Marek Cieplak

List of Publications by Year
in descending order

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172 papers	5,963 citations	71102 41 h-index	88630 70 g-index
175 all docs	175 docs citations	175 times ranked	3824 citing authors

#	Article	IF	Citations
1	Preface to the JPCM special issue on droplets and vesicles. Journal of Physics Condensed Matter, 2022, 34, 030401.	1.8	0
2	Contact-Based Analysis of Aggregation of Intrinsically Disordered Proteins. Methods in Molecular Biology, 2022, 2340, 105-120.	0.9	1
3	Final Remarks. Methods in Molecular Biology, 2022, 2340, 469-470.	0.9	0
4	Viscoelastic properties of wheat gluten in a molecular dynamics study. PLoS Computational Biology, 2021, 17, e1008840.	3.2	10
5	Gluten Adhesion and Shearing in a Contact-Based Coarse-Grained Model. Tribology Letters, 2021, 69, 1.	2.6	1
6	Cohesin-dockerin code in cellulosomal dual binding modes and its allosteric regulation by proline isomerization. Structure, 2021, 29, 587-597.e8.	3.3	10
7	Nascent Folding of Proteins Across the Three Domains of Life. Frontiers in Molecular Biosciences, 2021, 8, 692230.	3.5	3
8	Conformational Biases of Î±-Synuclein and Formation of Transient Knots. Journal of Physical Chemistry B, 2020, 124, 11-19.	2.6	12
9	Mechanical Unfolding of Proteinsâ€”A Comparative Nonequilibrium Molecular Dynamics Study. Biophysical Journal, 2020, 119, 939-949.	0.5	7
10	Protein droplets in systems of disordered homopeptides and the amyloid glass phase. Physical Chemistry Chemical Physics, 2020, 22, 15592-15599.	2.8	16
11	Properties of Cavities in Biological Structuresâ€”A Survey of the Protein Data Bank. Frontiers in Molecular Biosciences, 2020, 7, 591381.	3.5	11
12	Proteins at curved fluidâ€“fluid interfaces in a coarse-grained model. Journal of Physics Condensed Matter, 2020, 32, 404003.	1.8	4
13	Pseudo-Improper-Dihedral Model for Intrinsically Disordered Proteins. Journal of Chemical Theory and Computation, 2020, 16, 4726-4733.	5.3	17
14	Transient knots in intrinsically disordered proteins and neurodegeneration. Progress in Molecular Biology and Translational Science, 2020, 174, 79-103.	1.7	5
15	Networks of interbasin traffic in intrinsically disordered proteins. Physical Review Research, 2020, 2, .	3.6	7
16	Network of inter-basin traffic in intrinsically disordered PUMA protein. Europhysics Letters, 2020, 132, 28002.	2.0	0
17	Preliminary Study of Adhesive Properties of Surface Adsorbed Human Serum Albumin and Transforming Growth Factor-Î² Evaluated with AFM Force Spectroscopy. , 2019, , .		0
18	Differentiating between Inactive and Active States of Rhodopsin by Atomic Force Microscopy in Native Membranes. Analytical Chemistry, 2019, 91, 7226-7235.	6.5	25

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19	Self-entanglement of bovine serum albumin in shear flow: cumulative effects and irreversibility. European Physical Journal: Special Topics, 2019, 227, 2495-2500.	2.6	2
20	Mechanostability of Virus Capsids and Their Proteins in Structure-Based Coarse-Grained Models. Springer Series on Bio- and Neurosystems, 2019, , 307-330.	0.2	0
21	Proteins at the air-water interface in a lattice model. Journal of Chemical Physics, 2018, 148, 094704.	3.0	2
22	Stability of structurally entangled protein dimers. Proteins: Structure, Function and Bioinformatics, 2018, 86, 945-955.	2.6	12
23	Disordered peptide chains in an Î±-C-based coarse-grained model. Physical Chemistry Chemical Physics, 2018, 20, 19057-19070.	2.8	23
24	Dual binding in cohesin-dockerin complexes: the energy landscape and the role of short, terminal segments of the dockerin module. Scientific Reports, 2018, 8, 5051.	3.3	9
25	Steered molecular dynamics simulations reveal the role of Ca²⁺ in regulating mechanostability of cellulose-binding proteins. Physical Chemistry Chemical Physics, 2018, 20, 22674-22680.	2.8	7
26	Special Issue on the Physics of Viral Capsids. Journal of Physics Condensed Matter, 2018, 30, 290201.	1.8	1
27	Combining the MARTINI and Structure-Based Coarse-Grained Approaches for the Molecular Dynamics Studies of Conformational Transitions in Proteins. Journal of Chemical Theory and Computation, 2017, 13, 1366-1374.	5.3	136
28	Structural Changes in Barley Protein LTP1 Isoforms at Airâ€“Water Interfaces. Langmuir, 2017, 33, 4769-4780.	3.5	5
29	Topological transformations in proteins: effects of heating and proximity of an interface. Scientific Reports, 2017, 7, 39851.	3.3	15
30	Structural entanglements in protein complexes. Journal of Chemical Physics, 2017, 146, 225102.	3.0	14
31	Elastic moduli of biological fibers in a coarse-grained model: crystalline cellulose and Î²-amyloids. Physical Chemistry Chemical Physics, 2017, 19, 28195-28206.	2.8	27
32	Self-assembly of model proteins into virus capsids. Journal of Physics Condensed Matter, 2017, 29, 474003.	1.8	10
33	Non-local effects of point mutations on the stability of a protein module. Journal of Chemical Physics, 2017, 147, 105101.	3.0	6
34	Proteins at airâ€“water and oilâ€“water interfaces in an all-atom model. Physical Chemistry Chemical Physics, 2017, 19, 25197-25206.	2.8	19
35	The length but not the sequence of peptide linker modules exerts the primary influence on the conformations of protein domains in cellulosome multi-enzyme complexes. Physical Chemistry Chemical Physics, 2017, 19, 21414-21425.	2.8	17
36	The volume of cavities in proteins and virus capsids. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1275-1286.	2.6	22

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37	Structural fluctuations and thermal stability of proteins in crowded environments: effects of the excluded volume. Physical Biology, 2016, 13, 066002.	1.8	3
38	Dual binding mode in cohesin-dockerin complexes as assessed through stretching studies. Journal of Chemical Physics, 2016, 145, 134102.	3.0	4
39	Coarse-grained model of the native cellulose $$hbox {I}alpha$$ and the transformation pathways to the $$hbox {I}eta$$ allomorph. Cellulose, 2016, 23, 1573-1591.	4.9	29
40	Stiffness of the C-terminal disordered linker affects the geometry of the active site in endoglucanase Cel8A. Molecular BioSystems, 2016, 12, 3589-3599.	2.9	10
41	Unfolding knots by proteasome-like systems: simulations of the behaviour of folded and neurotoxic proteins. Molecular BioSystems, 2016, 12, 2700-2712.	2.9	33
42	Criteria for folding in structure-based models of proteins. Journal of Chemical Physics, 2016, 144, 185102.	3.0	16
43	Nanoscale Engineering of Designer Cellulosomes. Advanced Materials, 2016, 28, 5619-5647.	21.0	42
44	Peptide Recognition Capabilities of Cellulose in Molecular Dynamics Simulations. Journal of Physical Chemistry C, 2015, 119, 24404-24416.	3.1	16
45	Multiple folding pathways of proteins with shallow knots and co-translational folding. Journal of Chemical Physics, 2015, 143, 045101.	3.0	25
46	Determination of contact maps in proteins: A combination of structural and chemical approaches. Journal of Chemical Physics, 2015, 143, 243105.	3.0	60
47	An Exploration of the Universe of Polyglutamine Structures. PLoS Computational Biology, 2015, 11, e1004541.	3.2	15
48	Cotranslational folding of deeply knotted proteins. Journal of Physics Condensed Matter, 2015, 27, 354105.	1.8	40
49	Large conformational fluctuations of the multi-domain xylanase Z of Clostridium thermocellum. Journal of Structural Biology, 2015, 191, 68-75.	2.8	17
50	Statistical radii associated with amino acids to determine the contact map: fixing the structure of a type I cohesin domain in theClostridium thermocellumcellulosome. Physical Biology, 2015, 12, 046002.	1.8	22
51	Polysaccharideâ€“Protein Complexes in a Coarse-Grained Model. Journal of Physical Chemistry B, 2015, 119, 12028-12041.	2.6	38
52	Protein Mechanics at the Single-Molecule Level. , 2015, , 1-36.		0
53	Citrate synthase proteins in extremophilic organisms: Studies within a structure-based model. Journal of Chemical Physics, 2014, 141, 235102.	3.0	6
54	Theoretical tests of the mechanical protection strategy in protein nanomechanics. Proteins: Structure, Function and Bioinformatics, 2014, 82, 717-726.	2.6	13

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55	Knotted Proteins under Tension. Israel Journal of Chemistry, 2014, 54, 1241-1249.	2.3	3
56	Structureâ€based analysis of thermodynamic and mechanical properties of cavityâ€containing proteinsÂâ€“Âcase study of plant pathogenesisâ€related proteins of class 10. FEBS Journal, 2014, 281, 416-429.	4.7	30
57	Mechanostability of Virus Capsids and Their Proteins in Structure-Based Models. Springer Series in Bio-/neuroinformatics, 2014, , 295-315.	0.1	3
58	Interactions of aqueous amino acids and proteins with the (110) surface of ZnS in molecular dynamics simulations. Journal of Chemical Physics, 2014, 140, 095101.	3.0	13
59	Unbinding and unfolding of adhesion protein complexes through stretching: Interplay between shear and tensile mechanical clamps. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3144-3153.	2.6	16
60	Proteins at Airâ€“Water Interfaces: A Coarse-Grained Model. Langmuir, 2014, 30, 12888-12896.	3.5	25
61	Aqueous Amino Acids and Proteins Near the Surface of Gold in Hydrophilic and Hydrophobic Force Fields. Journal of Physical Chemistry C, 2014, 118, 12929-12943.	3.1	34
62	Protein Unfolding by Biological Unfoldases: Insights from Modeling. Biophysical Journal, 2014, 107, 1661-1668.	0.5	25
63	Mechanostability of cohesin-dockerin complexes in a structure-based model: Anisotropy and lack of universality in the force profiles. Journal of Chemical Physics, 2014, 141, 245103.	3.0	8
64	Amino acids and proteins at ZnOâ€“water interfaces in molecular dynamics simulations. Physical Chemistry Chemical Physics, 2013, 15, 13628.	2.8	42
65	Proteins in the electric field near the surface of mica. Journal of Chemical Physics, 2013, 139, 045102.	3.0	14
66	A multi-scale molecular dynamics study of the assembly of micron-size supraparticles from 30 nm alkyl-coated nanoparticles. Physical Chemistry Chemical Physics, 2013, 15, 8132.	2.8	7
67	Topological features in stretching of proteins. Biochemical Society Transactions, 2013, 41, 519-522.	3.4	3
68	Quantum dots as probes in biology. Journal of Physics Condensed Matter, 2013, 25, 190301.	1.8	2
69	Energy landscape and dynamics of an HP lattice model of proteins â€”The role of anisotropy. Europhysics Letters, 2013, 104, 58001.	2.0	3
70	Energy landscape and dynamics of proteins: An exact analysis of a simplified lattice model. Physical Review E, 2013, 88, 040702.	2.1	10
71	Formation of Cystine Slipknots in Dimeric Proteins. PLoS ONE, 2013, 8, e57443.	2.5	9
72	Nanoindentation of 35 Virus Capsids in a Molecular Model: Relating Mechanical Properties to Structure. PLoS ONE, 2013, 8, e63640.	2.5	62

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73	Cystine Plug and Other Novel Mechanisms of Large Mechanical Stability in Dimeric Proteins. Physical Review Letters, 2012, 109, 208101.	7.8	14
74	Geometrical and Electrical Properties of Indium Tin Oxide Clusters in Ink Dispersions. Langmuir, 2012, 28, 1523-1530.	3.5	1
75	Structure-Based Models of Biomolecules: Stretching of Proteins, Dynamics of Knots, Hydrodynamic Effects, and Indentation of Virus Capsids. , 2011, , 179-208.		3
76	Denaturation of proteins near polar surfaces. Journal of Chemical Physics, 2011, 135, 235103.	3.0	19
77	Mechanical stability of multidomain proteins and novel mechanical clamps. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1786-1799.	2.6	32
78	Hydrodynamic effects in proteins. Journal of Physics Condensed Matter, 2011, 23, 033102.	1.8	38
79	Linker-mediated assembly of gold nanoparticles into multimeric motifs. Nanotechnology, 2011, 22, 445601.	2.6	16
80	BSDB: the biomolecule stretching database. Nucleic Acids Research, 2011, 39, D443-D450.	14.5	35
81	Molecular jammingâ€"The cystine slipknot mechanical clamp in all-atom simulations. Journal of Chemical Physics, 2011, 134, 085102.	3.0	16
82	Understanding biology by stretching proteins: recent progress. Current Opinion in Structural Biology, 2010, 20, 63-69.	5.7	69
83	The influence of hydrodynamic interactions on protein dynamics in confined and crowded spacesâ€"assessment in simple models. Physical Biology, 2010, 7, 046011.	1.8	11
84	The folding of knotted proteins: insights from lattice simulations. Physical Biology, 2010, 7, 016009.	1.8	46
85	Nanoindentation of virus capsids in a molecular model. Journal of Chemical Physics, 2010, 132, 015101.	3.0	41
86	Untying Knots in Proteins. Journal of the American Chemical Society, 2010, 132, 13954-13956.	13.7	43
87	On the remarkable mechanostability of scaffoldins and the mechanical clamp motif. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13791-13796.	7.1	116
88	Stretching and twisting of the DNA duplexes in coarse-grained dynamical models. Journal of Physics Condensed Matter, 2009, 21, 474221.	1.8	21
89	Mechanical Strength of 17 134 Model Proteins and Cysteine Slipknots. PLoS Computational Biology, 2009, 5, e1000547.	3.2	104
90	Hydrodynamic interactions in protein folding. Journal of Chemical Physics, 2009, 130, 124906.	3.0	26

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91	Native state dynamics and mechanical properties of human topoisomerase I within a structureâ€based coarseâ€grained model. Proteins: Structure, Function and Bioinformatics, 2009, 77, 420-431.	2.6	11
92	Protein Mechanics at the Single-Molecule Level. , 2009, , 7026-7051.		6
93	Predicting the order in which contacts are broken during single molecule protein stretching experiments. Proteins: Structure, Function and Bioinformatics, 2008, 71, 45-60.	2.6	26
94	Effects of confinement and crowding on folding of model proteins. BioSystems, 2008, 94, 248-252.	2.0	17
95	Stretching to Understand Proteinsâ€"A Survey of the Protein Data Bank. Biophysical Journal, 2008, 94, 6-13.	0.5	45
96	Selection of Optimal Variants of GÅ•Like Models of Proteins through Studies of Stretching. Biophysical Journal, 2008, 95, 3174-3191.	0.5	119
97	Tightening of Knots in Proteins. Physical Review Letters, 2008, 100, 058106.	7.8	80
98	Coarse-grained molecular dynamics simulations of nanopatterning with multivalent inks. Journal of Chemical Physics, 2008, 128, 234906.	3.0	12
99	The folding transition state theory in simple model systems. Journal of Physics Condensed Matter, 2008, 20, 244134.	1.8	2
100	Molecular dynamics of immiscible fluids in chemically patterned nanochannels. Journal of Chemical Physics, 2008, 128, 104709.	3.0	5
101	Stabilizing effect of knots on proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19714-19719.	7.1	123
102	Coarse-grained modelling of pressure-related effects in staphylococcal nuclease and ubiquitin. Journal of Physics Condensed Matter, 2007, 19, 285218.	1.8	3
103	Proteins in a shear flow. Journal of Chemical Physics, 2007, 127, 155106.	3.0	52
104	Influence of hydrodynamic interactions on mechanical unfolding of proteins. Journal of Physics Condensed Matter, 2007, 19, 285224.	1.8	25
105	Mechanical stretching of proteinsâ€"a theoretical survey of the Protein Data Bank. Journal of Physics Condensed Matter, 2007, 19, 283201.	1.8	113
106	Pulling single bacteriorhodopsin out of a membrane: Comparison of simulation and experiment. Biochimica Et Biophysica Acta - Biomembranes, 2006, 1758, 537-544.	2.6	24
107	Stretching of proteins in a force-clamp. Journal of Physics Condensed Matter, 2006, 18, L21-L28.	1.8	26
108	Stretching of proteins in a uniform flow. Journal of Chemical Physics, 2006, 125, 164903.	3.0	47

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109	Nanoscale Fluid Flows in the Vicinity of Patterned Surfaces. Physical Review Letters, 2006, 96, 114502.	7.8	47
110	Protein folding in a force clamp. Journal of Chemical Physics, 2006, 124, 194901.	3.0	17
111	Using the principle of entropy maximization to infer genetic interaction networks from gene expression patterns. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 19033-19038.	7.1	209
112	Mechanical stretching of proteins: calmodulin and titin. Physica A: Statistical Mechanics and Its Applications, 2005, 352, 28-42.	2.6	9
113	Mechanical properties of the domains of titin in a Go-like model. Journal of Chemical Physics, 2005, 122, 054906.	3.0	27
114	Mechanical unfolding of ubiquitin molecules. Journal of Chemical Physics, 2005, 123, 194903.	3.0	28
115	Chirality and protein folding. Journal of Physics Condensed Matter, 2005, 17, S1565-S1580.	1.8	38
116	Thermal unfolding of proteins. Journal of Chemical Physics, 2005, 123, 194908.	3.0	25
117	Cooperativity and contact order in protein folding. Physical Review E, 2004, 69, 031907.	2.1	12
118	Stretching of proteins in the entropic limit. Physical Review E, 2004, 69, 011912.	2.1	20
119	Stretching of homopolymers and contact order. Physical Review E, 2004, 70, 011917.	2.1	13
120	Lattice Tube Model of Proteins. Physical Review Letters, 2004, 93, 238101.	7.8	24
121	Thermal effects in stretching of Go-like models of titin and secondary structures. Proteins: Structure, Function and Bioinformatics, 2004, 56, 285-297.	2.6	73
122	What can one learn from experiments about the elusive transition state?. Protein Science, 2004, 13, 2446-2457.	7.6	24
123	Folding of proteins in Go models with angular interactions. Physica A: Statistical Mechanics and Its Applications, 2003, 330, 195-205.	2.6	9
124	Universality Classes in Folding Times of Proteins. Biophysical Journal, 2003, 84, 475-488.	0.5	119
125	Effects of pore walls and randomness on phase transitions in porous media. Physical Review E, 2002, 66, 056124.	2.1	7
126	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.	1.7	19

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127	Folding and stretching in a Go-like model of titin. Proteins: Structure, Function and Bioinformatics, 2002, 49, 114-124.	2.6	64
128	Thermal folding and mechanical unfolding pathways of protein secondary structures. Proteins: Structure, Function and Bioinformatics, 2002, 49, 104-113.	2.6	62
129	Kinetic nonoptimality and vibrational stability of proteins. Proteins: Structure, Function and Bioinformatics, 2001, 44, 20-25.	2.6	18
130	Boundary Conditions at a Fluid-Solid Interface. Physical Review Letters, 2001, 86, 803-806.	7.8	293
131	Amino acid classes and the protein folding problem. Journal of Chemical Physics, 2001, 114, 1420-1423.	3.0	28
132	Molecular dynamics of flows in the Knudsen regime. Physica A: Statistical Mechanics and Its Applications, 2000, 287, 153-160.	2.6	46
133	Scaling of folding properties in go models of proteins. , 2000, 26, 273-294.		16
134	Molecular dynamics of folding of secondary structures in Go-type models of proteins. Journal of Chemical Physics, 2000, 112, 6851-6862.	3.0	117
135	Dynamical chaos and power spectra in toy models of heteropolymers and proteins. Physical Review E, 2000, 62, 4025-4031.	2.1	8
136	Sequencing of folding events in Go-type proteins. Journal of Chemical Physics, 2000, 113, 8319-8328.	3.0	100
137	Delineation of the native basin in continuum models of proteins. Journal of Physics A, 1999, 32, 5577-5584.	1.6	7
138	Scaling of Folding Properties in Simple Models of Proteins. Physical Review Letters, 1999, 83, 1684-1687.	7.8	67
139	Energy landscapes, supergraphs, and â€œfolding funnelsâ€•in spin systems. Physical Review E, 1999, 60, 3219-3226.	2.1	57
140	Folding in two-dimensional off-lattice models of proteins. Physical Review E, 1999, 59, 970-976.	2.1	31
141	Applications of statistical mechanics in subcontinuum fluid dynamics. Physica A: Statistical Mechanics and Its Applications, 1999, 274, 281-293.	2.6	42
142	Models of Fractal River Basins. Journal of Statistical Physics, 1998, 91, 1-15.	1.2	54
143	Structure-based design of model proteins. , 1998, 31, 10-20.		8
144	Protein folding and models of dynamics on the lattice. Journal of Chemical Physics, 1998, 109, 9192-9196.	3.0	8

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145	Master Equation Approach to Protein Folding and Kinetic Traps. Physical Review Letters, 1998, 80, 3654-3657.	7.8	75
146	Structureâ€based design of model proteins. Proteins: Structure, Function and Bioinformatics, 1998, 31, 10-20.	2.6	2
147	Topological disorder in cellular microstructures. The Philosophical Magazine: Physics of Condensed Matter B, Statistical Mechanics, Electronic, Optical and Magnetic Properties, 1997, 75, 669-679.	0.6	0
148	Cell dynamics of folding in two-dimensional model proteins. Folding & Design, 1997, 2, 235-245.	4.5	16
149	Cell Dynamics of Model Proteins. Physical Review Letters, 1996, 77, 3681-3684.	7.8	19
150	Friction on adsorbed monolayers. Physical Review B, 1996, 54, 8252-8260.	3.2	143
151	Invasion Percolation and Eden Growth: Geometry and Universality. Physical Review Letters, 1996, 76, 3754-3757.	7.8	97
152	DOMAIN WALLS IN THE TRANSVERSE FIELD ISING SPIN GLASSES. Fractals, 1996, 04, 401-406.	3.7	0
153	Two-color nonlinear Boltzmann cellular automata: Surface tension and wetting. Physical Review E, 1995, 51, 3718-3728.	2.1	76
154	FRACTAL DOMAIN WALLS IN ISING SPIN GLASSES. Fractals, 1994, 02, 481-484.	3.7	2
155	Optimal paths and domain walls in the strong disorder limit. Physical Review Letters, 1994, 72, 2320-2323.	7.8	138
156	Nematic-Isotropic Transition in Porous Media. Physical Review Letters, 1994, 72, 4113-4116.	7.8	63
157	Spin-flip avalanches and dynamics of first order phase transitions. Physical Review Letters, 1994, 72, 946-946.	7.8	21
158	Second Harmonic Generation in Spin-Glass Microstructures and Fabrication of Microstructures in IV-VI Epilayers. Acta Physica Polonica A, 1993, 84, 781-784.	0.5	2
159	Frustration, scaling, and local gauge invariance. Physical Review B, 1992, 45, 786-792.	3.2	44
160	Ordering and phase transitions in random-field Ising systems. AIP Conference Proceedings, 1992, , .	0.4	0
161	Universal conductance fluctuations in spin glasses. Physical Review B, 1991, 44, 12337-12347.	3.2	19
162	Monte Carlo mean-field theory. Physical Review Letters, 1991, 67, 1807-1807.	7.8	25

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163	Critical phenomena in fluid invasion of porous media. Physical Review Letters, 1991, 66, 1058-1061.	7.8	163
164	Ordering and phase transitions in random-field Ising systems. Physical Review Letters, 1991, 67, 1821-1824.	7.8	57
165	Scaling relations for interface motion through disordered media: Application to two-dimensional fluid invasion. Physical Review B, 1991, 44, 12294-12306.	3.2	89
166	Conductance Fluctuations in Microstructures of HgCdMnTe Bicrystals. Acta Physica Polonica A, 1991, 80, 307-310.	0.5	6
167	Site Percolation Thresholds of FCC Lattice. Acta Physica Polonica A, 1991, 80, 461-464.	0.5	12
168	Influence of contact angle on quasistatic fluid invasion of porous media. Physical Review B, 1990, 41, 11508-11521.	3.2	177
169	Dynamical Transition in Quasistatic Fluid Invasion in Porous Media. Physical Review Letters, 1988, 60, 2042-2045.	7.8	221
170	Lower critical dimensionality of Heisenberg spin-glasses. Physical Review B, 1984, 29, 469-471.	3.2	27
171	Renormalization-group analysis on fractals: Ising spin-glass and the SchrÃ¶dinger equation. Physical Review B, 1983, 28, 3813-3817.	3.2	25
172	Nature of Ordering in Spin-Glasses. Physical Review Letters, 1982, 48, 832-835.	7.8	154