

Amos Maritan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

234
papers

11,914
citations

55
h-index

102
g-index

243
ext. papers

13,347
ext. citations

8
avg, IF

6.27
L-index

#	Paper	IF	Citations
234	Pairing statistics and melting of random DNA oligomers: Finding your partner in superdiverse environments.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010051	5	0
233	Effective Resource Competition Model for Species Coexistence. <i>Physical Review Letters</i> , 2021 , 127, 208101	10.4	3
232	True scale-free networks hidden by finite size effects. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	13
231	Building blocks of protein structures: Physics meets biology. <i>Physical Review E</i> , 2021 , 104, 014402	2.4	1
230	Upscaling human activity data: A statistical ecology approach. <i>PLoS ONE</i> , 2021 , 16, e0253461	3.7	
229	Spontaneous dimensional reduction and ground state degeneracy in a simple chain model. <i>Physical Review E</i> , 2021 , 104, L012101	2.4	
228	Marginally compact phase and ordered ground states in a model polymer with side spheres. <i>Physical Review E</i> , 2021 , 104, L012501	2.4	
227	DNA sequence symmetries from randomness: the origin of the Chargaff's second parity rule. <i>Briefings in Bioinformatics</i> , 2021 , 22, 2172-2181	13.4	2
226	Local sequence-structure relationships in proteins. <i>Protein Science</i> , 2021 , 30, 818-829	6.3	3
225	Scaling of joint mass and metabolism fluctuations in in silico cell-laden spheroids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
224	Constrained proteome allocation affects coexistence in models of competitive microbial communities. <i>ISME Journal</i> , 2021 , 15, 1458-1477	11.9	4
223	Dynamic metabolic adaptation can promote species coexistence in competitive microbial communities. <i>PLoS Computational Biology</i> , 2020 , 16, e1007896	5	19
222	Emergence of Network Motifs in Deep Neural Networks. <i>Entropy</i> , 2020 , 22,	2.8	1
221	Optimal transport from a point-like source. <i>Continuum Mechanics and Thermodynamics</i> , 2020 , 32, 1325-1335	3.5	1
220	On the probabilistic nature of the species-area relation. <i>Journal of Theoretical Biology</i> , 2019 , 462, 391-407	7.3	3
219	Local symmetry determines the phases of linear chains: a simple model for the self-assembly of peptides. <i>Soft Matter</i> , 2019 , 15, 5596-5613	3.6	4
218	Reconciling cooperation, biodiversity and stability in complex ecological communities. <i>Scientific Reports</i> , 2019 , 9, 5580	4.9	11

217	Neutral and niche forces as drivers of species selection. <i>Journal of Theoretical Biology</i> , 2019 , 483, 109969-110000	2.3	4
216	Inferring macro-ecological patterns from local presence/absence data. <i>Oikos</i> , 2019 , 128, 1641-1652	4	4
215	Entropy production in master equations and Fokker-Planck equations: facing the coarse-graining and recovering the information loss. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2019 , 2019, 104013	1.9	8
214	Generalized size scaling of metabolic rates based on single-cell measurements with freshwater phytoplankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 17323-17329	11.5	11
213	The elixir phase of chain molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 176-184	4.2	5
212	Archetypes of human cognition defined by time preference for reward and their brain correlates: An evolutionary trade-off approach. <i>NeuroImage</i> , 2019 , 185, 322-334	7.9	8
211	River landscapes and optimal channel networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 6548-6553	11.5	23
210	Testing a general approach to assess the degree of disturbance in tropical forests. <i>Journal of Vegetation Science</i> , 2017 , 28, 659-668	3.1	7
209	Feasibility and coexistence of large ecological communities. <i>Nature Communications</i> , 2017 , 8,	17.4	63
208	Explorability and the origin of network sparsity in living systems. <i>Scientific Reports</i> , 2017 , 7, 12323	4.9	16
207	Upscaling species richness and abundances in tropical forests. <i>Science Advances</i> , 2017 , 3, e1701438	14.3	20
206	Covariations in ecological scaling laws fostered by community dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 10672-10677	11.5	14
205	Species coexistence in a neutral dynamics with environmental noise. <i>Journal of Theoretical Biology</i> , 2017 , 413, 1-10	2.3	29
204	Entropy production in systems with random transition rates close to equilibrium. <i>Physical Review E</i> , 2017 , 96, 062110	2.4	5
203	Generalized CNS arousal: An elementary force within the vertebrate nervous system. <i>Neuroscience and Biobehavioral Reviews</i> , 2016 , 68, 167-176	9	29
202	Application of optimal data-based binning method to spatial analysis of ecological datasets. <i>Spatial Statistics</i> , 2016 , 16, 137-151	2.2	4
201	Predicting the stability of large structured food webs. <i>Nature Communications</i> , 2015 , 6, 7842	17.4	75
200	Generalized receptor law governs phototaxis in the phytoplankton <i>Euglena gracilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7045-50	11.5	41

199	On entropy production in nonequilibrium systems. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2015 , 2015, P08014	1.9	8
198	New activity pattern in human interactive dynamics. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2015 , 2015, P09006	1.9	2
197	Resilience and reactivity of global food security. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6902-7	11.5	128
196	Sample and population exponents of generalized Taylor's law. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7755-60	11.5	45
195	Effect of localization on the stability of mutualistic ecological networks. <i>Nature Communications</i> , 2015 , 6, 10179	17.4	51
194	Towards a unified descriptive theory for spatial ecology: predicting biodiversity patterns across spatial scales. <i>Methods in Ecology and Evolution</i> , 2015 , 6, 324-332	7.7	43
193	Coexistence in neutral theories: interplay of criticality and mild local preferences. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2015 , 2015, P01030	1.9	6
192	Disentangling the effect of hybrid interactions and of the constant effort hypothesis on ecological community stability. <i>Oikos</i> , 2014 , 123, 525-532	4	38
191	Time to Absorption for a Heterogeneous Neutral Competition Model. <i>Journal of Statistical Physics</i> , 2014 , 156, 119-130	1.5	4
190	Diffusion of tagged particles in a crowded medium. <i>Europhysics Letters</i> , 2014 , 107, 20006	1.6	11
189	Information-based fitness and the emergence of criticality in living systems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10095-100	11.5	108
188	Form, function, and evolution of living organisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 3332-7	11.5	46
187	Evolution and selection of river networks: statics, dynamics, and complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2417-24	11.5	100
186	Emergence of structural and dynamical properties of ecological mutualistic networks. <i>Nature</i> , 2013 , 500, 449-52	50.4	170
185	Flory theory for polymers. <i>Journal of Physics Condensed Matter</i> , 2013 , 25, 503101	1.8	44
184	Scaling body size fluctuations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 4646-50	11.5	59
183	Analysis of noise-induced bimodality in a Michaelis-Menten single-step enzymatic cycle. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2013 , 392, 336-342	3.3	6
182	An allometry-based approach for understanding forest structure, predicting tree-size distribution and assessing the degree of disturbance. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013 , 280, 20122375	4.4	30

181	From cellular characteristics to disease diagnosis: uncovering phenotypes with supercells. <i>PLoS Computational Biology</i> , 2013 , 9, e1003215	5	28
180	Growth or reproduction: emergence of an evolutionary optimal strategy. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013 , 2013, P10020	1.9	2
179	Water-controlled wealth of nations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 4230-3	11.5	91
178	The effect of quenched disorder in neutral theories. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2013 , 2013, P04032	1.9	14
177	Human mobility in a continuum approach. <i>PLoS ONE</i> , 2013 , 8, e60069	3.7	57
176	On species persistence-time distributions. <i>Journal of Theoretical Biology</i> , 2012 , 303, 15-24	2.3	25
175	Inverse problem for multivariate time series using dynamical latent variables. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2012 , 391, 3159-3169	3.3	1
174	Scale invariance in the dynamics of spontaneous behavior. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 10564-9	11.5	78
173	Spatial aggregation and the species-area relationship across scales. <i>Journal of Theoretical Biology</i> , 2012 , 313, 87-97	2.3	20
172	Absence of detailed balance in ecology. <i>Europhysics Letters</i> , 2012 , 100, 38002	1.6	5
171	Protein Sequence and Structure: Is One More Fundamental than the Other?. <i>Journal of Statistical Physics</i> , 2012 , 148, 637-646	1.5	4
170	A universal model for mobility and migration patterns. <i>Nature</i> , 2012 , 484, 96-100	50.4	760
169	An exactly solvable coarse-grained model for species diversity. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2012 , 2012, P07017	1.9	4
168	Spatial effects on species persistence and implications for biodiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 4346-51	11.5	55
167	Self-similarity and scaling in forest communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 7658-62	11.5	23
166	A general basis for quarter-power scaling in animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 15816-20	11.5	133
165	Exploring the universe of protein structures beyond the Protein Data Bank. <i>PLoS Computational Biology</i> , 2010 , 6, e1000957	5	50
164	Simplified exactly solvable model for amyloid aggregation. <i>Physical Review Letters</i> , 2010 , 105, 108102	7.4	13

163	Predicting spatial similarity of freshwater fish biodiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 7058-62	11.5	18
162	First-principles design of nanomachines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6900-3	11.5	18
161	Inferring species interactions in tropical forests. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 13854-9	11.5	81
160	Phase diagrams for DNA denaturation under stretching forces. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, L04001	1.9	10
159	Microseconds dynamics simulations of the outer-membrane protease T. <i>Biophysical Journal</i> , 2008 , 94, 71-8	2.9	40
158	Incipient criticality in ecological communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18714-7	11.5	12
157	Self-templated nucleation in peptide and protein aggregation. <i>Physical Review Letters</i> , 2008 , 101, 258101	7.4	77
156	Structural motifs of biomolecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 17283-6	11.5	28
155	Patterns of relative species abundance in rainforests and coral reefs. <i>Nature</i> , 2007 , 450, 45-9	50.4	198
154	Aggregation of natively folded proteins: a theoretical approach. <i>Journal of Physics Condensed Matter</i> , 2007 , 19, 285221	1.8	4
153	Symmetry, shape, and order. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 19187-92	11.5	11
152	Marginal compactness of protein native structures. <i>Journal of Physics Condensed Matter</i> , 2006 , 18, S297-S306	5.3	5
151	Insight into the structure of amyloid fibrils from the analysis of globular proteins. <i>PLoS Computational Biology</i> , 2006 , 2, e170	5	167
150	A backbone-based theory of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 16623-33	11.5	355
149	Common attributes of native-state structures of proteins, disordered proteins, and amyloid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 6883-8	11.5	44
148	Using the principle of entropy maximization to infer genetic interaction networks from gene expression patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 19033-8	11.5	172
147	The origami of life. <i>Journal of Physics Condensed Matter</i> , 2006 , 18, 847-888	1.8	9
146	What determines the spectrum of protein native state structures?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 273-7	4.2	7

145	Comparing models of species abundance (Reply). <i>Nature</i> , 2006 , 441, E1-E2	50.4	10
144	Dynamical evolution of ecosystems. <i>Nature</i> , 2006 , 444, 926-8	50.4	93
143	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. <i>Journal of Theoretical Biology</i> , 2006 , 239, 391-3	2.3	7
142	Partially folded states of HIV-1 protease: Molecular dynamics simulations and ligand binding. <i>Computational and Theoretical Chemistry</i> , 2006 , 769, 111-121		3
141	A Novel Ensemble in Statistical Physics. <i>Journal of Statistical Physics</i> , 2006 , 123, 167-180	1.5	2
140	Linear One-Step Processes with Artificial Boundaries. <i>Journal of Statistical Physics</i> , 2006 , 125, 491-511	1.5	2
139	Non-neutral vegetation dynamics. <i>PLoS ONE</i> , 2006 , 1, e78	3.7	16
138	Coarse-grained model of proteins incorporating atomistic detail of the active site. <i>Physical Review Letters</i> , 2005 , 95, 218102	7.4	138
137	Species lifetime distribution for simple models of ecologies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15747-51	11.5	57
136	Proteins and polymers. <i>Journal of Chemical Physics</i> , 2005 , 122, 234910	3.9	11
135	Characterization and modeling of protein-protein interaction networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2005 , 352, 1-27	3.3	56
134	Geometrical model for the native-state folds of proteins. <i>Biophysical Chemistry</i> , 2005 , 115, 289-94	3.5	6
133	Density dependence explains tree species abundance and diversity in tropical forests. <i>Nature</i> , 2005 , 438, 658-61	50.4	250
132	A new interpolation formula for semiflexible polymers. <i>Biophysical Chemistry</i> , 2005 , 115, 251-4	3.5	16
131	Physics of thick polymers. <i>Journal of Polymer Science, Part B: Polymer Physics</i> , 2005 , 43, 650-679	2.6	19
130	What determines the structures of native folds of proteins?. <i>Journal of Physics Condensed Matter</i> , 2005 , 17, S1515-S1522	1.8	4
129	Pretransitional behavior of a water in liquid crystal microemulsion close to the demixing transition: evidence for intermicellar attraction mediated by paranematic fluctuations. <i>Journal of Chemical Physics</i> , 2005 , 122, 214721	3.9	17
128	Lattice tube model of proteins. <i>Physical Review Letters</i> , 2004 , 93, 238101	7.4	22

127	Organization of ecosystems in the vicinity of a novel phase transition. <i>Physical Review Letters</i> , 2004 , 92, 218703	7.4	15
126	Network structures from selection principles. <i>Physical Review Letters</i> , 2004 , 92, 198701	7.4	56
125	Unified perspective on proteins: a physics approach. <i>Physical Review E</i> , 2004 , 70, 041905	2.4	54
124	Geometry and symmetry prescript the free-energy landscape of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 7960-4	11.5	169
123	Accurate and efficient description of protein vibrational dynamics: comparing molecular dynamics and Gaussian models. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 635-45	4.2	146
122	Recognition of coarse-grained protein tertiary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 55, 536-47	4.2	2
121	On network form and function. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2004 , 340, 749-755	3.3	6
120	What can one learn from experiments about the elusive transition state?. <i>Protein Science</i> , 2004 , 13, 2446-57	6.57	23
119	Simulations of action of DNA topoisomerases to investigate boundaries and shapes of spaces of knots. <i>Biophysical Journal</i> , 2004 , 87, 2968-75	2.9	42
118	Coarse grained models: the kinetics of motor proteins. <i>Computational Materials Science</i> , 2004 , 30, 172-179	3.2	2
117	Modeling of Protein Interaction Networks. <i>Complexus</i> , 2003 , 1, 38-44		298
116	Tubes near the edge of compactness and folded protein structures *. <i>Journal of Physics Condensed Matter</i> , 2003 , 15, S1787-S1796	1.8	7
115	Geometry of Compact Tubes and Protein Structures. <i>Complexus</i> , 2003 , 1, 4-13		21
114	A knowledge-based scale for amino acid membrane propensity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 50, 114-21	4.2	24
113	Self-Interactions of Strands and Sheets. <i>Journal of Statistical Physics</i> , 2003 , 110, 35-50	1.5	35
112	A comment on the protein folds as platonic forms. <i>Journal of Theoretical Biology</i> , 2003 , 223, 263-5	2.3	3
111	Assembly of protein tertiary structures from secondary structures using optimized potentials. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 52, 155-65	4.2	13
110	Elucidation of the disulfide-folding pathway of hirudin by a topology-based approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003 , 53, 720-30	4.2	5

109	Neutral theory and relative species abundance in ecology. <i>Nature</i> , 2003 , 424, 1035-7	50.4	563
108	Physiology: Allometric cascades. <i>Nature</i> , 2003 , 421, 713-4; discussion 714	50.4	57
107	Global protein function prediction from protein-protein interaction networks. <i>Nature Biotechnology</i> , 2003 , 21, 697-700	44.5	494
106	Elasticity of Semiflexible Polymers with and without Self-Interactions. <i>Macromolecules</i> , 2003 , 36, 10095-10102	35.102	38
105	Colloquium: Geometrical approach to protein folding: a tube picture. <i>Reviews of Modern Physics</i> , 2003 , 75, 23-34	40.5	82
104	Geometry and physics of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 47, 315-22	4.2	61
103	Prediction of protein secondary structures from conformational biases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 558-65	4.2	5
102	Anisotropic effective interactions in a coarse-grained tube picture of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 49, 246-54	4.2	8
101	Crucial stages of protein folding through a solvable model: predicting target sites for enzyme-inhibiting drugs. <i>Protein Science</i> , 2002 , 11, 1878-87	6.3	16
100	Force dependent transition rates in chemical kinetics models for motor proteins. <i>Journal of Chemical Physics</i> , 2002 , 117, 10339-10349	3.9	10
99	Supply-demand balance and metabolic scaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 10506-9	11.5	172
98	Multiple Steering Molecular Dynamics Applied to Water Exchange at Alkali Ions. <i>Journal of Physical Chemistry B</i> , 2002 , 106, 13027-13032	3.4	15
97	The intracellular antibody capture technology (IACT): towards a consensus sequence for intracellular antibodies. <i>Journal of Molecular Biology</i> , 2002 , 317, 73-83	6.5	118
96	Energy landscape and native-state structure of proteins: a simplified model. <i>Europhysics Letters</i> , 2002 , 58, 623-629	1.6	27
95	Elastic properties of proteins: insight on the folding process and evolutionary selection of native structures. <i>Journal of Molecular Biology</i> , 2002 , 321, 909-21	6.5	54
94	Folding pathways of prion and doppel. <i>Biophysical Journal</i> , 2002 , 83, 3533-41	2.9	39
93	Network allometry. <i>Geophysical Research Letters</i> , 2002 , 29, 3-1	4.9	46
92	Molecular dynamics studies on HIV-1 protease: Drug resistance and folding pathways. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 43, 365-372	4.2	33

91	Learning effective amino acid interactions through iterative stochastic techniques. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 422-31	4.2	45
90	Computational approach to the protein-folding problem. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 433-435	4.2	16
89	Scaling, Optimality, and Landscape Evolution. <i>Journal of Statistical Physics</i> , 2001 , 104, 1-48	1.5	79
88	Protein threading by learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 14350-5	11.5	24
87	Dynamic modeling of gene expression data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 1693-8	11.5	24 ⁰
86	Field-induced anti-nematic ordering in assemblies of anisotropically polarizable particles. <i>Europhysics Letters</i> , 2001 , 55, 362-368	1.6	4
85	Amino acid classes and the protein folding problem. <i>Journal of Chemical Physics</i> , 2001 , 114, 1420-1423	3.9	25
84	Force dependence of the Michaelis constant in a two-state ratchet model for molecular motors. <i>Physical Review Letters</i> , 2001 , 86, 1134-7	7.4	23
83	Role of native-state topology in the stabilization of intracellular antibodies. <i>Biophysical Journal</i> , 2001 , 81, 2935-45	2.9	10
82	A self-consistent knowledge-based approach to protein design. <i>Biophysical Journal</i> , 2001 , 80, 480-90	2.9	17
81	An optimal procedure to extract interaction potentials for protein folding. <i>Computational Materials Science</i> , 2001 , 20, 305-310	3.2	5
80	Computational approach to the protein-folding problem 2001 , 42, 433		2
79	Scoring functions in protein folding and design. <i>Protein Science</i> , 2000 , 9, 812-9	6.3	14
78	Recurrent oligomers in proteins: an optimal scheme reconciling accurate and concise backbone representations in automated folding and design studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 40, 662-74	4.2	60
77	Optimal shapes of compact strings. <i>Nature</i> , 2000 , 406, 287-90	50.4	239
76	reply: Rivers, blood and transportation networks. <i>Nature</i> , 2000 , 408, 160-160	50.4	9
75	Fundamental patterns underlying gene expression profiles: simplicity from complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 8409-14	11.5	375
74	Deciphering the folding kinetics of transmembrane helical proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 14229-34	11.5	10

73	A novel iterative strategy for protein design. <i>Journal of Chemical Physics</i> , 2000 , 112, 2050-2055	3.9	10
72	Topology of the fittest transportation network. <i>Physical Review Letters</i> , 2000 , 84, 4745-8	7.4	99
71	Role of secondary motifs in fast folding polymers: a dynamical variational principle. <i>Physical Review Letters</i> , 2000 , 84, 3009-12	7.4	31
70	Extraction of interaction potentials between amino acids from native protein structures. <i>Journal of Chemical Physics</i> , 2000 , 112, 9151-9166	3.9	26
69	Scaling behavior in a nonlocal and nonlinear diffusion equation. <i>Physical Review E</i> , 2000 , 62, R5879-82	2.4	4
68	Compactness, aggregation, and prionlike behavior of protein: A lattice model study. <i>Journal of Chemical Physics</i> , 2000 , 113, 5072	3.9	38
67	Finite Size Scaling in Ecology. <i>Physical Review Letters</i> , 1999 , 83, 4212-4214	7.4	33
66	Depletion forces in hard-sphere colloids. <i>Physical Review E</i> , 1999 , 59, R1339-R1342	2.4	14
65	Protein Structures and Optimal Folding from a Geometrical Variational Principle. <i>Physical Review Letters</i> , 1999 , 82, 3372-3375	7.4	119
64	A comparative study of existing and new design techniques for protein models. <i>Journal of Chemical Physics</i> , 1999 , 110, 9730-9738	3.9	16
63	Optimal paths and growth processes. <i>Physica A: Statistical Mechanics and Its Applications</i> , 1999 , 266, 291-298	3.9	2
62	Size and form in efficient transportation networks. <i>Nature</i> , 1999 , 399, 130-2	50.4	591
61	Strategies for protein folding and design. <i>Annals of Combinatorics</i> , 1999 , 3, 431-450	0.7	8
60	Folding Lennard-Jones proteins by a contact potential. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999 , 37, 544-53	4.2	19
59	Determination of interaction potentials of amino acids from native protein structures: Tests on simple lattice models. <i>Journal of Chemical Physics</i> , 1999 , 110, 10123-10133	3.9	28
58	Models of Fractal River Basins. <i>Journal of Statistical Physics</i> , 1998 , 91, 1-15	1.5	44
57	Interaction potentials for protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 30, 244-252	4.2	32
56	Structure-based design of model proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 31, 10-20	2.0	7

55	Scale Invariant Correlations in a Driven Dissipative Gas. <i>Physical Review Letters</i> , 1998 , 80, 4410-4413	7.4	27
54	Folding, Design, and Determination of Interaction Potentials Using Off-Lattice Dynamics of Model Heteropolymers. <i>Physical Review Letters</i> , 1998 , 81, 3287-3290	7.4	46
53	Variational Approach to Protein Design and Extraction of Interaction Potentials. <i>Physical Review Letters</i> , 1998 , 81, 2172-2175	7.4	33
52	Bethe approximation for a semiflexible polymer chain. <i>Physical Review E</i> , 1998 , 58, R5241-R5244	2.4	26
51	Steric Constraints in Model Proteins. <i>Physical Review Letters</i> , 1998 , 80, 5683-5686	7.4	23
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1 Building blocks of protein structures [Physics meets Biology

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