2011**, 134, 044124	3.9	17
118	Velocity-scaling optimized replica exchange molecular dynamics of proteins in a hybrid explicit/implicit solvent. *Journal of Chemical Physics*, **2011**, 135, 084115	3.9	24
117	Replica exchange molecular dynamics of the thermodynamics of fibril growth of Alzheimer's A42 peptide. *Journal of Chemical Physics*, **2011**, 135, 065101	3.9	35
116	Internal and environmental effects on folding and dimerization of the Alzheimer's amyloid peptide. *Molecular Simulation*, **2011**, 37,	2	11
115	A numerical investigation into possible mechanisms by that the A629P mutant of ATP7A causes Menkes Disease. *Physical Chemistry Chemical Physics*, **2010**, 12, 11390-7	3.6	8
114	Temperature random walk sampling of protein configurations. *Physica A: Statistical Mechanics and Its Applications*, **2010**, 389, 1400-1404	3.3	4
113	Microcanonical replica exchange molecular dynamics simulation of proteins. *Physical Review E*, **2009**, 80, 056703	2.4	20
112	Free-energy-driven folding and thermodynamics of the 67-residue protein GS-alpha3W--a large-scale Monte Carlo study. *Journal of Computational Chemistry*, **2009**, 30, 1642-8	3.5	18
111	Optimized explicit-solvent replica exchange molecular dynamics from scratch. *Journal of Physical Chemistry B*, **2008**, 112, 10386-7	3.4	52
110	Caching of a chameleon segment facilitates folding of a protein with end-to-end beta-sheet. *Journal of Physical Chemistry B*, **2008**, 112, 15134-9	3.4	11
109	LOCUSTRA: accurate prediction of local protein structure using a two-layer support vector machine approach. *Journal of Chemical Information and Modeling*, **2008**, 48, 1903-8	6.1	32
108	The Alzheimer's beta amyloid (Abeta1-39) monomer in an implicit solvent. *Journal of Chemical Physics*, **2008**, 128, 165102	3.9	22
107	Toward reliable simulations of protein folding, misfolding and aggregation. *Progress in Molecular Biology and Translational Science*, **2008**, 84, 39-55	4	2
106	DETECTING SECONDARY BOTTLENECKS IN PARALLEL QUANTUM CHEMISTRY APPLICATIONS USING MPI. *International Journal of Modern Physics C*, **2008**, 19, 1-13	1.1	7
105	Simulation of Top7-CFr: a transient helix extension guides folding. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8004-7	11.5	42
104	Backbone and side-chain ordering in a small protein. *Journal of Chemical Physics*, **2008**, 128, 025105	3.9	14
103	The Alzheimer beta-amyloid (Abeta(1-39)) dimer in an implicit solvent. *Journal of Chemical Physics*, **2008**, 129, 195102	3.9	43

102	Folding proteins by first-passage-times-optimized replica exchange. *Physical Review E*, **2008**, 78, 061905	2.4	42
101	SMMP v. 3.0—simulating proteins and protein interactions in Python and Fortran. *Computer Physics Communications*, **2008**, 178, 459-470	4.2	19
100	Understanding protein folding: small proteins in silico. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2008**, 1784, 252-8	4	20
99	All-Atom Simulations of Proteins **2008**, 293-313		
98	Side-chain and backbone ordering in homopolymers. *Journal of Physical Chemistry B*, **2007**, 111, 4244-50	3.4	4
97	Dispersion terms and analysis of size- and charge dependence in an enhanced Poisson-Boltzmann approach. *Journal of Physical Chemistry B*, **2007**, 111, 8910-8	3.4	19
96	Short-time dynamics of polypeptides. *Journal of Chemical Physics*, **2007**, 126, 045107	3.9	12
95	Systematic study of the boundary composition in Poisson Boltzmann calculations. *Journal of Computational Chemistry*, **2007**, 28, 2538-44	3.5	17
94	Parallel tempering molecular dynamics folding simulation of a signal peptide in explicit water. *Proteins: Structure, Function and Bioinformatics*, **2007**, 68, 662-9	4.2	10
93	Protein simulations combining an all-atom force field with a Go term. *Journal of Physics Condensed Matter*, **2007**, 19, 285215	1.8	11
92	On the helix-coil transition in alanine based polypeptides in gas phase. *Journal of Chemical Physics*, **2007**, 126, 204307	3.9	11
91	Ring polymer simulations with global radius of curvature. *Physical Review E*, **2007**, 75, 051803	2.4	5
90	Dynamics and optimal number of replicas in parallel tempering simulations. *Physical Review E*, **2007**, 76, 065701	2.4	32
89	Optimizing replica exchange moves for molecular dynamics. *Physical Review E*, **2007**, 76, 057102	2.4	25
88	Aggregation of beta-amyloid fragments. *Journal of Chemical Physics*, **2007**, 126, 014706	3.9	19
87	Generalized ensemble and tempering simulations: a unified view. *Physical Review E*, **2007**, 75, 026109	2.4	86
86	BETTY: prediction of beta-strand type from sequence. *In Silico Biology*, **2007**, 7, 535-42	2	3
85	Support vector machines for prediction of dihedral angle regions. *Bioinformatics*, **2006**, 22, 3009-15	7.2	38

84	Short-time dynamics of the helix-coil transition in polypeptides. *Physical Review E*, **2006**, 73, 040902	2.4	19
83	Optimized parallel tempering simulations of proteins. *Journal of Chemical Physics*, **2006**, 124, 174903	3.9	193
82	NUMERICAL COMPARISON OF WANG□ANDAU SAMPLING AND PARALLEL TEMPERING FOR MET-ENKEPHALIN. *International Journal of Modern Physics C*, **2006**, 17, 817-824	1.1	10
81	Side-chain and backbone ordering in a polypeptide. *Journal of Chemical Physics*, **2006**, 125, 164902	3.9	9
80	Computational assessment of the entropy of solvation of small-sized hydrophobic entities. *Physical Chemistry Chemical Physics*, **2006**, 8, 5515-21	3.6	15
79	Folding of proteins with diverse folds. *Biophysical Journal*, **2006**, 91, 3573-8	2.9	17
78	An enhanced version of SMMP□pen-source software package for simulation of proteins. *Computer Physics Communications*, **2006**, 174, 422-429	4.2	48
77	Protein Folding in Silico □The Quest for Better Algorithms **2005**, 275-296		
76	Generalized-ensemble simulations of all-atom protein models. *Physica A: Statistical Mechanics and Its Applications*, **2005**, 350, 28-37	3.3	6
75	Efficient sampling of protein structures by model hopping. *Physical Review Letters*, **2005**, 95, 138102	7.4	77
74	Protein structure prediction by tempering spatial constraints. *Journal of Computer-Aided Molecular Design*, **2005**, 19, 603-8	4.2	2
73	Exploring protein energy landscapes with hierarchical clustering. *International Journal of Quantum Chemistry*, **2005**, 105, 826-830	2.1	19
72	A simple hydrophobicity-based score for profiling protein structures. *Journal of Physics Condensed Matter*, **2005**, 17, S1595-S1606	1.8	4
71	Energy landscape paving simulations of the trp-cage protein. *Journal of Chemical Physics*, **2005**, 122, 194711	3.9	61
70	Simulations of a small protein in a specifically designed generalized ensemble. *Physical Review E*, **2004**, 70, 012902	2.4	7
69	All-atom generalized-ensemble simulations of small proteins. *Journal of Molecular Graphics and Modelling*, **2004**, 22, 397-403	2.8	35
68	Generalized-ensemble simulations of the human parathyroid hormone fragment PTH(1-34). *Journal of Chemical Physics*, **2004**, 120, 417-22	3.9	17
67	New Algorithms and the Physics of Protein Folding **2004**, 173-192		

66	Parallel tempering simulations of HP-36. *Proteins: Structure, Function and Bioinformatics*, **2003**, 52, 436-45	4.2	86
65	New algorithms and the physics of proteins. *Physica A: Statistical Mechanics and Its Applications*, **2003**, 321, 152-163	3.3	5
64	Solution Effects and the Folding of an Artificial Peptide. *Journal of Physical Chemistry B*, **2003**, 107, 10284-10291	3.4	3
63	Solution effects and the order of the helix□coil transition in polyalanine. *Journal of Chemical Physics*, **2003**, 118, 2374-2380	3.9	41
62	Helix versus sheet formation in a small peptide. *Physical Review E*, **2003**, 68, 041911	2.4	21
61	Structural transitions in biomolecules - a numerical comparison of two approaches for the study of phase transitions in small systems. *International Journal of Molecular Sciences*, **2002**, 3, 17-29	6.3	7
60	Protein energy landscapes as studied by a generalized-ensemble approach with Tsallis statistics. *Chaos, Solitons and Fractals*, **2002**, 13, 507-512	9.3	4
59	Energy landscape paving for X-ray structure determination of organic molecules. *Acta Crystallographica Section A: Foundations and Advances*, **2002**, 58, 259-64		4
58	Protein-folding simulations in generalized ensembles. *International Journal of Quantum Chemistry*, **2002**, 90, 1515-1521	2.1	12
57	Generalized ensemble techniques and protein folding simulations. *Computer Physics Communications*, **2002**, 147, 604-607	4.2	13
56	Global optimization by energy landscape paving. *Physical Review Letters*, **2002**, 88, 068105	7.4	160
55	Numerical comparison of two approaches for the study of phase transitions in small systems. *Physical Review E*, **2002**, 65, 036110	2.4	18
54	Helix formation and folding in an artificial peptide. *Journal of Chemical Physics*, **2002**, 117, 2337-2343	3.9	27
53	Solvation model dependency of helix-coil transition in polyalanine. *Biophysical Journal*, **2002**, 82, 3269-76	2.9	34
52	Yang□Lee zeros and the helix□coil transition in a continuum model of polyalanine. *Physica A: Statistical Mechanics and Its Applications*, **2001**, 292, 509-518	3.3	24
51	[SMMP] A modern package for simulation of proteins. *Computer Physics Communications*, **2001**, 138, 192-212	4.2	110
50	Thermodynamics and kinetics of folding of a small peptide. *Journal of Chemical Physics*, **2001**, 115, 1601-1606	3.9	20
49	Proteinlike behavior of a spin system near the transition between a ferromagnet and a spin glass. *Physical Review E*, **2001**, 64, 052903	2.4	5

48	Structure determination of organic molecules from diffraction data by simulated annealing. *Physical Review E*, **2001**, 64, 056707	2.4	6
47	GLASS TRANSITION TEMPERATURE AND FRACTAL DIMENSION OF PROTEIN FREE ENERGY LANDSCAPES. *International Journal of Modern Physics C*, **2000**, 11, 301-308	1.1	3
46	Partition function zeros and leading-order scaling correction of the 3D Ising model from multicanonical simulations. *Journal of Physics A*, **2000**, 33, 7489-7498		10
45	Partition function zeros and finite size scaling of helix-coil transitions in a polypeptide. *Physical Review Letters*, **2000**, 84, 1836-9	7.4	70
44	Thermodynamics of Protein Folding The Generalized-Ensemble Approach. *Nonconvex Optimization and Its Applications*, **2000**, 91-105		
43	COMPUTER SIMULATION OF BIOLOGICAL MACROMOLECULES IN GENERALIZED ENSEMBLES. *International Journal of Modern Physics C*, **1999**, 10, 1521-1530	1.1	5
42	Finite-size scaling of helix coil transitions in poly-alanine studied by multicanonical simulations. *Journal of Chemical Physics*, **1999**, 110, 1267-1276	3.9	78
41	New Monte Carlo algorithms for protein folding. *Current Opinion in Structural Biology*, **1999**, 9, 177-83	8.1	245
40	The folding funnel landscape for the peptide Met-enkephalin. *Proteins: Structure, Function and Bioinformatics*, **1999**, 34, 472-83	4.2	57
39	Effects of Side-Chain Charges on Helix Stability in C-Peptide of Ribonuclease A Studied by Multicanonical Algorithm. *Journal of Physical Chemistry B*, **1999**, 103, 1595-1604	3.4	34
38	THE GENERALIZED-ENSEMBLE APPROACH FOR PROTEIN FOLDING SIMULATIONS **1999**, 129-157		76
37	Tackling the protein folding problem by a generalized-ensemble approach with Tsallis statistics. *Brazilian Journal of Physics*, **1999**, 29,	1.2	9
36	Recent Results from Protein-Folding Simulations in Generalized Ensembles. *Springer Proceedings in Physics*, **1999**, 62-67	0.2	
35	Stochastic dynamics simulations in a new generalized ensemble. *Chemical Physics Letters*, **1998**, 297, 374-382	2.5	12
34	Temperature dependence of distributions of conformations of a small peptide. *Journal of Molecular Graphics and Modelling*, **1998**, 16, 226-38, 262-3	2.8	25
33	Generalized ensembles: A new way of simulating proteins. *Physica A: Statistical Mechanics and Its Applications*, **1998**, 254, 15-23	3.3	1
32	Tertiary Structure Prediction of C-Peptide of Ribonuclease A by Multicanonical Algorithm. *Journal of Physical Chemistry B*, **1998**, 102, 653-656	3.4	32
31	A New Look at the 2D Ising Model from Exact Partition Function Zeros for Large Lattice Sizes. *International Journal of Modern Physics C*, **1997**, 08, 1063-1071	1.1	14

30	Generalized-ensemble Monte Carlo method for systems with rough energy landscape. *Physical Review E*, **1997**, 56, 2228-2233	2.4	104
29	Effective way for determination of multicanonical weights. *Physical Review E*, **1997**, 56, 6200-6203	2.4	26
28	A Simple Ansatz to Describe Thermodynamic Quantities of Peptides and Proteins at Low Temperatures. *International Journal of Modern Physics C*, **1997**, 08, 1085-1093	1.1	4
27	Variation of the Energy Landscape of a Small Peptide under a Change from the ECEPP/2 Force Field to ECEPP/3. *Journal of Physical Chemistry B*, **1997**, 101, 3304-3310	3.4	43
26	Simulated annealing with Tsallis weights a numerical comparison. *Physica A: Statistical Mechanics and Its Applications*, **1997**, 242, 250-257	3.3	24
25	Characteristic temperatures of folding of a small peptide. *Proceedings of the National Academy of Sciences of the United States of America*, **1997**, 94, 10652-6	11.5	69
24	Numerical comparisons of three recently proposed algorithms in the protein folding problem **1997**, 18, 920-933		141
23	Global minimum configuration of a small peptide for the ECEPP/2 and ECEPP/3 force fields. *Chemical Physics Letters*, **1997**, 268, 86-92	2.5	3
22	Parallel tempering algorithm for conformational studies of biological molecules. *Chemical Physics Letters*, **1997**, 281, 140-150	2.5	883
21	On the protein folding problem. *Nuclear Physics, Section B, Proceedings Supplements*, **1996**, 47, 188-195		
20	Thermodynamics of helix-coil transitions in amino-acid homopolymers studied by multicanonical algorithms. *Nuclear Physics, Section B, Proceedings Supplements*, **1996**, 47, 842-845		1
19	Molecular dynamics, Langevin and hydrid Monte Carlo simulations in a multicanonical ensemble. *Chemical Physics Letters*, **1996**, 259, 321-330	2.5	252
18	Monte Carlo simulations in generalized ensemble: Multicanonical algorithm versus simulated tempering. *Physical Review E*, **1996**, 54, 5863-5865	2.4	64
17	Groundstates of the 3d Edwards-Anderson spin glass model. *Nuclear Physics, Section B, Proceedings Supplements*, **1995**, 42, 905-907		2
16	Multicanonical approach in statistical mechanics of peptides. *Nuclear Physics, Section B, Proceedings Supplements*, **1995**, 42, 914-916		1
15	Thermodynamics of Helix-Coil Transitions Studied by Multicanonical Algorithms. *The Journal of Physical Chemistry*, **1995**, 99, 11276-11287		174
14	Comment on "Monte Carlo Simulation of a First-Order Transition for Protein Folding". *The Journal of Physical Chemistry*, **1995**, 99, 2236-2237		25
13	-Helix Propensities of Amino Acids Studied by Multicanonical Algorithm. *Chemistry Letters*, **1995**, 24, 391-392	1.7	9

List of Publications

12	SPIN GLASS GROUNDSTATE INVESTIGATION BY MULTICANONICAL ENSEMBLE. *International Journal of Modern Physics C*, **1994**, 05, 263-265	1.1	1
11	A MULTICANONICAL STUDY OF THE PROTEIN FOLDING PROBLEM. *International Journal of Modern Physics C*, **1994**, 05, 271-273	1.1	1
10	Ground-state properties of the three-dimensional Ising spin glass. *Physical Review B*, **1994**, 50, 16444-16452	3.3	37
9	Comparative study of multicanonical and simulated annealing algorithms in the protein folding problem. *Physica A: Statistical Mechanics and Its Applications*, **1994**, 212, 415-437	3.3	110
8	Approaching the protein folding problem. *Nuclear Physics, Section B, Proceedings Supplements*, **1994**, 34, 792-794		
7	Sampling Ground-State Configurations of a Peptide by Multicanonical Annealing. *Journal of the Physical Society of Japan*, **1994**, 63, 3945-3949	1.5	16
6	Simulation of an ensemble with varying magnetic field: A numerical determination of the order-order interface tension in the D=2 Ising model. *Physical Review B*, **1993**, 47, 497-500	3.3	89
5	Multicanonical Study of the 3D Ising Spin Glass. *Europhysics Letters*, **1993**, 22, 63-68	1.6	34
4	Prediction of peptide conformation by multicanonical algorithm: New approach to the multiple-minima problem. *Journal of Computational Chemistry*, **1993**, 14, 1333-1338	3.5	349
3	The van Hemmen spin glass revisited. *Journal of Statistical Physics*, **1993**, 73, 775-788	1.5	10
2	Multimagnetical simulation of the Ising model. *Nuclear Physics, Section B, Proceedings Supplements*, **1993**, 30, 285-288		2
1	Cleavage, down-regulation and aggregation of serum amyloid A		1