Peter G Wolynes

List of Publications by Year
in descending order

227 papers	22,129 citations	12322 69 h-index	10152 140 g-index
258 all docs	258 docs citations	258 times ranked	11392 citing authors

#	Article	IF	Citations
1	Funnels, pathways, and the energy landscape of protein folding: A synthesis. Proteins: Structure, Function and Bioinformatics, 1995, 21, 167-195.	1.5	2,415
2	THEORY OF PROTEIN FOLDING: The Energy Landscape Perspective. Annual Review of Physical Chemistry, 1997, 48, 545-600.	4.8	1,936
3	Theory of protein folding. Current Opinion in Structural Biology, 2004, 14, 70-75.	2.6	1,140
4	Intermediates and barrier crossing in a random energy model (with applications to protein folding). The Journal of Physical Chemistry, 1989, 93, 6902-6915.	2.9	714
5	Theory of Structural Glasses and Supercooled Liquids. Annual Review of Physical Chemistry, 2007, 58, 235-266.	4.8	683
6	The hinge-bending mode in lysozyme. Nature, 1976, 262, 325-326.	13.7	349
7	Protein topology determines binding mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 511-516.	3.3	318
8	Protein folding funnels: the nature of the transition state ensemble. Folding & Design, 1996, 1, 441-450.	4.5	304
9	From The Cover: Water in protein structure prediction. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3352-3357.	3.3	293
10	Localizing frustration in native proteins and protein assemblies. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19819-19824.	3.3	292
11	Transferable model for chromosome architecture. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12168-12173.	3.3	291
12	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, 11844-11849.	3.3	286
13	AWSEM-MD: Protein Structure Prediction Using Coarse-Grained Physical Potentials and Bioinformatically Based Local Structure Biasing. Journal of Physical Chemistry B, 2012, 116, 8494-8503.	1.2	276
14	Stochastic gene expression as a many-body problem. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2374-2379.	3.3	267
15	Microscopic Theory of Heterogeneity and Nonexponential Relaxations in Supercooled Liquids. Physical Review Letters, 2001, 86, 5526-5529.	2.9	259
16	The experimental survey of protein-folding energy landscapes. Quarterly Reviews of Biophysics, 2005, 38, 245-288.	2.4	254
17	Frustration in biomolecules. Quarterly Reviews of Biophysics, 2014, 47, 285-363.	2.4	253
18	The shapes of cooperatively rearranging regions in glass-forming liquids. Nature Physics, 2006, 2, 268-274.	6.5	245

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19	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, 586-591.	3.3	215
20	Stripe Glasses: Self-Generated Randomness in a Uniformly Frustrated System. Physical Review Letters, 2000, 85, 836-839.	2.9	204
21	Fly-Casting in Proteinâ^'DNA Binding:Â Frustration between Protein Folding and Electrostatics Facilitates Target Recognition. Journal of the American Chemical Society, 2007, 129, 738-739.	6.6	199
22	Chemical Dynamics in Solution. Physics Today, 1990, 43, 36-43.	0.3	194
23	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.	3.3	193
24	Topology, structures, and energy landscapes of human chromosomes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6062-6067.	3.3	190
25	Protein folding mechanisms and the multidimensional folding funnel. Proteins: Structure, Function and Bioinformatics, 1998, 32, 136-158.	1.5	181
26	Role of Water Mediated Interactions in Proteinâ^'Protein Recognition Landscapes. Journal of the American Chemical Society, 2003, 125, 9170-9178.	6.6	177
27	Protein Frustratometer 2: a tool to localize energetic frustration in protein molecules, now with electrostatics. Nucleic Acids Research, 2016, 44, W356-W360.	6.5	176
28	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, 3499-3503.	3.3	165
29	A simple statistical field theory of heteropolymer collapse with application to protein folding. Biopolymers, 1990, 30, 177-188.	1.2	164
30	Microscopic theory of protein folding rates. II. Local reaction coordinates and chain dynamics. Journal of Chemical Physics, 2001, 114, 5082-5096.	1.2	164
31	Domain swapping is a consequence of minimal frustration. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13786-13791.	3.3	164
32	Theory of aging in structural glasses. Journal of Chemical Physics, 2004, 121, 2852-2865.	1.2	157
33	Quantum localization and energy flow in manyâ€dimensional Fermi resonant systems. Journal of Chemical Physics, 1990, 93, 4994-5012.	1.2	154
34	Energy landscapes and solved proteinâ€"folding problems. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 453-467.	1.6	149
35	On the surface of glasses. Journal of Chemical Physics, 2008, 129, 234514.	1.2	148
36	Statistical mechanics of a correlated energy landscape model for protein folding funnels. Journal of Chemical Physics, 1997, 106, 2932-2948.	1.2	145

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37	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, 3504-3509.	3.3	143
38	Evolution, energy landscapes and the paradoxes of protein folding. Biochimie, 2015, 119, 218-230.	1.3	142
39	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, 1515-1518.	3.3	141
40	Protein frustratometer: a tool to localize energetic frustration in protein molecules. Nucleic Acids Research, 2012, 40, W348-W351.	6.5	135
41	Absolute rate theories of epigenetic stability. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18926-18931.	3.3	134
42	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.	3.3	133
43	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, 12408-12413.	3.3	126
44	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.	1.2	120
45	Exploring the Free Energy Landscape of Nucleosomes. Journal of the American Chemical Society, 2016, 138, 8126-8133.	6.6	119
46	Exploring the aggregation free energy landscape of the amyloid-Î² protein (1â€“40). Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11835-11840.	3.3	113
47	Predictive energy landscapes for proteinâ€“protein association. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19244-19249.	3.3	112
48	A universal origin for secondary relaxations in supercooled liquids and structural glasses. Nature Physics, 2010, 6, 62-68.	6.5	108
49	Simple Energy Landscape Model for the Kinetics of Functional Transitions in Proteins. Journal of Physical Chemistry B, 2005, 109, 1959-1969.	1.2	105
50	Stem cell differentiation as a many-body problem. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10185-10190.	3.3	102
51	Self-Consistent Proteomic Field Theory of Stochastic Gene Switches. Biophysical Journal, 2005, 88, 828-850.	0.2	101
52	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.	1.2	99
53	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, 16077-16082.	3.3	94
54	Intrinsic Quantum Excitations of Low Temperature Glasses. Physical Review Letters, 2001, 87, 195901.	2.9	93

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55	Some quantum weirdness in physiology. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17247-17248.	3.3	93
56	AWSEM-IDP: A Coarse-Grained Force Field for Intrinsically Disordered Proteins. Journal of Physical Chemistry B, 2018, 122, 11115-11125.	1.2	90
57	Dynamical orientation correlations in solution. Journal of Chemical Physics, 1977, 67, 733-741.	1.2	88
58	Correlated energy landscape model for finite, random heteropolymers. Physical Review E, 1996, 53, 6271-6296.	0.8	88
59	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, 2373-2378.	3.3	88
60	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. Accounts of Chemical Research, 2021, 54, 1251-1259.	7.6	88
61	Slip boundary conditions and the hydrodynamic effect on diffusion controlled reactions. Journal of Chemical Physics, 1976, 65, 450-454.	1.2	87
62	Comparing the Aggregation Free Energy Landscapes of Amyloid Beta(1â€“42) and Amyloid Beta(1â€“40). Journal of the American Chemical Society, 2017, 139, 16666-16676.	6.6	86
63	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, 19825-19830.	3.3	85
64	Frustration in the energy landscapes of multidomain protein misfolding. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1680-1685.	3.3	85
65	Optimizing physical energy functions for protein folding. Proteins: Structure, Function and Bioinformatics, 2003, 54, 88-103.	1.5	84
66	Quantum energy flow during molecular isomerization. Chemical Physics Letters, 1997, 280, 411-418.	1.2	83
67	Molecular stripping in the NF-ÎºB/IÎºB/DNA genetic regulatory network. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 110-115.	3.3	81
68	Role of explicitly cooperative interactions in protein folding funnels: A simulation study. Journal of Chemical Physics, 2001, 114, 4702.	1.2	80
69	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, 12401-12406.	3.3	80
70	Frustration, function and folding. Current Opinion in Structural Biology, 2018, 48, 68-73.	2.6	78
71	Mosaic Energy Landscapes of Liquids and the Control of Protein Conformational Dynamics by Glass-Forming Solvents. Journal of Physical Chemistry B, 2005, 109, 7488-7499.	1.2	73
72	Capillarity theory for the fly-casting mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2746-2750.	3.3	73

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73	The foldon universe: a survey of structural similarity and self-recognition of independently folding units 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1997, 272, 95-105.	2.0	72
74	Diffusion and the Mesoscopic Hydrodynamics of Supercooled Liquidsâ€. Journal of Physical Chemistry B, 2001, 105, 6570-6573.	1.2	72
75	Active contractility in actomyosin networks. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6446-6451.	3.3	72
76	Generalized protein tertiary structure recognition using associative memory hamiltonians. Journal of Molecular Biology, 1991, 222, 1013-1034.	2.0	71
77	Electrostatics, structure prediction, and the energy landscapes for protein folding and binding. Protein Science, 2016, 25, 255-269.	3.1	71
78	As simple as can be?. Nature Structural and Molecular Biology, 1997, 4, 871-874.	3.6	69
79	A scaling perspective on quantum energy flow in molecules. Journal of Chemical Physics, 1993, 98, 1123-1131.	1.2	68
80	Prediction of Native-State Hydrogen Exchange from Perfectly Funneled Energy Landscapes. Journal of the American Chemical Society, 2011, 133, 17463-17472.	6.6	68
81	Vibrational relaxation and energy localization in polyatomics: Effects of highâ€order resonances on flow rates and the quantum ergodicity transition. Journal of Chemical Physics, 1996, 105, 11226-11236.	1.2	67
82	The Ultimate Fate of Supercooled Liquids. Journal of Physical Chemistry A, 2011, 115, 3713-3719.	1.1	67
83	Self-generated randomness, defect wandering, and viscous flow in stripe glasses. Physical Review B, 2001, 64, .	1.1	66
84	Chemical physics of protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17770-17771.	3.3	66
85	Energy landscapes, glass transitions, and chemical reaction dynamics in biomolecular or solvent environment. Journal of Chemical Physics, 1993, 98, 2218-2224.	1.2	65
86	Exploring structures in protein folding funnels with free energy functionals: the denatured ensemble. Journal of Molecular Biology, 1999, 287, 657-674.	2.0	65
87	Vibrational Mixing and Energy Flow in Polyatomics:Â Quantitative Prediction Using Local Random Matrix Theory. Journal of Physical Chemistry A, 1997, 101, 541-548.	1.1	64
88	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, 434-439.	3.3	64
89	Aggregation landscapes of Huntingtin exon 1 protein fragments and the critical repeat length for the onset of Huntingtonâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4406-4411.	3.3	63
90	Communication: Effective temperature and glassy dynamics of active matter. Journal of Chemical Physics, 2011, 135, 051101.	1.2	62

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91	Local Conformational Signals and the Statistical Thermodynamics of Collapsed Helical Proteins. Journal of Molecular Biology, 1996, 257, 199-216.	2.0	59
92	Associative memory Hamiltonians for structure prediction without homology: Â/Â proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1679-1684.	3.3	59
93	Helix-Coil, Liquid Crystal, and Spin Glass Transitions of a Collapsed Heteropolymer. The Journal of Physical Chemistry, 1995, 99, 2177-2185.	2.9	58
94	Folding funnels: The key to robust protein structure prediction. Journal of Computational Chemistry, 2002, 23, 138-146.	1.5	58
95	Local frustration around enzyme active sites. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4037-4043.	3.3	58
96	Conformational Switching upon Phosphorylation:â€‰ A Predictive Framework Based on Energy Landscape Principles. Biochemistry, 2008, 47, 2110-2122.	1.2	57
97	Learning To Fold Proteins Using Energy Landscape Theory. Israel Journal of Chemistry, 2014, 54, 1311-1337.	1.0	57
98	Many-Dimensional Quantum Energy Flow at Low Energy. Physical Review Letters, 1996, 76, 216-219.	2.9	56
99	Effective Temperature in Stochastic Kinetics and Gene Networks. Biophysical Journal, 2006, 91, 84-94.	0.2	56
100	Dynamical Heterogeneity of the Glassy State. Journal of Physical Chemistry B, 2014, 118, 7835-7847.	1.2	56
101	Shape Transitions and Chiral Symmetry Breaking in the Energy Landscape of the Mitotic Chromosome. Physical Review Letters, 2016, 116, 248101.	2.9	56
102	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, 1796-1801.	3.3	55
103	Spatiotemporal structures in aging and rejuvenating glasses. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1353-1358.	3.3	55
104	Stochastic dynamic models of curve crossing phenomena in condensed phases. Journal of Chemical Physics, 1987, 86, 3836-3844.	1.2	54
105	Statistical Mechanics of the Combinatorial Synthesis and Analysis of Folding Macromolecules. Journal of Physical Chemistry B, 1997, 101, 8375-8389.	1.2	54
106	The folding energy landscape and phosphorylation: modeling the conformational switch of the NFAT regulatory domain. FASEB Journal, 2005, 19, 1389-1395.	0.2	53
107	On the strength of glasses. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16068-16072.	3.3	53
108	Statistical mechanical refinement of protein structure prediction schemes: Cumulant expansion approach. Journal of Chemical Physics, 2002, 117, 4602-4615.	1.2	52

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109	Frustration in Fuzzy Protein Complexes Leads to Interaction Versatility. Journal of Physical Chemistry B, 2021, 125, 2513-2520.	1.2	52
110	Activated events in glasses: The structure of entropic droplets. Physical Review B, 2005, 72, .	1.1	51
111	Genomic Energy Landscapes. Biophysical Journal, 2017, 112, 427-433.	0.2	50
112	Molecular Mechanism of Facilitated Dissociation of Fis Protein from DNA. Journal of the American Chemical Society, 2016, 138, 13497-13500.	6.6	47
113	Quantization of the Stochastic Pump Model of Arnold Diffusion. Physical Review Letters, 1997, 79, 55-58.	2.9	46
114	On the spontaneous collective motion of active matter. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15184-15189.	3.3	46
115	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.	3.3	46
116	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.	0.8	45
117	Exploring chromosomal structural heterogeneity across multiple cell lines. ELife, 2020, 9, .	2.8	43
118	Protein structure prediction using basin-hopping. Journal of Chemical Physics, 2008, 128, 225106.	1.2	42
119	On the hydrodynamics of swimming enzymes. Journal of Chemical Physics, 2015, 143, 165101.	1.2	42
120	Surveying biomolecular frustration at atomic resolution. Nature Communications, 2020, 11, 5944.	5.8	40
121	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, 20515-20520.	3.3	39
122	Predictive energy landscapes for folding Î±-helical transmembrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11031-11036.	3.3	38
123	Latest folding game results: Protein A barely frustrates computationalists. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6837-6838.	3.3	37
124	Protein Structure Prediction:Â The Next Generation. Journal of Chemical Theory and Computation, 2006, 2, 705-716.	2.3	37
125	Entropy crises in glasses and random heteropolymers. Journal of Research of the National Institute of Standards and Technology, 1997, 102, 187.	0.4	37
126	Tensegrity and motor-driven effective interactions in a model cytoskeleton. Journal of Chemical Physics, 2012, 136, 145102.	1.2	36

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127	Microscopic Theory of Network Glasses. Physical Review Letters, 2003, 90, 085505.	2.9	35
128	Role of Topology, Nonadditivity, and Water-Mediated Interactions in Predicting the Structures of Î±/Î² Proteins. Journal of the American Chemical Society, 2006, 128, 5168-5176.	6.6	35
129	Restriction versus guidance in protein structure prediction. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15302-15307.	3.3	34
130	The spectrum of biomolecular states and motions. HFSP Journal, 2008, 2, 307-313.	2.5	33
131	Scanning Malleable Transition State Ensembles:Â Comparing Theory and Experiment for Folding Protein U1Aâ€. Biochemistry, 2005, 44, 6433-6439.	1.2	32
132	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, 5006-5011.	3.3	32
133	The Aggregation Free Energy Landscapes of Polyglutamine Repeats. Journal of the American Chemical Society, 2016, 138, 15197-15203.	6.6	32
134	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.	3.3	32
135	Quantum theory of enhanced unimolecular reaction rates below the ergodicity threshold. Chemical Physics, 2006, 329, 163-167.	0.9	31
136	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.	3.3	31
137	OpenAWSEM with Open3SPN2: A fast, flexible, and accessible framework for large-scale coarse-grained biomolecular simulations. PLoS Computational Biology, 2021, 17, e1008308.	1.5	31
138	Complementary Variational Approximations for Intermittency and Reaction Dynamics in Fluctuating Environments. Journal of Physical Chemistry A, 1999, 103, 10602-10610.	1.1	30
139	Dynamical mean-field theory of quantum stripe glasses. Physical Review B, 2003, 68, .	1.1	29
140	Funneling and frustration in the energy landscapes of some designed and simplified proteins. Journal of Chemical Physics, 2013, 139, 121908.	1.2	29
141	The physics of protein folding. Physics World, 1999, 12, 39-44.	0.0	28
142	Fluctuating mobility generation and transport in glasses. Physical Review E, 2013, 88, 022308.	0.8	28
143	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, 8557-8565.	1.2	28
144	Dynamical theory of shear bands in structural glasses. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1287-1292.	3.3	28

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145	Resolving the NFÎºB Heterodimer Binding Paradox: Strain and Frustration Guide the Binding of Dimeric Transcription Factors. Journal of the American Chemical Society, 2017, 139, 18558-18566.	6.6	27
146	Computational study of manyâ€dimensional quantum vibrational energy redistribution. I. Statistics of the survival probability. Journal of Chemical Physics, 1996, 105, 940-952.	1.2	26
147	Ït-Value Analysis of Apo-Azurin Folding:â€‰ Comparison between Experiment and Theory. Biochemistry, 2006, 45, 6458-6466.	1.2	26
148	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, 3159-3164.	3.3	26
149	On the dephasing of genetic oscillators. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2391-2396.	3.3	26
150	Energy landscape underlying spontaneous insertion and folding of an alpha-helical transmembrane protein into a bilayer. Nature Communications, 2018, 9, 4949.	5.8	25
151	The Nucleome Data Bank: web-based resources to simulate and analyze the three-dimensional genome. Nucleic Acids Research, 2021, 49, D172-D182.	6.5	25
152	Molecular stripping, targets and decoys as modulators of oscillations in the NF-Î°B/IÎ°BÎ±/DNA genetic network. Journal of the Royal Society Interface, 2016, 13, 20160606.	1.5	24
153	Water Mediated Interactions and the Protein Folding Phase Diagram in the Temperatureâ€“Pressure Plane. Journal of Physical Chemistry B, 2015, 119, 11416-11427.	1.2	23
154	Protein structure prediction: making AWSEM AWSEMâ€ER by adding evolutionary restraints. Proteins: Structure, Function and Bioinformatics, 2017, 85, 2127-2142.	1.5	23
155	Energy Landscape Analysis of Protein Dimers. Israel Journal of Chemistry, 2004, 44, 281-297.	1.0	22
156	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, 15204-15219.	1.2	22
157	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.	3.3	22
158	FrustratometeR: an R-package to compute local frustration in protein structures, point mutants and MD simulations. Bioinformatics, 2021, 37, 3038-3040.	1.8	22
159	Molecular dynamics of associative memory hamiltonians for protein tertiary structure recognition. Tetrahedron Computer Methodology, 1990, 3, 175-190.	0.2	21
160	Replica theory for fluctuations of the activation barriers in glassy systems. Physical Review B, 2009, 80, .	1.1	21
161	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, 2098-2103.	3.3	21
162	Protein Folding and Structure Prediction from the Ground Up II: AAWSEM for Î±/Î² Proteins. Journal of Physical Chemistry B, 2017, 121, 3473-3482.	1.2	21

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163	Initial events of protein folding from an information-processing viewpoint. Physical Review A, 1992, 46, 5242-5248.	1.0	20
164	Dichotomous noise models of gene switches. Journal of Chemical Physics, 2015, 143, 195101.	1.2	20
165	PEST Control of Molecular Stripping of NFÎºB from DNA Transcription Sites. Journal of Physical Chemistry B, 2016, 120, 8532-8538.	1.2	20
166	Structural and Dynamical Order of a Disordered Protein: Molecular Insights into Conformational Switching of PAGE4 at the Systems Level. Biomolecules, 2019, 9, 77.	1.8	19
167	The role of atomic level steric effects and attractive forces in protein folding. Proteins: Structure, Function and Bioinformatics, 2012, 80, 362-373.	1.5	18
168	Aging, Jamming, and the Limits of Stability of Amorphous Solids. Journal of Physical Chemistry B, 2018, 122, 3280-3295.	1.2	18
169	Surveying the Energy Landscapes of AÎ² Fibril Polymorphism. Journal of Physical Chemistry B, 2018, 122, 11414-11430.	1.2	18
170	AWSEM-Suite: a protein structure prediction server based on template-guided, coevolutionary-enhanced optimized folding landscapes. Nucleic Acids Research, 2020, 48, W25-W30.	6.5	18
171	Discrete Kinetic Models from Funneled Energy Landscape Simulations. PLoS ONE, 2012, 7, e50635.	1.1	17
172	Examining the Ensembles of Amyloid-Î² Monomer Variants and Their Propensities to Form Fibers Using an Energy Landscape Visualization Method. Journal of Physical Chemistry B, 2022, 126, 93-99.	1.2	17
173	Statistical mechanical refinement of protein structure prediction schemes. II. Mayer cluster expansion approach. Journal of Chemical Physics, 2003, 118, 8500-8512.	1.2	16
174	The Associative Memory, Water Mediated, Structure and Energy Model (AWSEM)-Amylometer: Predicting Amyloid Propensity and Fibril Topology Using an Optimized Folding Landscape Model. ACS Chemical Neuroscience, 2018, 9, 1027-1039.	1.7	16
175	Steady, Symmetric, and Reversible Growth and Dissolution of Individual Amyloid-Î² Fibrils. ACS Chemical Neuroscience, 2019, 10, 2967-2976.	1.7	16
176	Spin Glass Ideas and the Protein Folding Problems. Series on Directions in Condensed Matter Physics, 1992, , 225-259.	0.1	15
177	Microscopic theory of the glassy dynamics of passive and active network materials. Journal of Chemical Physics, 2013, 138, 12A521.	1.2	15
178	Template-Guided Protein Structure Prediction and Refinement Using Optimized Folding Landscape Force Fields. Journal of Chemical Theory and Computation, 2018, 14, 6102-6116.	2.3	15
179	Forging tools for refining predicted protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9400-9409.	3.3	15
180	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.	3.3	15

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181	Protein Structure Prediction in CASP13 Using AWSEM-Suite. Journal of Chemical Theory and Computation, 2020, 16, 3977-3988.	2.3	15
182	Solution of local-field equations for self-generated glasses. Physical Review B, 2004, 70, .	1.1	14
183	Statistical mechanics of a cat's cradle. New Journal of Physics, 2006, 8, 273-273.	1.2	14
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