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	Boundary Conditions at a Fluid-Solid Interface. Physical Review Letters, 2001, 86, 803-806.	7.8	293
2	Dynamical Transition in Quasistatic Fluid Invasion in Porous Media. Physical Review Letters, 1988, 60, 2042-2045.	7.8	221
3	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
4	Influence of contact angle on quasistatic fluid invasion of porous media. Physical Review B, 1990, 41, 11508-11521.	3.2	177
5	Critical phenomena in fluid invasion of porous media. Physical Review Letters, 1991, 66, 1058-1061.	7.8	163
6	Nature of Ordering in Spin-Glasses. Physical Review Letters, 1982, 48, 832-835.	7.8	154
7	Friction on adsorbed monolayers. Physical Review B, 1996, 54, 8252-8260.	3.2	143
8	Optimal paths and domain walls in the strong disorder limit. Physical Review Letters, 1994, 72, 2320-2323.	7.8	138
9	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
10	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
11	Universality Classes in Folding Times of Proteins. Biophysical Journal, 2003, 84, 475-488.	0.5	119
12	Selection of Optimal Variants of GÅ•Like Models of Proteins through Studies of Stretching. Biophysical Journal, 2008, 95, 3174-3191.	0.5	119
13	Molecular dynamics of folding of secondary structures in Go-type models of proteins. Journal of Chemical Physics, 2000, 112, 6851-6862.	3.0	117
14	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
15	Mechanical stretching of proteinsâ€"a theoretical survey of the Protein Data Bank. Journal of Physics Condensed Matter, 2007, 19, 283201.	1.8	113
16	Mechanical Strength of 17 134 Model Proteins and Cysteine Slipknots. PLoS Computational Biology, 2009, 5, e1000547.	3.2	104
17	Sequencing of folding events in Go-type proteins. Journal of Chemical Physics, 2000, 113, 8319-8328.	3.0	100
18	Invasion Percolation and Eden Growth: Geometry and Universality. Physical Review Letters, 1996, 76, 3754-3757.	7.8	97

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19	Scaling relations for interface motion through disordered media: Application to two-dimensional fluid invasion. Physical Review B, 1991, 44, 12294-12306.	3.2	89
20	Tightening of Knots in Proteins. Physical Review Letters, 2008, 100, 058106.	7.8	80
21	Two-color nonlinear Boltzmann cellular automata: Surface tension and wetting. Physical Review E, 1995, 51, 3718-3728.	2.1	76
22	Master Equation Approach to Protein Folding and Kinetic Traps. Physical Review Letters, 1998, 80, 3654-3657.	7.8	75
23	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
24	Understanding biology by stretching proteins: recent progress. Current Opinion in Structural Biology, 2010, 20, 63-69.	5.7	69
25	Scaling of Folding Properties in Simple Models of Proteins. Physical Review Letters, 1999, 83, 1684-1687.	7.8	67
26	Folding and stretching in a Go-like model of titin. Proteins: Structure, Function and Bioinformatics, 2002, 49, 114-124.	2.6	64
27	Nematic-Isotropic Transition in Porous Media. Physical Review Letters, 1994, 72, 4113-4116.	7.8	63
28	Thermal folding and mechanical unfolding pathways of protein secondary structures. Proteins: Structure, Function and Bioinformatics, 2002, 49, 104-113.	2.6	62
29	Nanoindentation of 35 Virus Capsids in a Molecular Model: Relating Mechanical Properties to Structure. PLoS ONE, 2013, 8, e63640.	2.5	62
30	Determination of contact maps in proteins: A combination of structural and chemical approaches. Journal of Chemical Physics, 2015, 143, 243105.	3.0	60
31	Ordering and phase transitions in random-field Ising systems. Physical Review Letters, 1991, 67, 1821-1824.	7.8	57
32	Energy landscapes, supergraphs, and â€œfolding funnelsâ€•in spin systems. Physical Review E, 1999, 60, 3219-3226.	2.1	57
33	Models of Fractal River Basins. Journal of Statistical Physics, 1998, 91, 1-15.	1.2	54
34	Proteins in a shear flow. Journal of Chemical Physics, 2007, 127, 155106.	3.0	52
35	Stretching of proteins in a uniform flow. Journal of Chemical Physics, 2006, 125, 164903.	3.0	47
36	Nanoscale Fluid Flows in the Vicinity of Patterned Surfaces. Physical Review Letters, 2006, 96, 114502.	7.8	47

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37	Molecular dynamics of flows in the Knudsen regime. Physica A: Statistical Mechanics and Its Applications, 2000, 287, 153-160.	2.6	46
38	The folding of knotted proteins: insights from lattice simulations. Physical Biology, 2010, 7, 016009.	1.8	46
39	Stretching to Understand Proteinsâ€"A Survey of the Protein Data Bank. Biophysical Journal, 2008, 94, 6-13.	0.5	45
40	Frustration, scaling, and local gauge invariance. Physical Review B, 1992, 45, 786-792.	3.2	44
41	Untying Knots in Proteins. Journal of the American Chemical Society, 2010, 132, 13954-13956.	13.7	43
42	Applications of statistical mechanics in subcontinuum fluid dynamics. Physica A: Statistical Mechanics and Its Applications, 1999, 274, 281-293.	2.6	42
43	Amino acids and proteins at ZnOâ€"water interfaces in molecular dynamics simulations. Physical Chemistry Chemical Physics, 2013, 15, 13628.	2.8	42
44	Nanoscale Engineering of Designer Cellulosomes. Advanced Materials, 2016, 28, 5619-5647.	21.0	42
45	Nanoindentation of virus capsids in a molecular model. Journal of Chemical Physics, 2010, 132, 015101.	3.0	41
46	Cotranslational folding of deeply knotted proteins. Journal of Physics Condensed Matter, 2015, 27, 354105.	1.8	40
47	Chirality and protein folding. Journal of Physics Condensed Matter, 2005, 17, S1565-S1580.	1.8	38
48	Hydrodynamic effects in proteins. Journal of Physics Condensed Matter, 2011, 23, 033102.	1.8	38
49	Polysaccharideâ€"Protein Complexes in a Coarse-Grained Model. Journal of Physical Chemistry B, 2015, 119, 12028-12041.	2.6	38
50	BSDB: the biomolecule stretching database. Nucleic Acids Research, 2011, 39, D443-D450.	14.5	35
51	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
52	Unfolding knots by proteasome-like systems: simulations of the behaviour of folded and neurotoxic proteins. Molecular BioSystems, 2016, 12, 2700-2712.	2.9	33
53	Mechanical stability of multidomain proteins and novel mechanical clamps. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1786-1799.	2.6	32
54	Folding in two-dimensional off-lattice models of proteins. Physical Review E, 1999, 59, 970-976.	2.1	31

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55	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
56	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
57	Amino acid classes and the protein folding problem. Journal of Chemical Physics, 2001, 114, 1420-1423.	3.0	28
58	Mechanical unfolding of ubiquitin molecules. Journal of Chemical Physics, 2005, 123, 194903.	3.0	28
59	Lower critical dimensionality of Heisenberg spin-glasses. Physical Review B, 1984, 29, 469-471.	3.2	27
60	Mechanical properties of the domains of titin in a Go-like model. Journal of Chemical Physics, 2005, 122, 054906.	3.0	27
61	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
62	Stretching of proteins in a force-clamp. Journal of Physics Condensed Matter, 2006, 18, L21-L28.	1.8	26
63	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
64	Hydrodynamic interactions in protein folding. Journal of Chemical Physics, 2009, 130, 124906.	3.0	26
65	Renormalization-group analysis on fractals: Ising spin-glass and the SchrÃ¶dinger equation. Physical Review B, 1983, 28, 3813-3817.	3.2	25
66	Monte Carlo mean-field theory. Physical Review Letters, 1991, 67, 1807-1807.	7.8	25
67	Thermal unfolding of proteins. Journal of Chemical Physics, 2005, 123, 194908.	3.0	25
68	Influence of hydrodynamic interactions on mechanical unfolding of proteins. Journal of Physics Condensed Matter, 2007, 19, 285224.	1.8	25
69	Proteins at Airâ€“Water Interfaces: A Coarse-Grained Model. Langmuir, 2014, 30, 12888-12896.	3.5	25
70	Protein Unfolding by Biological Unfoldases: Insights from Modeling. Biophysical Journal, 2014, 107, 1661-1668.	0.5	25
71	Multiple folding pathways of proteins with shallow knots and co-translational folding. Journal of Chemical Physics, 2015, 143, 045101.	3.0	25
72	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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73	Lattice Tube Model of Proteins. Physical Review Letters, 2004, 93, 238101.	7.8	24
74	What can one learn from experiments about the elusive transition state?. Protein Science, 2004, 13, 2446-2457.	7.6	24
75	Pulling single bacteriorhodopsin out of a membrane: Comparison of simulation and experiment. Biochimica Et Biophysica Acta - Biomembranes, 2006, 1758, 537-544.	2.6	24
76	Disordered peptide chains in an Î±-C-based coarse-grained model. Physical Chemistry Chemical Physics, 2018, 20, 19057-19070.	2.8	23
77	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
78	The volume of cavities in proteins and virus capsids. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1275-1286.	2.6	22
79	Spin-flip avalanches and dynamics of first order phase transitions. Physical Review Letters, 1994, 72, 946-946.	7.8	21
80	Stretching and twisting of the DNA duplexes in coarse-grained dynamical models. Journal of Physics Condensed Matter, 2009, 21, 474221.	1.8	21
81	Stretching of proteins in the entropic limit. Physical Review E, 2004, 69, 011912.	2.1	20
82	Universal conductance fluctuations in spin glasses. Physical Review B, 1991, 44, 12337-12347.	3.2	19
83	Cell Dynamics of Model Proteins. Physical Review Letters, 1996, 77, 3681-3684.	7.8	19
84	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
85	Denaturation of proteins near polar surfaces. Journal of Chemical Physics, 2011, 135, 235103.	3.0	19
86	Proteins at airâ€“water and oilâ€“water interfaces in an all-atom model. Physical Chemistry Chemical Physics, 2017, 19, 25197-25206.	2.8	19
87	Kinetic nonoptimality and vibrational stability of proteins. Proteins: Structure, Function and Bioinformatics, 2001, 44, 20-25.	2.6	18
88	Protein folding in a force clamp. Journal of Chemical Physics, 2006, 124, 194901.	3.0	17
89	Effects of confinement and crowding on folding of model proteins. BioSystems, 2008, 94, 248-252.	2.0	17
90	Large conformational fluctuations of the multi-domain xylanase Z of Clostridium thermocellum. Journal of Structural Biology, 2015, 191, 68-75.	2.8	17

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91	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
92	Pseudo-Improper-Dihedral Model for Intrinsically Disordered Proteins. Journal of Chemical Theory and Computation, 2020, 16, 4726-4733.	5.3	17
93	Cell dynamics of folding in two-dimensional model proteins. Folding & Design, 1997, 2, 235-245.	4.5	16
94	Scaling of folding properties in go models of proteins. , 2000, 26, 273-294.		16
95	Linker-mediated assembly of gold nanoparticles into multimeric motifs. Nanotechnology, 2011, 22, 445601.	2.6	16
96	Molecular jammingâ€"The cystine slipknot mechanical clamp in all-atom simulations. Journal of Chemical Physics, 2011, 134, 085102.	3.0	16
97	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
98	Peptide Recognition Capabilities of Cellulose in Molecular Dynamics Simulations. Journal of Physical Chemistry C, 2015, 119, 24404-24416.	3.1	16
99	Criteria for folding in structure-based models of proteins. Journal of Chemical Physics, 2016, 144, 185102.	3.0	16
100	Protein droplets in systems of disordered homopeptides and the amyloid glass phase. Physical Chemistry Chemical Physics, 2020, 22, 15592-15599.	2.8	16
101	An Exploration of the Universe of Polyglutamine Structures. PLoS Computational Biology, 2015, 11, e1004541.	3.2	15
102	Topological transformations in proteins: effects of heating and proximity of an interface. Scientific Reports, 2017, 7, 39851.	3.3	15
103	Cystine Plug and Other Novel Mechanisms of Large Mechanical Stability in Dimeric Proteins. Physical Review Letters, 2012, 109, 208101.	7.8	14
104	Proteins in the electric field near the surface of mica. Journal of Chemical Physics, 2013, 139, 045102.	3.0	14
105	Structural entanglements in protein complexes. Journal of Chemical Physics, 2017, 146, 225102.	3.0	14
106	Stretching of homopolymers and contact order. Physical Review E, 2004, 70, 011917.	2.1	13
107	Theoretical tests of the mechanical protection strategy in protein nanomechanics. Proteins: Structure, Function and Bioinformatics, 2014, 82, 717-726.	2.6	13
108	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

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109	Cooperativity and contact order in protein folding. Physical Review E, 2004, 69, 031907.	2.1	12
110	Coarse-grained molecular dynamics simulations of nanopatterning with multivalent inks. Journal of Chemical Physics, 2008, 128, 234906.	3.0	12
111	Stability of structurally entangled protein dimers. Proteins: Structure, Function and Bioinformatics, 2018, 86, 945-955.	2.6	12
112	Conformational Biases of Î±-Synuclein and Formation of Transient Knots. Journal of Physical Chemistry B, 2020, 124, 11-19.	2.6	12
113	Site Percolation Thresholds of FCC Lattice. Acta Physica Polonica A, 1991, 80, 461-464.	0.5	12
114	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
115	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
116	Properties of Cavities in Biological Structuresâ€”A Survey of the Protein Data Bank. Frontiers in Molecular Biosciences, 2020, 7, 591381.	3.5	11
117	Energy landscape and dynamics of proteins: An exact analysis of a simplified lattice model. Physical Review E, 2013, 88, 040702.	2.1	10
118	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
119	Self-assembly of model proteins into virus capsids. Journal of Physics Condensed Matter, 2017, 29, 474003.	1.8	10
120	Viscoelastic properties of wheat gluten in a molecular dynamics study. PLoS Computational Biology, 2021, 17, e1008840.	3.2	10
121	Cohesin-dockerin code in cellulosomal dual binding modes and its allosteric regulation by proline isomerization. Structure, 2021, 29, 587-597.e8.	3.3	10
122	Folding of proteins in Go models with angular interactions. Physica A: Statistical Mechanics and Its Applications, 2003, 330, 195-205.	2.6	9
123	Mechanical stretching of proteins: calmodulin and titin. Physica A: Statistical Mechanics and Its Applications, 2005, 352, 28-42.	2.6	9
124	Formation of Cystine Slipknots in Dimeric Proteins. PLoS ONE, 2013, 8, e57443.	2.5	9
125	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
126	Structure-based design of model proteins. , 1998, 31, 10-20.		8

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127	Protein folding and models of dynamics on the lattice. Journal of Chemical Physics, 1998, 109, 9192-9196.	3.0	8
128	Dynamical chaos and power spectra in toy models of heteropolymers and proteins. Physical Review E, 2000, 62, 4025-4031.	2.1	8
129	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
130	Delineation of the native basin in continuum models of proteins. Journal of Physics A, 1999, 32, 5577-5584.	1.6	7
131	Effects of pore walls and randomness on phase transitions in porous media. Physical Review E, 2002, 66, 056124.	2.1	7
132	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
133	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
134	Mechanical Unfolding of Proteinsâ€"A Comparative Nonequilibrium Molecular Dynamics Study. Biophysical Journal, 2020, 119, 939-949.	0.5	7
135	Networks of interbasin traffic in intrinsically disordered proteins. Physical Review Research, 2020, 2, .	3.6	7
136	Citrate synthase proteins in extremophilic organisms: Studies within a structure-based model. Journal of Chemical Physics, 2014, 141, 235102.	3.0	6
137	Non-local effects of point mutations on the stability of a protein module. Journal of Chemical Physics, 2017, 147, 105101.	3.0	6
138	Protein Mechanics at the Single-Molecule Level. , 2009, , 7026-7051.		6
139	Conductance Fluctuations in Microstructures of HgCdMnTe Bicrystals. Acta Physica Polonica A, 1991, 80, 307-310.	0.5	6
140	Molecular dynamics of immiscible fluids in chemically patterned nanochannels. Journal of Chemical Physics, 2008, 128, 104709.	3.0	5
141	Structural Changes in Barley Protein LTP1 Isoforms at Airâ€"Water Interfaces. Langmuir, 2017, 33, 4769-4780.	3.5	5
142	Transient knots in intrinsically disordered proteins and neurodegeneration. Progress in Molecular Biology and Translational Science, 2020, 174, 79-103.	1.7	5
143	Dual binding mode in cohesin-dockerin complexes as assessed through stretching studies. Journal of Chemical Physics, 2016, 145, 134102.	3.0	4
144	Proteins at curved fluidâ€"fluid interfaces in a coarse-grained model. Journal of Physics Condensed Matter, 2020, 32, 404003.	1.8	4

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145	Coarse-grained modelling of pressure-related effects in staphylococcal nuclease and ubiquitin. Journal of Physics Condensed Matter, 2007, 19, 285218.	1.8	3
146	Structure-Based Models of Biomolecules: Stretching of Proteins, Dynamics of Knots, Hydrodynamic Effects, and Indentation of Virus Capsids. , 2011, , 179-208.		3
147	Topological features in stretching of proteins. Biochemical Society Transactions, 2013, 41, 519-522.	3.4	3
148	Energy landscape and dynamics of an HP lattice model of proteins â€"The role of anisotropy. Europhysics Letters, 2013, 104, 58001.	2.0	3
149	Knotted Proteins under Tension. Israel Journal of Chemistry, 2014, 54, 1241-1249.	2.3	3
150	Mechanostability of Virus Capsids and Their Proteins in Structure-Based Models. Springer Series in Bio-/neuroinformatics, 2014, , 295-315.	0.1	3
151	Structural fluctuations and thermal stability of proteins in crowded environments: effects of the excluded volume. Physical Biology, 2016, 13, 066002.	1.8	3
152	Nascent Folding of Proteins Across the Three Domains of Life. Frontiers in Molecular Biosciences, 2021, 8, 692230.	3.5	3
153	FRACTAL DOMAIN WALLS IN ISING SPIN GLASSES. Fractals, 1994, 02, 481-484.	3.7	2
154	The folding transition state theory in simple model systems. Journal of Physics Condensed Matter, 2008, 20, 244134.	1.8	2
155	Quantum dots as probes in biology. Journal of Physics Condensed Matter, 2013, 25, 190301.	1.8	2
156	Proteins at the air-water interface in a lattice model. Journal of Chemical Physics, 2018, 148, 094704.	3.0	2
157	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
158	Structureâ€based design of model proteins. Proteins: Structure, Function and Bioinformatics, 1998, 31, 10-20.	2.6	2
159	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
160	Geometrical and Electrical Properties of Indium Tin Oxide Clusters in Ink Dispersions. Langmuir, 2012, 28, 1523-1530.	3.5	1
161	Special Issue on the Physics of Viral Capsids. Journal of Physics Condensed Matter, 2018, 30, 290201.	1.8	1
162	Gluten Adhesion and Shearing in a Contact-Based Coarse-Grained Model. Tribology Letters, 2021, 69, 1.	2.6	1

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163	Contact-Based Analysis of Aggregation of Intrinsically Disordered Proteins. Methods in Molecular Biology, 2022, 2340, 105-120.	0.9	1
164	Ordering and phase transitions in random-field Ising systems. AIP Conference Proceedings, 1992, , .	0.4	0
165	DOMAIN WALLS IN THE TRANSVERSE FIELD ISING SPIN GLASSES. Fractals, 1996, 04, 401-406.	3.7	0
166	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
167	Preliminary Study of Adhesive Properties of Surface Adsorbed Human Serum Albumin and Transforming Growth Factor-Î² Evaluated with AFM Force Spectroscopy. , 2019, , .		0
168	Protein Mechanics at the Single-Molecule Level. , 2015, , 1-36.		0
169	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
170	Preface to the JPCM special issue on droplets and vesicles. Journal of Physics Condensed Matter, 2022, 34, 030401.	1.8	0
171	Network of inter-basin traffic in intrinsically disordered PUMA protein. Europhysics Letters, 2020, 132, 28002.	2.0	0
172	Final Remarks. Methods in Molecular Biology, 2022, 2340, 469-470.	0.9	0