Peter G Wolynes

List of Publications by Citations

234 papers	18,642 citations	68 h-index	132 g-index
258 ext. papers	20,654 ext. citations	7.6 avg, IF	7.12 L-index

#	Paper	IF	Citations
234	Funnels, pathways, and the energy landscape of protein folding: a synthesis. *Proteins: Structure, Function and Bioinformatics*, **1995**, 21, 167-95	4.2	2175
233	Theory of protein folding: the energy landscape perspective. *Annual Review of Physical Chemistry*, **1997**, 48, 545-600	15.7	1719
232	Theory of protein folding. *Current Opinion in Structural Biology*, **2004**, 14, 70-5	8.1	992
231	Intermediates and barrier crossing in a random energy model (with applications to protein folding). *The Journal of Physical Chemistry*, **1989**, 93, 6902-6915		664
230	Theory of structural glasses and supercooled liquids. *Annual Review of Physical Chemistry*, **2007**, 58, 235-66	15.7	589
229	The hinge-bending mode in lysozyme. *Nature*, **1976**, 262, 325-6	50.4	324
228	Protein topology determines binding mechanism. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 511-6	11.5	297
227	Protein folding funnels: the nature of the transition state ensemble. *Folding & Design*, **1996**, 1, 441-50		277
226	Water in protein structure prediction. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 3352-7	11.5	263
225	Multiple-basin energy landscapes for large-amplitude conformational motions of proteins: Structure-based molecular dynamics simulations. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 11844-9	11.5	247
224	Microscopic theory of heterogeneity and nonexponential relaxations in supercooled liquids. *Physical Review Letters*, **2001**, 86, 5526-9	7.4	246
223	Stochastic gene expression as a many-body problem. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 2374-9	11.5	233
222	The experimental survey of protein-folding energy landscapes. *Quarterly Reviews of Biophysics*, **2005**, 38, 245-88	7	232
221	Localizing frustration in native proteins and protein assemblies. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 19819-24	11.5	226
220	The shapes of cooperatively rearranging regions in glass-forming liquids. *Nature Physics*, **2006**, 2, 268-274	6.2	217
219	Stripe glasses: self-generated randomness in a uniformly frustrated system. *Physical Review Letters*, **2000**, 85, 836-9	7.4	185
218	AWSEM-MD: protein structure prediction using coarse-grained physical potentials and bioinformatically based local structure biasing. *Journal of Physical Chemistry B*, **2012**, 116, 8494-503	3.4	184

217	Chemical Dynamics in Solution. *Physics Today*, **1990**, 43, 36-43	0.9	182
216	P versus Q: structural reaction coordinates capture protein folding on smooth landscapes. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 586-91	11.5	179
215	Transferable model for chromosome architecture. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 12168-12173	11.5	179
214	Protein folding mechanisms and the multidimensional folding funnel. *Proteins: Structure, Function and Bioinformatics*, **1998**, 32, 136-158	4.2	174
213	Frustration in biomolecules. *Quarterly Reviews of Biophysics*, **2014**, 47, 285-363	7	168
212	Fly-casting in protein-DNA binding: frustration between protein folding and electrostatics facilitates target recognition. *Journal of the American Chemical Society*, **2007**, 129, 738-9	16.4	168
211	Role of water mediated interactions in protein-protein recognition landscapes. *Journal of the American Chemical Society*, **2003**, 125, 9170-8	16.4	158
210	Microscopic theory of protein folding rates. II. Local reaction coordinates and chain dynamics. *Journal of Chemical Physics*, **2001**, 114, 5082-5096	3.9	158
209	A simple statistical field theory of heteropolymer collapse with application to protein folding. *Biopolymers*, **1990**, 30, 177-188	2.2	158
208	Domain swapping is a consequence of minimal frustration. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 13786-91	11.5	152
207	Theory of aging in structural glasses. *Journal of Chemical Physics*, **2004**, 121, 2852-65	3.9	146
206	Statistical mechanics of a correlated energy landscape model for protein folding funnels. *Journal of Chemical Physics*, **1997**, 106, 2932-2948	3.9	140
205	Quantum localization and energy flow in many-dimensional Fermi resonant systems. *Journal of Chemical Physics*, **1990**, 93, 4994-5012	3.9	140
204	Energy landscapes and solved protein-folding problems. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2005**, 363, 453-64; discussion 464-7	3	135
203	On the surface of glasses. *Journal of Chemical Physics*, **2008**, 129, 234514	3.9	133
202	Absolute rate theories of epigenetic stability. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 18926-31	11.5	128
201	On the role of frustration in the energy landscapes of allosteric proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 3499-503	11.5	127
200	Frustration, specific sequence dependence, and nonlinearity in large-amplitude fluctuations of allosteric proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 3504-9	11.5	125

199	De novo prediction of human chromosome structures: Epigenetic marking patterns encode genome architecture. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 12126-12131	11.5	122
198	Topology, structures, and energy landscapes of human chromosomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 6062-7	11.5	121
197	Barrier softening near the onset of nonactivated transport in supercooled liquids: Implications for establishing detailed connection between thermodynamic and kinetic anomalies in supercooled liquids. *Journal of Chemical Physics*, **2003**, 119, 9088-9105	3.9	112
196	The origin of the boson peak and thermal conductivity plateau in low-temperature glasses. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 1515-8	11.5	111
195	Protein Frustratometer 2: a tool to localize energetic frustration in protein molecules, now with electrostatics. *Nucleic Acids Research*, **2016**, 44, W356-60	20.1	110
194	Evolution, energy landscapes and the paradoxes of protein folding. *Biochimie*, **2015**, 119, 218-30	4.6	109
193	Protein frustratometer: a tool to localize energetic frustration in protein molecules. *Nucleic Acids Research*, **2012**, 40, W348-51	20.1	109
192	Microscopic theory of protein folding rates. I. Fine structure of the free energy profile and folding routes from a variational approach. *Journal of Chemical Physics*, **2001**, 114, 5069-5081	3.9	96
191	Simple energy landscape model for the kinetics of functional transitions in proteins. *Journal of Physical Chemistry B*, **2005**, 109, 1959-69	3.4	94
190	Coevolutionary information, protein folding landscapes, and the thermodynamics of natural selection. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 12408-13	11.5	90
189	A universal origin for secondary relaxations in supercooled liquids and structural glasses. *Nature Physics*, **2009**, 6, 62-68	16.2	90
188	Self-consistent proteomic field theory of stochastic gene switches. *Biophysical Journal*, **2005**, 88, 828-50	2.9	89
187	Predictive energy landscapes for protein-protein association. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 19244-9	11.5	87
186	Facilitation, complexity growth, mode coupling, and activated dynamics in supercooled liquids. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 16077-82	11.5	87
185	Intrinsic quantum excitations of low temperature glasses. *Physical Review Letters*, **2001**, 87, 195901	7.4	86
184	Correlated energy landscape model for finite, random heteropolymers. *Physical Review E*, **1996**, 53, 6271-6296	2.4	85
183	Symmetry and frustration in protein energy landscapes: a near degeneracy resolves the Rop dimer-folding mystery. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 2373-8	11.5	83
182	Dynamical orientation correlations in solution. *Journal of Chemical Physics*, **1977**, 67, 733-741	3.9	82

181	Some quantum weirdness in physiology. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 17247-8	11.5	79
180	Slip boundary conditions and the hydrodynamic effect on diffusion controlled reactions. *Journal of Chemical Physics*, **1976**, 65, 450-454	3.9	79
179	Exploring the aggregation free energy landscape of the amyloid-β protein (1-40). *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 11835-11840	11.5	79
178	Quantum energy flow during molecular isomerization. *Chemical Physics Letters*, **1997**, 280, 411-418	2.5	78
177	Exploring the Free Energy Landscape of Nucleosomes. *Journal of the American Chemical Society*, **2016**, 138, 8126-33	16.4	77
176	Anomalous diffusion, spatial coherence, and viscoelasticity from the energy landscape of human chromosomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 7753-7758	11.5	77
175	Consequences of localized frustration for the folding mechanism of the IM7 protein. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 19825-30	11.5	76
174	Optimizing physical energy functions for protein folding. *Proteins: Structure, Function and Bioinformatics*, **2004**, 54, 88-103	4.2	76
173	Stem cell differentiation as a many-body problem. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 10185-90	11.5	75
172	A funneled energy landscape for cytochrome c directly predicts the sequential folding route inferred from hydrogen exchange experiments. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 12401-6	11.5	75
171	Mosaic energy landscapes of liquids and the control of protein conformational dynamics by glass-forming solvents. *Journal of Physical Chemistry B*, **2005**, 109, 7488-99	3.4	70
170	Role of explicitly cooperative interactions in protein folding funnels: A simulation study. *Journal of Chemical Physics*, **2001**, 114, 4702	3.9	69
169	Diffusion and the Mesoscopic Hydrodynamics of Supercooled Liquids. *Journal of Physical Chemistry B*, **2001**, 105, 6570-6573	3.4	69
168	Frustration in the energy landscapes of multidomain protein misfolding. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 1680-5	11.5	68
167	A scaling perspective on quantum energy flow in molecules. *Journal of Chemical Physics*, **1993**, 98, 1123-1131	3.9	68
166	The foldon universe: a survey of structural similarity and self-recognition of independently folding units. *Journal of Molecular Biology*, **1997**, 272, 95-105	6.5	66
165	Generalized protein tertiary structure recognition using associative memory Hamiltonians. *Journal of Molecular Biology*, **1991**, 222, 1013-34	6.5	65
164	Capillarity theory for the fly-casting mechanism. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 2746-50	11.5	63

163	Self-generated randomness, defect wandering, and viscous flow in stripe glasses. *Physical Review B*, **2001**, 64,	3.3	63
162	Active contractility in actomyosin networks. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 6446-51	11.5	62
161	Comparing the Aggregation Free Energy Landscapes of Amyloid Beta(1-42) and Amyloid Beta(1-40). *Journal of the American Chemical Society*, **2017**, 139, 16666-16676	16.4	61
160	The ultimate fate of supercooled liquids. *Journal of Physical Chemistry A*, **2011**, 115, 3713-9	2.8	61
159	Energy landscapes, glass transitions, and chemical reaction dynamics in biomolecular or solvent environment. *Journal of Chemical Physics*, **1993**, 98, 2218-2224	3.9	61
158	Quantitative criteria for native energetic heterogeneity influences in the prediction of protein folding kinetics. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 434-9	11.5	59
157	Vibrational Mixing and Energy Flow in Polyatomics: Quantitative Prediction Using Local Random Matrix Theory. *Journal of Physical Chemistry A*, **1997**, 101, 541-548	2.8	59
156	Exploring structures in protein folding funnels with free energy functionals: the denatured ensemble. *Journal of Molecular Biology*, **1999**, 287, 657-74	6.5	58
155	Local conformational signals and the statistical thermodynamics of collapsed helical proteins. *Journal of Molecular Biology*, **1996**, 257, 199-216	6.5	58
154	Vibrational relaxation and energy localization in polyatomics: Effects of high-order resonances on flow rates and the quantum ergodicity transition. *Journal of Chemical Physics*, **1996**, 105, 11226-11236	3.9	58
153	Electrostatics, structure prediction, and the energy landscapes for protein folding and binding. *Protein Science*, **2016**, 25, 255-69	6.3	55
152	Communication: Effective temperature and glassy dynamics of active matter. *Journal of Chemical Physics*, **2011**, 135, 051101	3.9	55
151	Prediction of native-state hydrogen exchange from perfectly funneled energy landscapes. *Journal of the American Chemical Society*, **2011**, 133, 17463-72	16.4	54
150	Effective temperature in stochastic kinetics and gene networks. *Biophysical Journal*, **2006**, 91, 84-94	2.9	54
149	Helix-Coil, Liquid Crystal, and Spin Glass Transitions of a Collapsed Heteropolymer. *The Journal of Physical Chemistry*, **1995**, 99, 2177-2185		54
148	Folding funnels: the key to robust protein structure prediction. *Journal of Computational Chemistry*, **2002**, 23, 138-46	3.5	53
147	Molecular stripping in the NF-B/IB/DNA genetic regulatory network. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 110-5	11.5	52
146	Chemical physics of protein folding. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 17770-1	11.5	52

145	Electrostatic effects on funneled landscapes and structural diversity in denatured protein ensembles. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 1796-801	11.5	52
144	Stochastic dynamic models of curve crossing phenomena in condensed phases. *Journal of Chemical Physics*, **1987**, 86, 3836-3844	3.9	52
143	Many-dimensional quantum energy flow at low energy. *Physical Review Letters*, **1996**, 76, 216-219	7.4	51
142	Statistical mechanical refinement of protein structure prediction schemes: Cumulant expansion approach. *Journal of Chemical Physics*, **2002**, 117, 4602-4615	3.9	49
141	AWSEM-IDP: A Coarse-Grained Force Field for Intrinsically Disordered Proteins. *Journal of Physical Chemistry B*, **2018**, 122, 11115-11125	3.4	48
140	Activated events in glasses: The structure of entropic droplets. *Physical Review B*, **2005**, 72,	3.3	48
139	Spatiotemporal structures in aging and rejuvenating glasses. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 1353-8	11.5	47
138	Statistical Mechanics of the Combinatorial Synthesis and Analysis of Folding Macromolecules. *Journal of Physical Chemistry B*, **1997**, 101, 8375-8389	3.4	47
137	Conformational switching upon phosphorylation: a predictive framework based on energy landscape principles. *Biochemistry*, **2008**, 47, 2110-22	3.2	46
136	Learning To Fold Proteins Using Energy Landscape Theory. *Israel Journal of Chemistry*, **2014**, 54, 1311-1337	3.4	44
135	On the strength of glasses. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 16068-72	11.5	44
134	Frustration, function and folding. *Current Opinion in Structural Biology*, **2018**, 48, 68-73	8.1	43
133	Quantization of the Stochastic Pump Model of Arnold Diffusion. *Physical Review Letters*, **1997**, 79, 55-58	7.4	42
132	The folding energy landscape and phosphorylation: modeling the conformational switch of the NFAT regulatory domain. *FASEB Journal*, **2005**, 19, 1389-95	0.9	41
131	Aggregation landscapes of Huntingtin exon 1 protein fragments and the critical repeat length for the onset of Huntington's disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 4406-4411	11.5	40
130	Bridging the gap between the mode coupling and the random first order transition theories of structural relaxation in liquids. *Physical Review E*, **2005**, 72, 031509	2.4	40
129	On the spontaneous collective motion of active matter. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 15184-9	11.5	39
128	Dynamical heterogeneity of the glassy state. *Journal of Physical Chemistry B*, **2014**, 118, 7835-47	3.4	38

127	Free energy landscapes for initiation and branching of protein aggregation. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 20515-20	11.5	38
126	Associative memory Hamiltonians for structure prediction without homology: alpha/beta proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 1679-84	11.5	38
125	Protein structure prediction using basin-hopping. *Journal of Chemical Physics*, **2008**, 128, 225106	3.9	37
124	On the hydrodynamics of swimming enzymes. *Journal of Chemical Physics*, **2015**, 143, 165101	3.9	36
123	Protein Structure Prediction: The Next Generation. *Journal of Chemical Theory and Computation*, **2006**, 2, 705-16	6.4	36
122	Shape Transitions and Chiral Symmetry Breaking in the Energy Landscape of the Mitotic Chromosome. *Physical Review Letters*, **2016**, 116, 248101	7.4	34
121	Latest folding game results: protein A barely frustrates computationalists. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 6837-8	11.5	34
120	Genomic Energy Landscapes. *Biophysical Journal*, **2017**, 112, 427-433	2.9	33
119	Tensegrity and motor-driven effective interactions in a model cytoskeleton. *Journal of Chemical Physics*, **2012**, 136, 145102	3.9	33
118	Entropy Crises in Glasses and Random Heteropolymers. *Journal of Research of the National Institute of Standards and Technology*, **1997**, 102, 187-194	1.3	33
117	Theory, simulations, and experiments show that proteins fold by multiple pathways. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E9759-E9760	11.5	32
116	The Random First-Order Transition Theory of Glasses: A Critical Assessment **2012**, 31-113		32
115	Restriction versus guidance in protein structure prediction. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 15302-7	11.5	32
114	Role of topology, nonadditivity, and water-mediated interactions in predicting the structures of alpha/beta proteins. *Journal of the American Chemical Society*, **2006**, 128, 5168-76	16.4	32
113	The spectrum of biomolecular states and motions. *HFSP Journal*, **2008**, 2, 307-13		31
112	Predictive energy landscapes for folding α-helical transmembrane proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 11031-6	11.5	30
111	Scanning malleable transition state ensembles: comparing theory and experiment for folding protein U1A. *Biochemistry*, **2005**, 44, 6433-9	3.2	30
110	Complementary Variational Approximations for Intermittency and Reaction Dynamics in Fluctuating Environments. *Journal of Physical Chemistry A*, **1999**, 103, 10602-10610	2.8	30

109	Local frustration around enzyme active sites. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 4037-4043	11.5	30
108	Molecular Mechanism of Facilitated Dissociation of Fis Protein from DNA. *Journal of the American Chemical Society*, **2016**, 138, 13497-13500	16.4	29
107	Quantum theory of enhanced unimolecular reaction rates below the ergodicity threshold. *Chemical Physics*, **2006**, 329, 163-167	2.3	28
106	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. *Accounts of Chemical Research*, **2021**, 54, 1251-1259	24.3	28
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103	Fluctuating mobility generation and transport in glasses. *Physical Review E*, **2013**, 88, 022308	2.4	26
102	Dynamical mean-field theory of quantum stripe glasses. *Physical Review B*, **2003**, 68,	3.3	26
101	The physics of protein folding. *Physics World*, **1999**, 12, 39-44	0.5	26
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99	Establishing the entatic state in folding metallated Pseudomonas aeruginosa azurin. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 3159-64	11.5	25
98	The Aggregation Free Energy Landscapes of Polyglutamine Repeats. *Journal of the American Chemical Society*, **2016**, 138, 15197-15203	16.4	24
97	Energy landscapes of a mechanical prion and their implications for the molecular mechanism of long-term memory. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 5006-11	11.5	23
96	Computational study of many-dimensional quantum vibrational energy redistribution. I. Statistics of the survival probability. *Journal of Chemical Physics*, **1996**, 105, 940-952	3.9	22
95	Protein Folding and Structure Prediction from the Ground Up: The Atomistic Associative Memory, Water Mediated, Structure and Energy Model. *Journal of Physical Chemistry B*, **2016**, 120, 8557-65	3.4	22
94	Microscopically based calculations of the free energy barrier and dynamic length scale in supercooled liquids: the comparative role of configurational entropy and elasticity. *Journal of Physical Chemistry B*, **2013**, 117, 15204-19	3.4	21
93	Phi-value analysis of apo-azurin folding: comparison between experiment and theory. *Biochemistry*, **2006**, 45, 6458-66	3.2	21
92	Water Mediated Interactions and the Protein Folding Phase Diagram in the Temperature-Pressure Plane. *Journal of Physical Chemistry B*, **2015**, 119, 11416-27	3.4	20

91	The Microscopic Quantum Theory of Low Temperature Amorphous Solids. *Advances in Chemical Physics*, **2008**, 95-206		19
90	Protein structure prediction: making AWSEM AWSEM-ER by adding evolutionary restraints. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 2127-2142	4.2	18
89	Resolving the NFB Heterodimer Binding Paradox: Strain and Frustration Guide the Binding of Dimeric Transcription Factors. *Journal of the American Chemical Society*, **2017**, 139, 18558-18566	16.4	18
88	Dichotomous noise models of gene switches. *Journal of Chemical Physics*, **2015**, 143, 195101	3.9	18
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84	Initial events of protein folding from an information-processing viewpoint. *Physical Review A*, **1992**, 46, 5242-5248	2.6	18
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82	Exploring the interplay between fibrillization and amorphous aggregation channels on the energy landscapes of tau repeat isoforms. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 4125-4130	11.5	17
81	The role of atomic level steric effects and attractive forces in protein folding. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 362-73	4.2	17
80	Frustration in Fuzzy Protein Complexes Leads to Interaction Versatility. *Journal of Physical Chemistry B*, **2021**, 125, 2513-2520	3.4	17
79	Assemblies of calcium/calmodulin-dependent kinase II with actin and their dynamic regulation by calmodulin in dendritic spines. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 18937-18942	11.5	17
78	Topological constraints and modular structure in the folding and functional motions of GlpG, an intramembrane protease. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 2098-103	11.5	16
77	Protein Folding and Structure Prediction from the Ground Up II: AAWSEM for Proteins. *Journal of Physical Chemistry B*, **2017**, 121, 3473-3482	3.4	16
76	Discrete kinetic models from funneled energy landscape simulations. *PLoS ONE*, **2012**, 7, e50635	3.7	16
75	Energy landscape underlying spontaneous insertion and folding of an alpha-helical transmembrane protein into a bilayer. *Nature Communications*, **2018**, 9, 4949	17.4	16
74	Statistical mechanical refinement of protein structure prediction schemes. II. Mayer cluster expansion approach. *Journal of Chemical Physics*, **2003**, 118, 8500-8512	3.9	15

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72	Aging, Jamming, and the Limits of Stability of Amorphous Solids. *Journal of Physical Chemistry B*, **2018**, 122, 3280-3295	3.4	15
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70	Glasses and Replicas **2012**, 151-191		14
69	Molecular stripping, targets and decoys as modulators of oscillations in the NF-B/IB/DNA genetic network. *Journal of the Royal Society Interface*, **2016**, 13,	4.1	14
68	PEST Control of Molecular Stripping of NFB from DNA Transcription Sites. *Journal of Physical Chemistry B*, **2016**, 120, 8532-8	3.4	14
67	The interplay of nonlinearity and architecture in equilibrium cytoskeletal mechanics. *Journal of Chemical Physics*, **2011**, 134, 014510	3.9	13
66	Statistical mechanics of a cat's cradle. *New Journal of Physics*, **2006**, 8, 273-273	2.9	13
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64	Solution of local-field equations for self-generated glasses. *Physical Review B*, **2004**, 70,	3.3	13
63	Surveying biomolecular frustration at atomic resolution. *Nature Communications*, **2020**, 11, 5944	17.4	13
62	The role of the Arp2/3 complex in shaping the dynamics and structures of branched actomyosin networks. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 10825-10831	11.5	12
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60	The Nucleome Data Bank: web-based resources to simulate and analyze the three-dimensional genome. *Nucleic Acids Research*, **2021**, 49, D172-D182	20.1	12
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58	Dielectric Spectroscopy of Glassy Dynamics **2012**, 115-149		11
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54	Forging tools for refining predicted protein structures. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 9400-9409	11.5	10
53	Supercooled Liquid Dynamics: Advances and Challenges **2012**, 1-30		10
52	Braiding topology and the energy landscape of chromosome organization proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 1468-1477	11.5	10
51	Template-Guided Protein Structure Prediction and Refinement Using Optimized Folding Landscape Force Fields. *Journal of Chemical Theory and Computation*, **2018**, 14, 6102-6116	6.4	10
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7	FrustratometeR: an R-package to compute local frustration in protein structures, point mutants and MD simulations		1
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