Amos Maritan

List of Publications by Year in descending order

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238 papers

14,550 citations

58 h-index 26792 111 g-index

243 all docs

 $\begin{array}{c} 243 \\ \text{docs citations} \end{array}$

times ranked

243

15342 citing authors

#	Article	IF	CITATIONS
1	A universal model for mobility and migration patterns. Nature, 2012, 484, 96-100.	13.7	1,027
2	Size and form in efficient transportation networks. Nature, 1999, 399, 130-132.	13.7	713
3	Neutral theory and relative species abundance in ecology. Nature, 2003, 424, 1035-1037.	13.7	672
4	Global protein function prediction from protein-protein interaction networks. Nature Biotechnology, 2003, 21, 697-700.	9.4	611
5	Fundamental patterns underlying gene expression profiles: Simplicity from complexity. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 8409-8414.	3.3	433
6	A backbone-based theory of protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16623-16633.	3.3	433
7	Modeling of Protein Interaction Networks. Complexus, 2003, 1, 38-44.	0.7	392
8	Density dependence explains tree species abundance and diversity in tropical forests. Nature, 2005, 438, 658-661.	13.7	287
9	Dynamic modeling of gene expression data. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1693-1698.	3.3	274
10	Optimal shapes of compact strings. Nature, 2000, 406, 287-290.	13.7	270
11	Patterns of relative species abundance in rainforests and coral reefs. Nature, 2007, 450, 45-49.	13.7	244
12	Emergence of structural and dynamical properties of ecological mutualistic networks. Nature, 2013, 500, 449-452.	13.7	221
13	Chaos, noise, and synchronization. Physical Review Letters, 1994, 72, 1451-1454.	2.9	210
14	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.	3.3	209
15	Scaling laws for river networks. Physical Review E, 1996, 53, 1510-1515.	0.8	208
16	Geometry and symmetry presculpt the free-energy landscape of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7960-7964.	3.3	203
17	On Hack's Law. Water Resources Research, 1996, 32, 3367-3374.	1.7	202
18	Supply-demand balance and metabolic scaling. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10506-10509.	3.3	201

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19	Insight into the Structure of Amyloid Fibrils from the Analysis of Globular Proteins. PLoS Computational Biology, 2006, 2, e170.	1.5	180
20	Resilience and reactivity of global food security. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6902-6907.	3.3	179
21	A general basis for quarter-power scaling in animals. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15816-15820.	3.3	171
22	Accurate and efficient description of protein vibrational dynamics: Comparing molecular dynamics and Gaussian models. Proteins: Structure, Function and Bioinformatics, 2004, 55, 635-645.	1.5	160
23	Coarse-Grained Model of Proteins Incorporating Atomistic Detail of the Active Site. Physical Review Letters, 2005, 95, 218102.	2.9	157
24	Information-based fitness and the emergence of criticality in living systems. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10095-10100.	3.3	145
25	Evolution and selection of river networks: Statics, dynamics, and complexity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2417-2424.	3.3	143
26	Optimal paths and domain walls in the strong disorder limit. Physical Review Letters, 1994, 72, 2320-2323.	2.9	138
27	Stochastic growth equations and reparametrization invariance. Reviews of Modern Physics, 1996, 68, 963-983.	16.4	133
28	The intracellular antibody capture technology (IACT): towards a consensus sequence for intracellular antibodies. Journal of Molecular Biology, 2002, 317, 73-83.	2.0	130
29	Protein Structures and Optimal Folding from a Geometrical Variational Principle. Physical Review Letters, 1999, 82, 3372-3375.	2.9	124
30	Topology of the Fittest Transportation Network. Physical Review Letters, 2000, 84, 4745-4748.	2.9	117
31	Dynamical evolution of ecosystems. Nature, 2006, 444, 926-928.	13.7	117
32	Feasibility and coexistence of large ecological communities. Nature Communications, 2017, 8, .	5.8	115
33	Water-controlled wealth of nations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4230-4233.	3.3	108
34	Predicting the stability of large structured food webs. Nature Communications, 2015, 6, 7842.	5.8	108
35	Network allometry. Geophysical Research Letters, 2002, 29, 3-1.	1.5	107
36	Inferring species interactions in tropical forests. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13854-13859.	3.3	103

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37	Scale invariance in the dynamics of spontaneous behavior. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 10564-10569.	3.3	100
38	Invasion Percolation and Eden Growth: Geometry and Universality. Physical Review Letters, 1996, 76, 3754-3757.	2.9	97
39	On skewed ARC plots of impedance of electrodes with an irreversible electrode process. Electrochimica Acta, 1990, 35, 141-145.	2.6	96
40	Scaling, Optimality, and Landscape Evolution. Journal of Statistical Physics, 2001, 104, 1-48.	0.5	92
41	Thermodynamics of Fractal Networks. Physical Review Letters, 1996, 76, 3364-3367.	2.9	89
42	Self-Templated Nucleation in Peptide and Protein Aggregation. Physical Review Letters, 2008, 101, 258101.	2.9	89
43	Optimal Protein Design Procedure. Physical Review Letters, 1996, 77, 1901-1904.	2.9	87
44	Colloquium: Geometrical approach to protein folding: a tube picture. Reviews of Modern Physics, 2003, 75, 23-34.	16.4	86
45	Sculpting of a Fractal River Basin. Physical Review Letters, 1997, 78, 4522-4525.	2.9	78
46	Scaling body size fluctuations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4646-4650.	3.3	77
47	Recurrent oligomers in proteins: An optimal scheme reconciling accurate and concise backbone representations in automated folding and design studies. Proteins: Structure, Function and Bioinformatics, 2000, 40, 662-674.	1.5	72
48	Dynamics of phase separation of binary fluids. Physical Review A, 1992, 45, R5347-R5350.	1.0	70
49	Spatial effects on species persistence and implications for biodiversity. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4346-4351.	3.3	70
50	Effect of localization on the stability of mutualistic ecological networks. Nature Communications, 2015, 6, 10179.	5.8	70
51	Geometry and physics of proteins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 315-322.	1.5	69
52	Characterization and modeling of protein–protein interaction networks. Physica A: Statistical Mechanics and Its Applications, 2005, 352, 1-27.	1.2	68
53	Human Mobility in a Continuum Approach. PLoS ONE, 2013, 8, e60069.	1.1	67
54	Species lifetime distribution for simple models of ecologies. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15747-15751.	3.3	66

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55	Form, function, and evolution of living organisms. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 3332-3337.	3.3	66
56	Allometric cascades. Nature, 2003, 421, 713-714.	13.7	64
57	Sample and population exponents of generalized Taylor's law. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7755-7760.	3.3	64
58	Nematic-Isotropic Transition in Porous Media. Physical Review Letters, 1994, 72, 4113-4116.	2.9	63
59	Network Structures from Selection Principles. Physical Review Letters, 2004, 92, 198701.	2.9	62
60	Exploring the Universe of Protein Structures beyond the Protein Data Bank. PLoS Computational Biology, 2010, 6, e1000957.	1.5	62
61	Unified perspective on proteins: A physics approach. Physical Review E, 2004, 70, 041905.	0.8	61
62	Generalized receptor law governs phototaxis in the phytoplankton <i>Euglena gracilis</i> Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 7045-7050.	3.3	60
63	Dynamic metabolic adaptation can promote species coexistence in competitive microbial communities. PLoS Computational Biology, 2020, 16, e1007896.	1.5	60
64	Elastic Properties of Proteins: Insight on the Folding Process and Evolutionary Selection of Native Structures. Journal of Molecular Biology, 2002, 321, 909-921.	2.0	59
65	Ordering and phase transitions in random-field Ising systems. Physical Review Letters, 1991, 67, 1821-1824.	2.9	57
66	Flory theory for polymers. Journal of Physics Condensed Matter, 2013, 25, 503101.	0.7	57
67	Towards a unified descriptive theory for spatial ecology: predicting biodiversity patterns across spatial scales. Methods in Ecology and Evolution, 2015, 6, 324-332.	2.2	57
68	Disentangling the effect of hybrid interactions and of the constant effort hypothesis on ecological community stability. Oikos, 2014, 123, 525-532.	1.2	56
69	Models of Fractal River Basins. Journal of Statistical Physics, 1998, 91, 1-15.	0.5	54
70	Learning effective amino acid interactions through iterative stochastic techniques. Proteins: Structure, Function and Bioinformatics, 2001, 42, 422-431.	1.5	51
71	Randomly pinned landscape evolution. Physical Review E, 1997, 55, R4865-R4868.	0.8	50
72	Folding, Design, and Determination of Interaction Potentials Using Off-Lattice Dynamics of Model Heteropolymers. Physical Review Letters, 1998, 81, 3287-3290.	2.9	50

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73	Simulations of Action of DNA Topoisomerases to Investigate Boundaries and Shapes of Spaces of Knots. Biophysical Journal, 2004, 87, 2968-2975.	0.2	48
74	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6883-6888.	3.3	48
75	Self-Interactions of Strands and Sheets. Journal of Statistical Physics, 2003, 110, 35-50.	0.5	45
76	Microseconds Dynamics Simulations of the Outer-Membrane Protease T. Biophysical Journal, 2008, 94, 71-78.	0.2	43
77	Generalized CNS arousal: An elementary force within the vertebrate nervous system. Neuroscience and Biobehavioral Reviews, 2016, 68, 167-176.	2.9	42
78	Species coexistence in a neutral dynamics with environmental noise. Journal of Theoretical Biology, 2017, 413, 1-10.	0.8	42
79	Scaling Behavior of Self-Avoiding Random Surfaces. Physical Review Letters, 1984, 53, 123-126.	2.9	41
80	Protein Design in a Lattice Model of Hydrophobic and Polar Amino Acids. Physical Review Letters, 1998, 80, 2237-2240.	2.9	41
81	Folding Pathways of Prion and Doppel. Biophysical Journal, 2002, 83, 3533-3541.	0.2	40
82	Elasticity of Semiflexible Polymers with and without Self-Interactions. Macromolecules, 2003, 36, 10095-10102.	2.2	40
83	True scale-free networks hidden by finite size effects. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	40
84	Compactness, aggregation, and prionlike behavior of protein: A lattice model study. Journal of Chemical Physics, 2000, 113, 5072.	1.2	39
85	Dynamics of growing interfaces. Physical Review Letters, 1992, 69, 3193-3195.	2.9	37
86	Random walk and the ideal chain problem on self-similar structures. Physical Review Letters, 1989, 62, 2845-2848.	2.9	35
87	Interfacial Roughening Induced by Phase Separation. Physical Review Letters, 1996, 76, 1106-1109.	2.9	35
88	Variational Approach to Protein Design and Extraction of Interaction Potentials. Physical Review Letters, 1998, 81, 2172-2175.	2.9	35
89	Molecular dynamics studies on HIV-1 protease: Drug resistance and folding pathways. Proteins: Structure, Function and Bioinformatics, 2001, 43, 365-372.	1.5	35
90	An allometry-based approach for understanding forest structure, predicting tree-size distribution and assessing the degree of disturbance. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20122375.	1.2	35

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91	Interaction potentials for protein folding. , 1998, 30, 244-248.		34
92	Finite Size Scaling in Ecology. Physical Review Letters, 1999, 83, 4212-4214.	2.9	34
93	From Cellular Characteristics to Disease Diagnosis: Uncovering Phenotypes with Supercells. PLoS Computational Biology, 2013, 9, e1003215.	1.5	34
94	Explorability and the origin of network sparsity in living systems. Scientific Reports, 2017, 7, 12323.	1.6	34
95	Continuum Model for River Networks. Physical Review Letters, 1995, 75, 577-580.	2.9	33
96	Continuum model for the growth of interfaces. Physical Review E, 1996, 53, 759-778.	0.8	33
97	Stability Threshold as a Selection Principle for Protein Design. Physical Review Letters, 1997, 78, 3967-3970.	2.9	32
98	Role of Secondary Motifs in Fast Folding Polymers: A Dynamical Variational Principle. Physical Review Letters, 2000, 84, 3009-3012.	2.9	32
99	Extraction of interaction potentials between amino acids from native protein structures. Journal of Chemical Physics, 2000, 112, 9151-9166.	1.2	32
100	On species persistence-time distributions. Journal of Theoretical Biology, 2012, 303, 15-24.	0.8	32
101	River landscapes and optimal channel networks. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6548-6553.	3.3	32
102	Adhesion of solids. Physical Review E, 1997, 56, 2626-2634.	0.8	31
103	Structural motifs of biomolecules. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17283-17286.	3.3	31
104	Determination of interaction potentials of amino acids from native protein structures: Tests on simple lattice models. Journal of Chemical Physics, 1999, 110, 10123-10133.	1.2	29
105	Energy landscape and native-state structure of proteins—A simplified model. Europhysics Letters, 2002, 58, 623-629.	0.7	29
106	Upscaling species richness and abundances in tropical forests. Science Advances, 2017, 3, e1701438.	4.7	29
107	Scale Invariant Correlations in a Driven Dissipative Gas. Physical Review Letters, 1998, 80, 4410-4413.	2.9	28
108	Bethe approximation for a semiflexible polymer chain. Physical Review E, 1998, 58, R5241-R5244.	0.8	28

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109	Protein threading by learning. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 14350-14355.	3.3	28
110	Amino acid classes and the protein folding problem. Journal of Chemical Physics, 2001, 114, 1420-1423.	1.2	28
111	A knowledge-based scale for amino acid membrane propensity. Proteins: Structure, Function and Bioinformatics, 2002, 50, 114-121.	1.5	27
112	Self-similarity and scaling in forest communities. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7658-7662.	3.3	27
113	Maritan and Banavar Reply. Physical Review Letters, 1994, 73, 2932-2932.	2.9	26
114	Monte Carlo mean-field theory. Physical Review Letters, 1991, 67, 1807-1807.	2.9	25
115	Molecular dynamics of phase separation in narrow channels. Physical Review E, 1993, 47, R2265-R2268.	0.8	25
116	Steric Constraints in Model Proteins. Physical Review Letters, 1998, 80, 5683-5686.	2.9	25
117	First-principles design of nanomachines. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6900-6903.	3.3	25
118	Covariations in ecological scaling laws fostered by community dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10672-10677.	3.3	25
119	Diffusion on two-dimensional random walks. Physical Review Letters, 1987, 58, 1758-1760.	2.9	24
120	Critical behavior of two-dimensional vesicles in the deflated regime. Physical Review A, 1991, 43, 5752-5754.	1.0	24
121	Lattice Tube Model of Proteins. Physical Review Letters, 2004, 93, 238101.	2.9	24
122	What can one learn from experiments about the elusive transition state?. Protein Science, 2004, 13, 2446-2457.	3.1	24
123	Spatial aggregation and the species–area relationship across scales. Journal of Theoretical Biology, 2012, 313, 87-97.	0.8	24
124	Force Dependence of the Michaelis Constant in a Two-State Ratchet Model for Molecular Motors. Physical Review Letters, 2001, 86, 1134-1137.	2.9	23
125	Spectral dimension of a fractal structure with long-range interactions. Physical Review B, 1986, 34, 456-459.	1.1	22
126	Computational approach to the protein-folding problem. Proteins: Structure, Function and Bioinformatics, 2001, 42, 433-435.	1.5	22

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127	Geometry of Compact Tubes and Protein Structures. Complexus, 2003, 1, 4-13.	0.7	22
128	Spin-flip avalanches and dynamics of first order phase transitions. Physical Review Letters, 1994, 72, 946-946.	2.9	21
129	Physics of thick polymers. Journal of Polymer Science, Part B: Polymer Physics, 2005, 43, 650-679.	2.4	21
130	Random walks with intersections: Static and dynamic fractal properties. Physical Review A, 1987, 36, 2338-2351.	1.0	20
131	The spectrum of a one-dimensional hierarchical model. Journal of Statistical Physics, 1988, 52, 595-608.	0.5	20
132	Folding Lennard-Jones proteins by a contact potential. , 1999, 37, 544-553.		20
133	Dynamical relaxation of the surface tension of miscible phases. Physical Review Letters, 1993, 71, 3465-3468.	2.9	19
134	A Self-Consistent Knowledge-Based Approach to Protein Design. Biophysical Journal, 2001, 80, 480-490.	0.2	19
135	A new interpolation formula for semiflexible polymers. Biophysical Chemistry, 2005, 115, 251-254.	1.5	19
136	Predicting spatial similarity of freshwater fish biodiversity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7058-7062.	3.3	19
137	The effect of quenched disorder in neutral theories. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P04032.	0.9	19
138	Reconciling cooperation, biodiversity and stability in complex ecological communities. Scientific Reports, 2019, 9, 5580.	1.6	19
139	Statistical mechanics of random paths on disordered lattices. Journal of Statistical Physics, 1994, 75, 669-706.	0.5	18
140	Pretransitional behavior of a water in liquid crystal microemulsion close to the demixing transition: Evidence for intermicellar attraction mediated by paranematic fluctuations. Journal of Chemical Physics, 2005, 122, 214721.	1.2	18
141	Scoring functions in protein folding and design. Protein Science, 2000, 9, 812-819.	3.1	18
142	A comparative study of existing and new design techniques for protein models. Journal of Chemical Physics, 1999, 110, 9730-9738.	1.2	17
143	Towards a theory of biodiversity. Nature, 2009, 460, 334-335.	13.7	17
144	Crucial stages of protein folding through a solvable model: Predicting target sites for enzyme-inhibiting drugs. Protein Science, 2002, 11, 1878-1887.	3.1	16

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145	Organization of Ecosystems in the Vicinity of a Novel Phase Transition. Physical Review Letters, 2004, 92, 218703.	2.9	16
146	Generalized size scaling of metabolic rates based on single-cell measurements with freshwater phytoplankton. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17323-17329.	3.3	16
147	DNA sequence symmetries from randomness: the origin of the Chargaff's second parity rule. Briefings in Bioinformatics, 2021, 22, 2172-2181.	3.2	16
148	Non-Neutral Vegetation Dynamics. PLoS ONE, 2006, 1, e78.	1.1	16
149	Weak non-self-averaging behavior for diffusion in a trapping environment. Physical Review E, 1994, 49, 227-231.	0.8	15
150	Multiple Steering Molecular Dynamics Applied to Water Exchange at Alkali Ions. Journal of Physical Chemistry B, 2002, 106, 13027-13032.	1.2	15
151	Proteins and polymers. Journal of Chemical Physics, 2005, 122, 234910.	1.2	15
152	Simplified Exactly Solvable Model for <mml:math display="inline" xmlns:mml="http://www.w3.org/1998/Math/MathML"> <mml:mi>\hat{l}^2</mml:mi></mml:math> -Amyloid Aggregation. Physical Review Letters, 2010, 105, 108102.	2.9	15
153	Entropy production in master equations and Fokker–Planck equations: facing the coarse-graining and recovering the information loss. Journal of Statistical Mechanics: Theory and Experiment, 2019, 2019, 104013.	0.9	15
154	Archetypes of human cognition defined by time preference for reward and their brain correlates: An evolutionary trade-off approach. Neurolmage, 2019, 185, 322-334.	2.1	15
155	Local sequenceâ€structure relationships in proteins. Protein Science, 2021, 30, 818-829.	3.1	15
156	Depletion forces in hard-sphere colloids. Physical Review E, 1999, 59, R1339-R1342.	0.8	14
157	Symmetry, shape, and order. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19187-19192.	3.3	14
158	Diffusion of tagged particles in a crowded medium. Europhysics Letters, 2014, 107, 20006.	0.7	14
159	Composition waves in confined geometries. Physical Review E, 1993, 48, R2362-R2365.	0.8	13
160	Continuum approach to diffusion-limited-aggregation type of growth. Physical Review E, 1994, 49, R4795-R4798.	0.8	13
161	Assembly of protein tertiary structures from secondary structures using optimized potentials. Proteins: Structure, Function and Bioinformatics, 2003, 52, 155-165.	1.5	13
162	The origami of life. Journal of Physics Condensed Matter, 2006, 18, 847-888.	0.7	13

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163	Incipient criticality in ecological communities. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18714-18717.	3.3	13
164	Local symmetry determines the phases of linear chains: a simple model for the self-assembly of peptides. Soft Matter, 2019, 15, 5596-5613.	1.2	13
165	Deciphering the folding kinetics of transmembrane helical proteins. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 14229-14234.	3.3	12
166	A novel iterative strategy for protein design. Journal of Chemical Physics, 2000, 112, 2050-2055.	1.2	12
167	Force dependent transition rates in chemical kinetics models for motor proteins. Journal of Chemical Physics, 2002, 117, 10339-10349.	1.2	12
168	Comparing models of species abundance (Reply). Nature, 2006, 441, E1-E2.	13.7	12
169	reply: Rivers, blood and transportation networks. Nature, 2000, 408, 160-160.	13.7	11
170	Phase diagrams for DNA denaturation under stretching forces. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, L04001.	0.9	11
171	Testing a general approach to assess the degree of disturbance in tropical forests. Journal of Vegetation Science, 2017, 28, 659-668.	1.1	11
172	The elixir phase of chain molecules. Proteins: Structure, Function and Bioinformatics, 2019, 87, 176-184.	1.5	11
173	Morphology and Scaling in Continuum Ballistic Deposition. Physical Review Letters, 1995, 74, 1783-1786.	2.9	10
174	Role of Native-State Topology in the Stabilization of Intracellular Antibodies. Biophysical Journal, 2001, 81, 2935-2945.	0.2	10
175	Neutral and niche forces as drivers of species selection. Journal of Theoretical Biology, 2019, 483, 109969.	0.8	10
176	Building blocks of protein structures: Physics meets biology. Physical Review E, 2021, 104, 014402.	0.8	10
177	Constrained proteome allocation affects coexistence in models of competitive microbial communities. ISME Journal, 2021, 15, 1458-1477.	4.4	10
178	Effective Resource Competition Model for Species Coexistence. Physical Review Letters, 2021, 127, 208101.	2.9	10
179	Scattering function for a model of interacting surfaces. Physical Review E, 1993, 47, 411-418.	0.8	9
180	sMean-field theory of sandpiles. Physical Review E, 1997, 55, 1998-2000.	0.8	9

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181	Anisotropic effective interactions in a coarse-grained tube picture of proteins. Proteins: Structure, Function and Bioinformatics, 2002, 49, 246-254.	1.5	9
182	Analysis of noise-induced bimodality in a Michaelis–Menten single-step enzymatic cycle. Physica A: Statistical Mechanics and Its Applications, 2013, 392, 336-342.	1.2	9
183	On entropy production in nonequilibrium systems. Journal of Statistical Mechanics: Theory and Experiment, 2015, 2015, P08014.	0.9	9
184	Scaling Properties of Suboptimal Interfaces. Physical Review Letters, 1996, 77, 5288-5291.	2.9	8
185	Structure-based design of model proteins. , 1998, 31, 10-20.		8
186	Strategies for protein folding and design. Annals of Combinatorics, 1999, 3, 431-450.	0.3	8
187	Tubes near the edge of compactness and folded protein structures *. Journal of Physics Condensed Matter, 2003, 15, S1787-S1796.	0.7	8
188	Scaling Relationships in Agglomeration and Annihilation Models. Physical Review Letters, 1997, 79, 3278-3281.	2.9	7
189	Geometrical model for the native-state folds of proteins. Biophysical Chemistry, 2005, 115, 289-294.	1.5	7
190	What determines the spectrum of protein native state structures? Proteins: Structure, Function and Bioinformatics, 2006, 63, 273-277.	1.5	7
191	Comment on "Revising the distributive networks models of West, Brown and Enquist (1997) and Banavar, Maritan and Rinaldo (1999): Metabolic inequity of living tissues provides clues for the observed allometric scaling rules―by Makarieva, Gorshkov and Li. Journal of Theoretical Biology, 2006, 239, 391-393.	0.8	7
192	Absence of detailed balance in ecology. Europhysics Letters, 2012, 100, 38002.	0.7	7
193	Application of optimal data-based binning method to spatial analysis of ecological datasets. Spatial Statistics, 2016, 16, 137-151.	0.9	7
194	Entropy production in systems with random transition rates close to equilibrium. Physical Review E, 2017, 96, 062110.	0.8	7
195	An optimal procedure to extract interaction potentials for protein folding. Computational Materials Science, 2001, 20, 305-310.	1.4	6
196	Field-induced anti-nematic ordering in assemblies of anisotropically polarizable particles. Europhysics Letters, 2001, 55, 362-368.	0.7	6
197	On network form and function. Physica A: Statistical Mechanics and Its Applications, 2004, 340, 749-755.	1.2	6
198	Partially folded states of HIV-1 protease: Molecular dynamics simulations and ligand binding. Computational and Theoretical Chemistry, 2006, 769, 111-121.	1.5	6

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199	Marginal compactness of protein native structures. Journal of Physics Condensed Matter, 2006, 18, S297-S306.	0.7	6
200	Emergence of Network Motifs in Deep Neural Networks. Entropy, 2020, 22, 204.	1.1	6
201	Coexistence in neutral theories: interplay of criticality and mild local preferences. Journal of Statistical Mechanics: Theory and Experiment, 2015, 2015, P01030.	0.9	6
202	Dynamics of rough surfaces with an arbitrary topology. Physical Review E, 1994, 49, R937-R940.	0.8	5
203	Real-space renormalization group for Langevin dynamics in absence of translational invariance. Journal of Statistical Physics, 1995, 79, 649-668.	0.5	5
204	Optimal path and directed percolation. Physical Review E, 1996, 53, R2029-R2032.	0.8	5
205	Scaling behavior in a nonlocal and nonlinear diffusion equation. Physical Review E, 2000, 62, R5879-R5882.	0.8	5
206	Prediction of protein secondary structures from conformational biases. Proteins: Structure, Function and Bioinformatics, 2002, 48, 558-565.	1.5	5
207	Elucidation of the disulfide-folding pathway of hirudin by a topology-based approach. Proteins: Structure, Function and Bioinformatics, 2003, 53, 720-730.	1.5	5
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