Peter G Wolynes

List of Publications by Year in Descending Order

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	Localization of Energetic Frustration in Proteins. *Methods in Molecular Biology*, **2022**, 2376, 387-398	1.4	2
233	Exploring the folding energy landscapes of heme proteins using a hybrid AWSEM-heme model.. *Journal of Biological Physics*, **2022**, 1	1.6	0
232	A generalized Flory-Stockmayer kinetic theory of connectivity percolation and rigidity percolation of cytoskeletal networks.. *PLoS Computational Biology*, **2022**, 18, e1010105	5	0
231	Vectorial channeling as a mechanism for translational control by functional prions and condensates. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	1
230	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
229	Frustration in Fuzzy Protein Complexes Leads to Interaction Versatility. *Journal of Physical Chemistry B*, **2021**, 125, 2513-2520	3.4	17
228	FrustratometeR: an R-package to compute local frustration in protein structures, point mutants and MD simulations. *Bioinformatics*, **2021**,	7.2	5
227	Single-molecule conformational dynamics of a transcription factor reveals a continuum of binding modes controlling association and dissociation. *Nucleic Acids Research*, **2021**, 49, 11211-11223	20.1	0
226	Frustration and Direct-Coupling Analyses to Predict Formation and Function of Adeno-Associated Virus. *Biophysical Journal*, **2021**, 120, 489-503	2.9	3
225	OpenAWSEM with Open3SPN2: A fast, flexible, and accessible framework for large-scale coarse-grained biomolecular simulations. *PLoS Computational Biology*, **2021**, 17, e1008308	5	8
224	Fuzziness and Frustration in the Energy Landscape of Protein Folding, Function, and Assembly. *Accounts of Chemical Research*, **2021**, 54, 1251-1259	24.3	28
223	Glass Dynamics Deep in the Energy Landscape. *Journal of Physical Chemistry B*, **2021**, 125, 9052-9068	3.4	5
222	Coarse-Grained Modeling and Molecular Dynamics Simulations of Ca-Calmodulin. *Frontiers in Molecular Biosciences*, **2021**, 8, 661322	5.6	3
221	Modeling Protein Aggregation Kinetics: The Method of Second Stochasticization. *Journal of Physical Chemistry B*, **2021**, 125, 1118-1133	3.4	4
220	Examining the Ensembles of Amyloid-β Monomer Variants and Their Propensities to Form Fibers Using an Energy Landscape Visualization Method.. *Journal of Physical Chemistry B*, **2021**,	3.4	4
219	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
218	Protein Structure Prediction in CASP13 Using AWSEM-Suite. *Journal of Chemical Theory and Computation*, **2020**, 16, 3977-3988	6.4	6

217	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
216	Molecular-replacement phasing using predicted protein structures from. *IUCrJ*, **2020**, 7, 1168-1178	4.7	4
215	Exploring chromosomal structural heterogeneity across multiple cell lines. *ELife*, **2020**, 9,	8.9	15
214	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
213	AWSEM-Suite: a protein structure prediction server based on template-guided, coevolutionary-enhanced optimized folding landscapes. *Nucleic Acids Research*, **2020**, 48, W25-W30	20.1	9
212	Protein Structure Refinement Guided by Atomic Packing Frustration Analysis. *Journal of Physical Chemistry B*, **2020**, 124, 10889-10898	3.4	0
211	Surveying biomolecular frustration at atomic resolution. *Nature Communications*, **2020**, 11, 5944	17.4	13
210	Photon Activation of Glassy Dynamics: A Mechanism for Photoinduced Fluidization, Aging, and Information Storage in Amorphous Materials. *Journal of Physical Chemistry B*, **2020**, 124, 8434-8453	3.4	2
209	Exploring the F-actin/CPEB3 interaction and its possible role in the molecular mechanism of long-term memory. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 22128-22134	11.5	4
208	Multiple Binding Configurations of Fis Protein Pairs on DNA: Facilitated Dissociation versus Cooperative Dissociation. *Journal of the American Chemical Society*, **2019**, 141, 18113-18126	16.4	4
207	Localizing Frustration in Proteins Using All-Atom Energy Functions. *Journal of Physical Chemistry B*, **2019**, 123, 4497-4504	3.4	8
206	Steady, Symmetric, and Reversible Growth and Dissolution of Individual Amyloid-╫Fibrils. *ACS Chemical Neuroscience*, **2019**, 10, 2967-2976	5.7	10
205	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
204	Structural and Dynamical Order of a Disordered Protein: Molecular Insights into Conformational Switching of PAGE4 at the Systems Level. *Biomolecules*, **2019**, 9,	5.9	11
203	Learning Genomic Energy Landscapes from Experiments **2019**, 305-330		4
202	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
201	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
200	Stochastic resonances in a distributed genetic broadcasting system: the NFB/IB paradigm. *Journal of the Royal Society Interface*, **2018**, 15,	4.1	1

199	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
198	Modeling the therapeutic efficacy of NFB synthetic decoy oligodeoxynucleotides (ODNs). *BMC Systems Biology*, **2018**, 12, 4	3.5	5
197	AWSEM-IDP: A Coarse-Grained Force Field for Intrinsically Disordered Proteins. *Journal of Physical Chemistry B*, **2018**, 122, 11115-11125	3.4	48
196	Aging, Jamming, and the Limits of Stability of Amorphous Solids. *Journal of Physical Chemistry B*, **2018**, 122, 3280-3295	3.4	15
195	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	5.7	9
194	Frustration, function and folding. *Current Opinion in Structural Biology*, **2018**, 48, 68-73	8.1	43
193	Energy landscape underlying spontaneous insertion and folding of an alpha-helical transmembrane protein into a bilayer. *Nature Communications*, **2018**, 9, 4949	17.4	16
192	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
191	Surveying the Energy Landscapes of AFibril Polymorphism. *Journal of Physical Chemistry B*, **2018**, 122, 11414-11430	3.4	8
190	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	11.5	26
189	Aggregation landscapes of Huntingtin exon 1 protein fragments and the critical repeat length for the onset of Huntingtons disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 4406-4411	11.5	40
188	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
187	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
186	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
185	Protein structure prediction: making AWSEM AWSEM-ER by adding evolutionary restraints. *Proteins: Structure, Function and Bioinformatics*, **2017**, 85, 2127-2142	4.2	18
184	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
183	Stochastic dynamics of genetic broadcasting networks. *Physical Review E*, **2017**, 96, 052305	2.4	5
182	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

181	Genomic Energy Landscapes. *Biophysical Journal*, **2017**, 112, 427-433	2.9	33
180	AWSEM-MD **2017**, 121-190		5
179	Shape Transitions and Chiral Symmetry Breaking in the Energy Landscape of the Mitotic Chromosome. *Physical Review Letters*, **2016**, 116, 248101	7.4	34
178	The Aggregation Free Energy Landscapes of Polyglutamine Repeats. *Journal of the American Chemical Society*, **2016**, 138, 15197-15203	16.4	24
177	Exploring the Free Energy Landscape of Nucleosomes. *Journal of the American Chemical Society*, **2016**, 138, 8126-33	16.4	77
176	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
175	Electrostatics, structure prediction, and the energy landscapes for protein folding and binding. *Protein Science*, **2016**, 25, 255-69	6.3	55
174	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
173	Binding of NFB Appears to Twist the Ankyrin Repeat Domain of IB. *Biophysical Journal*, **2016**, 110, 887-95	2.9	8
172	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
171	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
170	BIOMOLECULAR FOLDING. Moments of excitement. *Science*, **2016**, 352, 150-1	33.3	7
169	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
168	PEST Control of Molecular Stripping of NFB from DNA Transcription Sites. *Journal of Physical Chemistry B*, **2016**, 120, 8532-8	3.4	14
167	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
166	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
165	Molecular Mechanism of Facilitated Dissociation of Fis Protein from DNA. *Journal of the American Chemical Society*, **2016**, 138, 13497-13500	16.4	29
164	Exploring the aggregation free energy landscape of the amyloid- protein (1-40). *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 11835-11840	11.5	79

163	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
162	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
161	Evolution, energy landscapes and the paradoxes of protein folding. *Biochimie*, **2015**, 119, 218-30	4.6	109
160	Predictive energy landscapes for folding membrane protein assemblies. *Journal of Chemical Physics*, **2015**, 143, 243101	3.9	12
159	On the hydrodynamics of swimming enzymes. *Journal of Chemical Physics*, **2015**, 143, 165101	3.9	36
158	Dichotomous noise models of gene switches. *Journal of Chemical Physics*, **2015**, 143, 195101	3.9	18
157	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
156	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
155	Dynamical heterogeneity of the glassy state. *Journal of Physical Chemistry B*, **2014**, 118, 7835-47	3.4	38
154	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
153	On the dephasing of genetic oscillators. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 2391-6	11.5	18
152	Frustration in biomolecules. *Quarterly Reviews of Biophysics*, **2014**, 47, 285-363	7	168
151	Learning To Fold Proteins Using Energy Landscape Theory. *Israel Journal of Chemistry*, **2014**, 54, 1311-1337	3.4	44
150	Funneling and frustration in the energy landscapes of some designed and simplified proteins. *Journal of Chemical Physics*, **2013**, 139, 121908	3.9	25
149	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
148	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
147	Microscopic theory of the glassy dynamics of passive and active network materials. *Journal of Chemical Physics*, **2013**, 138, 12A521	3.9	14
146	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

145	Fluctuating mobility generation and transport in glasses. *Physical Review E*, **2013**, 88, 022308	2.4	26
144	Active patterning and asymmetric transport in a model actomyosin network. *Journal of Chemical Physics*, **2013**, 139, 235103	3.9	4
143	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
142	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
141	Protein frustratometer: a tool to localize energetic frustration in protein molecules. *Nucleic Acids Research*, **2012**, 40, W348-51	20.1	109
140	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
139	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
138	Supercooled Liquid Dynamics: Advances and Challenges **2012**, 1-30		10
137	Dielectric Spectroscopy of Glassy Dynamics **2012**, 115-149		11
136	Glassiness in Uniformly Frustrated Systems **2012**, 193-221		6
135	Fragile Glass Formers: Evidence for a New Paradigm, and a New Relation to Strong Liquids **2012**, 237-278		4
134	Glassy Dynamics of Proteins **2012**, 319-339		1
133	The Random First-Order Transition Theory of Glasses: A Critical Assessment **2012**, 31-113		32
132	Glasses and Replicas **2012**, 151-191		14
131	Random First-Order Phase Transition Theory of the Structural Glass Transition **2012**, 223-236		6
130	Dynamics in the Crossover Region of Supercooled Liquids **2012**, 279-317		
129	Theories of Structural Glass Dynamics: Mosaics, Jamming, and All That **2012**, 341-379		8
128	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

127	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
126	Tensegrity and motor-driven effective interactions in a model cytoskeleton. *Journal of Chemical Physics*, **2012**, 136, 145102	3.9	33
125	Discrete kinetic models from funneled energy landscape simulations. *PLoS ONE*, **2012**, 7, e50635	3.7	16
124	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
123	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
122	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
121	Prediction of native-state hydrogen exchange from perfectly funneled energy landscapes. *Journal of the American Chemical Society*, **2011**, 133, 17463-72	16.4	54
120	The ultimate fate of supercooled liquids. *Journal of Physical Chemistry A*, **2011**, 115, 3713-9	2.8	61
119	The interplay of nonlinearity and architecture in equilibrium cytoskeletal mechanics. *Journal of Chemical Physics*, **2011**, 134, 014510	3.9	13
118	Communication: Effective temperature and glassy dynamics of active matter. *Journal of Chemical Physics*, **2011**, 135, 051101	3.9	55
117	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
116	Protein structure prediction: do hydrogen bonding and water-mediated interactions suffice?. *Methods*, **2010**, 52, 84-90	4.6	8
115	A universal origin for secondary relaxations in supercooled liquids and structural glasses. *Nature Physics*, **2009**, 6, 62-68	16.2	90
114	Replica theory for fluctuations of the activation barriers in glassy systems. *Physical Review B*, **2009**, 80,	3.3	18
113	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
112	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
111	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
110	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

109	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
108	Variationally determined free energy profiles for structural models of proteins: characteristic temperatures for folding and trapping. *Journal of Physical Chemistry B*, **2008**, 112, 6074-82	3.4	7
107	Conformational switching upon phosphorylation: a predictive framework based on energy landscape principles. *Biochemistry*, **2008**, 47, 2110-22	3.2	46
106	The spectrum of biomolecular states and motions. *HFSP Journal*, **2008**, 2, 307-13		31
105	Protein structure prediction using basin-hopping. *Journal of Chemical Physics*, **2008**, 128, 225106	3.9	37
104	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
103	On the surface of glasses. *Journal of Chemical Physics*, **2008**, 129, 234514	3.9	133
102	The Microscopic Quantum Theory of Low Temperature Amorphous Solids. *Advances in Chemical Physics*, **2008**, 95-206		19
101	Protein Folding and Beyond: Energy Landscapes and the Organization of Living Matter in Time and Space **2008**, 267-288		1
100	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
99	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
98	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
97	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
96	Theory of structural glasses and supercooled liquids. *Annual Review of Physical Chemistry*, **2007**, 58, 235-66	25.7	589
95	Statistical mechanics of a cat's cradle. *New Journal of Physics*, **2006**, 8, 273-273	2.9	13
94	Simulation studies of the fidelity of biomolecular structure ensemble recreation. *Journal of Chemical Physics*, **2006**, 125, 214905	3.9	13
93	Electrodynamics of amorphous media at low temperatures. *Molecular Physics*, **2006**, 104, 1325-1335	1.7	11
92	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

91	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
90	Effective temperature in stochastic kinetics and gene networks. *Biophysical Journal*, **2006**, 91, 84-94	2.9	54
89	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
88	Protein Structure Prediction: The Next Generation. *Journal of Chemical Theory and Computation*, **2006**, 2, 705-16	6.4	36
87	Phi-value analysis of apo-azurin folding: comparison between experiment and theory. *Biochemistry*, **2006**, 45, 6458-66	3.2	21
86	The shapes of cooperatively rearranging regions in glass-forming liquids. *Nature Physics*, **2006**, 2, 268-274	6.2	217
85	Quantum theory of enhanced unimolecular reaction rates below the ergodicity threshold. *Chemical Physics*, **2006**, 329, 163-167	2.3	28
84	The experimental survey of protein-folding energy landscapes. *Quarterly Reviews of Biophysics*, **2005**, 38, 245-88	7	232
83	Scanning malleable transition state ensembles: comparing theory and experiment for folding protein U1A. *Biochemistry*, **2005**, 44, 6433-9	3.2	30
82	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
81	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
80	Self-consistent proteomic field theory of stochastic gene switches. *Biophysical Journal*, **2005**, 88, 828-50	2.9	89
79	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
78	Activated events in glasses: The structure of entropic droplets. *Physical Review B*, **2005**, 72,	3.3	48
77	Simple energy landscape model for the kinetics of functional transitions in proteins. *Journal of Physical Chemistry B*, **2005**, 109, 1959-69	3.4	94
76	The folding energy landscape and phosphorylation: modeling the conformational switch of the NFAT regulatory domain. *FASEB Journal*, **2005**, 19, 1389-95	0.9	41
75	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
74	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

73	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
72	Solution of local-field equations for self-generated glasses. *Physical Review B*, **2004**, 70,	3.3	13
71	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
70	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
69	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
68	Theory of protein folding. *Current Opinion in Structural Biology*, **2004**, 14, 70-5	8.1	992
67	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
66	Energy Landscape Analysis of Protein Dimers. *Israel Journal of Chemistry*, **2004**, 44, 281-297	3.4	18
65	Optimizing physical energy functions for protein folding. *Proteins: Structure, Function and Bioinformatics*, **2004**, 54, 88-103	4.2	76
64	Theory of aging in structural glasses. *Journal of Chemical Physics*, **2004**, 121, 2852-65	3.9	146
63	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
62	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
61	Role of water mediated interactions in protein-protein recognition landscapes. *Journal of the American Chemical Society*, **2003**, 125, 9170-8	16.4	158
60	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
59	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
58	Microscopic theory of network glasses. *Physical Review Letters*, **2003**, 90, 085505	7.4	27
57	Dynamical mean-field theory of quantum stripe glasses. *Physical Review B*, **2003**, 68,	3.3	26
56	Statistical mechanical refinement of protein structure prediction schemes. II. Mayer cluster expansion approach. *Journal of Chemical Physics*, **2003**, 118, 8500-8512	3.9	15

55	Folding funnels: the key to robust protein structure prediction. *Journal of Computational Chemistry*, **2002**, 23, 138-46	3.5	53
54	Statistical mechanical refinement of protein structure prediction schemes: Cumulant expansion approach. *Journal of Chemical Physics*, **2002**, 117, 4602-4615	3.9	49
53	Microscopic theory of heterogeneity and nonexponential relaxations in supercooled liquids. *Physical Review Letters*, **2001**, 86, 5526-9	7.4	246
52	Intrinsic quantum excitations of low temperature glasses. *Physical Review Letters*, **2001**, 87, 195901	7.4	86
51	Microscopic theory of protein folding rates. II. Local reaction coordinates and chain dynamics. *Journal of Chemical Physics*, **2001**, 114, 5082-5096	3.9	158
50	Self-generated randomness, defect wandering, and viscous flow in stripe glasses. *Physical Review B*, **2001**, 64,	3.3	63
49	Role of explicitly cooperative interactions in protein folding funnels: A simulation study. *Journal of Chemical Physics*, **2001**, 114, 4702	3.9	69
48	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
47	Diffusion and the Mesoscopic Hydrodynamics of Supercooled Liquids *Journal of Physical Chemistry B*, **2001**, 105, 6570-6573	3.4	69
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4	The Nucleome Data Bank: Web-based Resources to Simulate and Analyze the Three-Dimensional Genome		2
3	Frustration in protein complexes leads to interaction versatility		3
2	FrustratometeR: an R-package to compute local frustration in protein structures, point mutants and MD simulations		1

List of Publications

1 Vectorial Channeling as a Mechanism for Translational Control by Functional Prions and Condensates 1