Robert B Best

List of Publications by Year
in descending order

170	20,340	14644 66	12258 133
papers	citations	h-index	g-index

193	193	193	16330
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Analysis of Molecular Dynamics Simulations of Protein Folding. Methods in Molecular Biology, 2022, 2376, 317-329.	0.4	4
2	Release of linker histone from the nucleosome driven by polyelectrolyte competition with a disordered protein. Nature Chemistry, 2022, 14, 224-231.	6.6	37
3	Tuning Formation of Proteinâ€“DNA Coacervates by Sequence and Environment. Journal of Physical Chemistry B, 2022, 126, 2407-2419.	1.2	10
4	Single-molecule Detection of Ultrafast Biomolecular Dynamics with Nanophotonics. Journal of the American Chemical Society, 2022, 144, 52-56.	6.6	18
5	Mechanism of membrane-tethered mitochondrial protein synthesis. Science, 2021, 371, 846-849.	6.0	76
6	Estimating transition path times and shapes from single-molecule photon trajectories: A simulation analysis. Journal of Chemical Physics, 2021, 154, 115101.	1.2	3
7	Martini 3: a general purpose force field for coarse-grained molecular dynamics. Nature Methods, 2021, 18, 382-388.	9.0	557
8	Physics-based computational and theoretical approaches to intrinsically disordered proteins. Current Opinion in Structural Biology, 2021, 67, 219-225.	2.6	101
9	A Data-Driven Hydrophobicity Scale for Predicting Liquidâ€“Liquid Phase Separation of Proteins. Journal of Physical Chemistry B, 2021, 125, 4046-4056.	1.2	71
10	The ribosome modulates folding inside the ribosomal exit tunnel. Communications Biology, 2021, 4, 523.	2.0	27
11	Treatment of sickle cell disease by increasing oxygen affinity of hemoglobin. Blood, 2021, 138, 1172-1181.	0.6	52
12	Atomic view of cosolute-induced protein denaturation probed by NMR solvent paramagnetic relaxation enhancement. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
13	Mechanism of Hydrogen Sulfide-Dependent Inhibition of FeFe Hydrogenase. ACS Catalysis, 2021, 11, 15162-15176.	5.5	13
14	Emerging consensus on the collapse of unfolded and intrinsically disordered proteins in water. Current Opinion in Structural Biology, 2020, 60, 27-38.	2.6	26
15	Polyelectrolyte interactions enable rapid association and dissociation in high-affinity disordered protein complexes. Nature Communications, 2020, 11, 5736.	5.8	74
16	A Tale of Two Tyrosines. Biophysical Journal, 2020, 119, 1927-1928.	0.2	0
17	Molecular Details of Protein Condensates Probed by Microsecond Long Atomistic Simulations. Journal of Physical Chemistry B, 2020, 124, 11671-11679.	1.2	127
18	Atomistic mechanism of transmembrane helix association. PLoS Computational Biology, 2020, 16, e1007919.	1.5	16

#	Article	IF	Citations
19	Cotranslational folding cooperativity of contiguous domains of Î±-spectrin. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14119-14126.	3.3	24
20	Multiple lipid binding sites determine the affinity of PH domains for phosphoinositide-containing membranes. Science Advances, 2020, 6, eaay5736.	4.7	44
21	Cutting antiparallel DNA strands in a single active site. Nature Structural and Molecular Biology, 2020, 27, 119-126.	3.6	25
22	Biomolecular Phase Separation: From Molecular Driving Forces to Macroscopic Properties. Annual Review of Physical Chemistry, 2020, 71, 53-75.	4.8	368
23	Exploring the sequence fitness landscape of a bridge between protein folds. PLoS Computational Biology, 2020, 16, e1008285.	1.5	20
24	Computational Protocol for Determining Conformational Ensembles of Intrinsically Disordered Proteins. Methods in Molecular Biology, 2020, 2141, 413-427.	0.4	1
25	Tandem domain swapping: determinants of multidomain protein misfolding. Current Opinion in Structural Biology, 2019, 58, 97-104.	2.6	28
26	Disordered RNA chaperones can enhance nucleic acid folding via local charge screening. Nature Communications, 2019, 10, 2453.	5.8	59
27	Evolution of All-Atom Protein Force Fields to Improve Local and Global Properties. Journal of Physical Chemistry Letters, 2019, 10, 2227-2234.	2.1	65
28	Improving the Performance of the Amber RNA Force Field by Tuning the Hydrogen-Bonding Interactions. Journal of Chemical Theory and Computation, 2019, 15, 3288-3305.	2.3	97
29	TADOSS: computational estimation of tandem domain swap stability. Bioinformatics, 2019, 35, 2507-2508.	1.8	6
30	Atomistic Force Fields for Proteins. Methods in Molecular Biology, 2019, 2022, 3-19.	0.4	14
31	Extreme disorder in an ultrahigh-affinity protein complex. Nature, 2018, 555, 61-66.	13.7	538
32	Coâ€Evolutionary Fitness Landscapes for Sequence Design. Angewandte Chemie - International Edition, 2018, 57, 5674-5678.	7.2	58
33	Coâ€Evolutionary Fitness Landscapes for Sequence Design. Angewandte Chemie, 2018, 130, 5776-5780.	1.6	5
34	Race to the native state. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2267-2269.	3.3	1
35	Highly Disordered Amyloid-Î² Monomer Probed by Single-Molecule FRET and MD Simulation. Biophysical Journal, 2018, 114, 870-884.	0.2	88
36	InnenrÃ¼cktitelbild: Co-Evolutionary Fitness Landscapes for Sequence Design (Angew. Chem. 20/2018). Angewandte Chemie, 2018, 130, 6061-6061.	1.6	1

#	Article	IF	Citations
37	Inferring properties of disordered chains from FRET transfer efficiencies. Journal of Chemical Physics, 2018, 148, 123329.	1.2	84
38	Balancing Force Field Proteinâ€“Lipid Interactions To Capture Transmembrane Helixâ€“Helix Association. Journal of Chemical Theory and Computation, 2018, 14, 1706-1715.	2.3	40
39	An Extended Guinier Analysis for Intrinsically Disordered Proteins. Journal of Molecular Biology, 2018, 430, 2540-2553.	2.0	64
40	A small single-domain protein folds through the same pathway on and off the ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12206-12211.	3.3	51
41	Folding pathway of an Ig domain is conserved on and off the ribosome. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11284-E11293.	3.3	86
42	Accurate Transfer Efficiencies, Distance Distributions, and Ensembles of Unfolded and Intrinsically Disordered Proteins From Single-Molecule FRET. Methods in Enzymology, 2018, 611, 287-325.	0.4	46
43	Origin of Internal Friction in Disordered Proteins Depends on Solvent Quality. Journal of Physical Chemistry B, 2018, 122, 11478-11487.	1.2	19
44	Reversible two-state folding of the ultrafast protein gpW under mechanical force. Communications Chemistry, 2018, 1, .	2.0	16
45	Molecular Determinants of AÎ²₄₂ Adsorption to Amyloid Fibril Surfaces. Journal of Physical Chemistry Letters, 2018, 9, 6437-6443.	2.1	19
46	Relation between single-molecule properties and phase behavior of intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9929-9934.	3.3	283
47	Comment on â€œInnovative scattering analysis shows that hydrophobic disordered proteins are expanded in waterâ€. Science, 2018, 361, .	6.0	36
48	Instrumental Effects in the Dynamics of an Ultrafast Folding Protein under Mechanical Force. Journal of Physical Chemistry B, 2018, 122, 11147-11154.	1.2	15
49	Editorial overview: Theory and simulation: Interpreting experimental data at the molecular level. Current Opinion in Structural Biology, 2018, 49, iv-v.	2.6	4
50	Sequence determinants of protein phase behavior from a coarse-grained model. PLoS Computational Biology, 2018, 14, e1005941.	1.5	427
51	The shape of the bacterial ribosome exit tunnel affects cotranslational protein folding. ELife, 2018, 7, .	2.8	65
52	Computational and theoretical advances in studies of intrinsically disordered proteins. Current Opinion in Structural Biology, 2017, 42, 147-154.	2.6	186
53	How Many Protein Sequences Fold to a Given Structure? A Coevolutionary Analysis. Biophysical Journal, 2017, 113, 1719-1730.	0.2	38
54	Phosphorylation of the <scp>FUS</scp> lowâ€complexity domain disrupts phase separation, aggregation, and toxicity. EMBO Journal, 2017, 36, 2951-2967.	3.5	544

#	Article	IF	Citations
55	Convergence and Sampling in Determining Free Energy Landscapes for Membrane Protein Association. Journal of Physical Chemistry B, 2017, 121, 3364-3375.	1.2	93
56	Mechanism of O2 diffusion and reduction in FeFe hydrogenases. Nature Chemistry, 2017, 9, 88-95.	6.6	105
57	Markov state models of protein misfolding. Journal of Chemical Physics, 2016, 144, 075101.	1.2	26
58	Probing the Action of Chemical Denaturant on an Intrinsically Disordered Protein by Simulation and Experiment. Journal of the American Chemical Society, 2016, 138, 11702-11713.	6.6	121
59	Consistent View of Polypeptide Chain Expansion in Chemical Denaturants from Multiple Experimental Methods. Journal of the American Chemical Society, 2016, 138, 11714-11726.	6.6	171
60	Reconciling Intermediates in Mechanical Unfolding Experiments with Two-State Protein Folding in Bulk. Journal of Physical Chemistry Letters, 2016, 7, 3798-3803.	2.1	13
61	Computer Folding of RNA Tetraloops: Identification of Key Force Field Deficiencies. Journal of Chemical Theory and Computation, 2016, 12, 4534-4548.	2.3	125
62	Modulation of Folding Internal Friction by Local and Global Barrier Heights. Journal of Physical Chemistry Letters, 2016, 7, 1028-1034.	2.1	15
63	Diffusive Dynamics of Contact Formation in Disordered Polypeptides. Physical Review Letters, 2016, 116, 068102.	2.9	21
64	Microscopic interpretation of folding Ï•-values using the transition path ensemble. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3263-3268.	3.3	55
65	Structural Determinants of Misfolding in Multidomain Proteins. PLoS Computational Biology, 2016, 12, e1004933.	1.5	30
66	Surprising Abundance of Misfolding during Refolding of Multidomain Proteins. Biophysical Journal, 2015, 108, 501a.	0.2	0
67	Dependence of Internal Friction on Native Topology. Biophysical Journal, 2015, 108, 518a.	0.2	0
68	Molecular Simulations of Unfolded and Intrinsically Disordered Proteins. Biophysical Journal, 2015, 108, 194a.	0.2	0
69	Pressureâ€induced structural transition of mature <scp>HIV</scp>â€1 protease from a combined <scp>NMR/MD</scp> simulation approach. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2117-2123.	1.5	21
70	Quantitative Interpretation of FRET Experiments via Molecular Simulation: Force Field and Validation. Biophysical Journal, 2015, 108, 2721-2731.	0.2	59
71	Empirical Optimization of Interactions between Proteins and Chemical Denaturants in Molecular Simulations. Journal of Chemical Theory and Computation, 2015, 11, 5543-5553.	2.3	23
72	Reduction of All-Atom Protein Folding Dynamics to One-Dimensional Diffusion. Journal of Physical Chemistry B, 2015, 119, 15247-15255.	1.2	31

#	Article	IF	Citations
73	Dependence of Internal Friction on Folding Mechanism. Journal of the American Chemical Society, 2015, 137, 3283-3290.	6.6	41
74	Identification of Mutational Hot Spots for Substrate Diffusion: Application to Myoglobin. Journal of Chemical Theory and Computation, 2015, 11, 1919-1927.	2.3	12
75	Sequence- and Temperature-Dependent Properties of Unfolded and Disordered Proteins from Atomistic Simulations. Journal of Physical Chemistry B, 2015, 119, 14622-14630.	1.2	70
76	Transient misfolding dominates multidomain protein folding. Nature Communications, 2015, 6, 8861.	5.8	97
77	Role of solvation in pressure-induced helix stabilization. Journal of Chemical Physics, 2014, 141, 22D522.	1.2	16
78	Insights into the binding of intrinsically disordered proteins from molecular dynamics simulation. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2014, 4, 182-198.	6.2	56
79	Temperature-dependent solvation modulates the dimensions of disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5213-5218.	3.3	161
80	Effect of interactions with the chaperonin cavity on protein folding and misfolding. Physical Chemistry Chemical Physics, 2014, 16, 6358-6366.	1.3	17
81	Discriminating binding mechanisms of an intrinsically disordered protein via a multi-state coarse-grained model. Journal of Chemical Physics, 2014, 140, 175102.	1.2	46
82	Molecular origins of internal friction effects on protein-folding rates. Nature Communications, 2014, 5, 4307.	5.8	98
83	Balanced Proteinâ€“Water Interactions Improve Properties of Disordered Proteins and Non-Specific Protein Association. Journal of Chemical Theory and Computation, 2014, 10, 5113-5124.	2.3	564
84	Modest Influence of FRET Chromophores on the Properties of Unfolded Proteins. Biophysical Journal, 2014, 107, 1654-1660.	0.2	29
85	Bootstrapping New Protein Folds. Biophysical Journal, 2014, 107, 1040-1041.	0.2	3
86	Aerobic Damage to [FeFe]â€Hydrogenases: Activation Barriers for the Chemical Attachment of O₂. Angewandte Chemie - International Edition, 2014, 53, 4081-4084.	7.2	26
87	How Well Does a Funneled Energy Landscape Capture the Folding Mechanism of Spectrin Domains?. Journal of Physical Chemistry B, 2013, 117, 13235-13244.	1.2	16
88	Polarizable Atomic Multipole-Based AMOEBA Force Field for Proteins. Journal of Chemical Theory and Computation, 2013, 9, 4046-4063.	2.3	524
89	Native contacts determine protein folding mechanisms in atomistic simulations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17874-17879.	3.3	490
90	Engineering Folding Dynamics from Two-State to Downhill: Application to Î»-Repressor. Journal of Physical Chemistry B, 2013, 117, 13435-13443.	1.2	11

#	Article	IF	Citations
91	Cyclic N-Terminal Loop of Amylin Forms Non Amyloid Fibers. Biophysical Journal, 2013, 105, 1661-1669.	0.2	9
92	Complex Energy Landscape of a Giant Repeat Protein. Structure, 2013, 21, 1954-1965.	1.6	33
93	Cyclic N Terminal Fragment of Amylin Forms Non Amyloid Fibers: Implications for Intra- and Inter-Molecular Interactions in Amylin. Biophysical Journal, 2013, 104, 389a-390a.	0.2	0
94	Folding and Binding: When the Force is Against You. Biophysical Journal, 2013, 105, 2611-2612.	0.2	2
95	Effects of Interactions with the GroEL Cavity on Protein Folding Rates. Biophysical Journal, 2013, 104, 1098-1106.	0.2	34
96	Computer Folding of RNA Tetraloops? Are We There Yet?. Journal of Chemical Theory and Computation, 2013, 9, 2115-2125.	2.3	84
97	Matching of Additive and Polarizable Force Fields for Multiscale Condensed Phase Simulations. Journal of Chemical Theory and Computation, 2013, 9, 2826-2837.	2.3	24
98	Variational Optimization of an All-Atom Implicit Solvent Force Field To Match Explicit Solvent Simulation Data. Journal of Chemical Theory and Computation, 2013, 9, 5641-5652.	2.3	46
99	Comparing a simple theoretical model for protein folding with all-atom molecular dynamics simulations. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17880-17885.	3.3	94
100	Folding Kinetics and Unfolded State Dynamics of the GB1 Hairpin from Molecular Simulation. Journal of Chemical Theory and Computation, 2013, 9, 1743-1753.	2.3	35
101	A â€œslowâ€•protein folds quickly in the end. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5744-5745.	3.3	3
102	(Ala)₄â€Xâ€(Ala)₄ as a model system for the optimization of the Ï‡₁ and Ï‡₂ amino acid sideâ€chain dihedral empirical force field parameters. Journal of Computational Chemistry, 2013, 34, 593-603.	1.5	5
103	A Preformed Binding Interface in the Unbound Ensemble of an Intrinsically Disordered Protein: Evidence from Molecular Simulations. PLoS Computational Biology, 2012, 8, e1002605.	1.5	104
104	Residue-Specific Î±-Helix Propensities from Molecular Simulation. Biophysical Journal, 2012, 102, 1462-1467.	0.2	97
105	Peptide Chain Dynamics in Light and Heavy Water: Zooming in on Internal Friction. Journal of the American Chemical Society, 2012, 134, 6273-6279.	6.6	86
106	Modulation of an IDP binding mechanism and rates by helix propensity and non-native interactions: association of HIF1Î± with CBP. Molecular BioSystems, 2012, 8, 256-267.	2.9	83
107	Using Ligandâ€Mapping Simulations to Design a Ligand Selectively Targeting a Cryptic Surface Pocket of Poloâ€Like Kinase 1. Angewandte Chemie - International Edition, 2012, 51, 10078-10081.	7.2	71
108	Force-Field Dependence of Chignolin Folding and Misfolding: Comparison with Experiment and Redesign. Biophysical Journal, 2012, 102, 1897-1906.	0.2	71

#	Article	IF	Citations
109	Smoothing of the GB1 Hairpin Folding Landscape by Interfacial Confinement. Biophysical Journal, 2012, 103, 596-600.	0.2	21
110	Inclusion of Many-Body Effects in the Additive CHARMM Protein CMAP Potential Results in Enhanced Cooperativity of Î±-Helix and Î²-Hairpin Formation. Biophysical Journal, 2012, 103, 1045-1051.	0.2	130
111	Optimization of the Additive CHARMM All-Atom Protein Force Field Targeting Improved Sampling of the Backbone Ï•, Ï^ and Side-Chain Ï‡₁ and Ï‡₂ Dihedral Angles. Journal of Chemical Theory and Computation, 2012, 8, 3257-3273.	2.3	3,696
112	Atomistic molecular simulations of protein folding. Current Opinion in Structural Biology, 2012, 22, 52-61.	2.6	129
113	Force-Induced Change in Protein Unfolding Mechanism: Discrete or Continuous Switch?. Journal of Physical Chemistry B, 2011, 115, 1546-1561.	1.2	50
114	A microscopic model for gas diffusion dynamics in a [NiFe]-hydrogenase. Physical Chemistry Chemical Physics, 2011, 13, 7708.	1.3	27
115	What Is the Time Scale for Î±-Helix Nucleation?. Journal of the American Chemical Society, 2011, 133, 6809-6816.	6.6	68
116	Diffusion models of protein folding. Physical Chemistry Chemical Physics, 2011, 13, 16902.	1.3	76
117	Locating the Barrier for Folding of Single Molecules under an External Force. Physical Review Letters, 2011, 107, 208301.	2.9	69
118	Multiscale Simulation Reveals Multiple Pathways for H2and O2Transport in a [NiFe]-Hydrogenase. Journal of the American Chemical Society, 2011, 133, 3548-3556.	6.6	65
119	Single-molecule fluorescence reveals sequence-specific misfolding in multidomain proteins. Nature, 2011, 474, 662-665.	13.7	158
120	Freeâ€energy landscape of the GB1 hairpin in allâ€atom explicit solvent simulations with different force fields: Similarities and differences. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1318-1328.	1.5	112
121	Microscopic events in Î²-hairpin folding from alternative unfolded ensembles. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11087-11092.	3.3	67
122	Coordinate-dependent diffusion in protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1088-1093.	3.3	253
123	Protein Folding Landscapes for Alpha- and Beta-Miniproteins Using All-Atom Simulations with an Optimized Force-Field. Biophysical Journal, 2010, 98, 200a.	0.2	1
124	Insights from Molecular Simulations into the Temperature-Induced Collapse of Unfolded Proteins. Biophysical Journal, 2010, 98, 634a.	0.2	0
125	Dependence of Protein Folding Stability and Dynamics on the Density and Composition of Macromolecular Crowders. Biophysical Journal, 2010, 98, 315-320.	0.2	81
126	Replica Exchange Simulations For Macromolecular Crowding Effects on Multiprotein Binding. Biophysical Journal, 2010, 98, 57a.	0.2	0

#	Article	IF	Citations
127	Tackling Force-Field Bias in Protein Folding Simulations: Folding of Villin HP35 and Pin WW Domains in Explicit Water. Biophysical Journal, 2010, 99, L26-L28.	0.2	105
128	Simulation of Coarse-Grained Proteinâ^'Protein Interactions with Graphics Processing Units. Journal of Chemical Theory and Computation, 2010, 6, 3588-3600.	2.3	11
129	Protein Simulations with an Optimized Water Model: Cooperative Helix Formation and Temperature-Induced Unfolded State Collapse. Journal of Physical Chemistry B, 2010, 114, 14916-14923.	1.2	233
130	Balance between Î± and Î² Structures in Ab Initio Protein Folding. Journal of Physical Chemistry B, 2010, 114, 8790-8798.	1.2	96
131	Macromolecular crowding effects on proteinâ€“protein binding affinity and specificity. Journal of Chemical Physics, 2010, 133, 205101.	1.2	68
132	Single-molecule spectroscopy of the temperature-induced collapse of unfolded proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20740-20745.	3.3	211
133	Unfolding the Secrets of Calmodulin. Science, 2009, 323, 593-594.	6.0	13
134	Evidence for a Partially Structured State of the Amylin Monomer. Biophysical Journal, 2009, 97, 2948-2957.	0.2	45
135	Optimized Molecular Dynamics Force Fields Applied to the Helixâ^'Coil Transition of Polypeptides. Journal of Physical Chemistry B, 2009, 113, 9004-9015.	1.2	767
136	Are Current Molecular Dynamics Force Fields too Helical?. Biophysical Journal, 2008, 95, L07-L09.	0.2	419
137	Pulling Direction as a Reaction Coordinate for the Mechanical Unfolding of Single Molecules. Journal of Physical Chemistry B, 2008, 112, 5968-5976.	1.2	135
138	Crosstalk between the Protein Surface and Hydrophobic Core in a Core-swapped Fibronectin Type III Domain. Journal of Molecular Biology, 2008, 375, 560-571.	2.0	23
139	Atomistic Insights into Rhodopsin Activation from a Dynamic Model. Journal of the American Chemical Society, 2008, 130, 10141-10149.	6.6	35
140	Protein Folding Kinetics Under Force from Molecular Simulation. Journal of the American Chemical Society, 2008, 130, 3706-3707.	6.6	40
141	Binding-Induced Folding of a Natively Unstructured Transcription Factor. PLoS Computational Biology, 2008, 4, e1000060.	1.5	189
142	Thermodynamics and kinetics of protein folding under confinement. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20233-20238.	3.3	146
143	Effect of flexibility and cis residues in single-molecule FRET studies of polyproline. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18964-18969.	3.3	201
144	Designing an extracellular matrix protein with enhanced mechanical stability. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9633-9637.	3.3	66

#	Article	IF	Citations
145	Characterizing the unfolded states of proteins using single-molecule FRET spectroscopy and molecular simulations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1528-1533.	3.3	327
146	Structural Comparison of the Two Alternative Transition States for Folding of TI I27. Biophysical Journal, 2006, 91, 263-275.	0.2	21
147	Characterization of the residual structure in the unfolded state of the Î”131Î” fragment of staphylococcal nuclease. Proteins: Structure, Function and Bioinformatics, 2006, 65, 145-152.	1.5	38
148	Structural Interpretation of Hydrogen Exchange Protection Factors in Proteins: Characterization of the Native State Fluctuations of CI2. Structure, 2006, 14, 97-106.	1.6	115
149	Diffusive Model of Protein Folding Dynamics with Kramers Turnover in Rate. Physical Review Letters, 2006, 96, 228104.	2.9	165
150	Relation between native ensembles and experimental structures of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10901-10906.	3.3	136
151	Simultaneous determination of protein structure and dynamics. Nature, 2005, 433, 128-132.	13.7	641
152	Slow Protein Conformational Dynamics from Multiple Experimental Structures: The Helix/Sheet Transition of Arc Repressor. Structure, 2005, 13, 1755-1763.	1.6	160
153	Interpreting Dynamically-Averaged Scalar Couplings in Proteins. Journal of Biomolecular NMR, 2005, 32, 273-280.	1.6	46
154	Reaction coordinates and rates from transition paths. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6732-6737.	3.3	433
155	Comment on "Force-Clamp Spectroscopy Monitors the Folding Trajectory of a Single Protein". Science, 2005, 308, 498b-498b.	6.0	37
156	What Contributions to Protein Side-chain Dynamics are Probed by NMR Experiments? A Molecular Dynamics Simulation Analysis. Journal of Molecular Biology, 2005, 349, 185-203.	2.0	92
157	The Origin of Protein Sidechain Order Parameter Distributions. Journal of the American Chemical Society, 2004, 126, 7734-7735.	6.6	59
158	A mutant chaperonin with rearranged inter-ring electrostatic contacts and temperature-sensitive dissociation. Nature Structural and Molecular Biology, 2004, 11, 1128-1133.	3.6	39
159	Hydrophobic Core Fluidity of Homologous Protein Domains:Â Relation of Side-Chain Dynamics to Core Composition and Packingâ€. Biochemistry, 2004, 43, 1145-1155.	1.2	38
160	Determination of Protein Structures Consistent with NMR Order Parameters. Journal of the American Chemical Society, 2004, 126, 8090-8091.	6.6	126
161	Force mode atomic force microscopy as a tool for protein folding studies. Analytica Chimica Acta, 2003, 479, 87-105.	2.6	120
162	Hidden complexity in the mechanical properties of titin. Nature, 2003, 422, 446-449.	13.7	268

#	Article	IF	Citations
163	Mechanical Unfolding of a Titin Ig Domain: Structure of Transition State Revealed by Combining Atomic Force Microscopy, Protein Engineering and Molecular Dynamics Simulations. Journal of Molecular Biology, 2003, 330, 867-877.	2.0	168
164	A simple method for probing the mechanical unfolding pathway of proteins in detail. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12143-12148.	3.3	93
165	Modeling the Î±(1â†'6) Branch Point of Amylopectin in Solution. Journal of Physical Chemistry B, 2002, 106, 5091-5098.	1.2	18
166	AN NMR INVESTIGATION INTO THE DYNAMICS OF PANOSE, AN Î±(1â†'4) AND Î±(1â†'6)-LINKED TRISACCHARIDE. Spectroscopy Letters, 2002, 35, 625-632.	0.5	3
167	What can atomic force microscopy tell us about protein folding?. Chemical Communications, 2002, , 183-192.	2.2	50
168	Mechanical Unfolding of a Titin Ig Domain: Structure of Unfolding Intermediate Revealed by Combining AFM, Molecular Dynamics Simulations, NMR and Protein Engineering. Journal of Molecular Biology, 2002, 322, 841-849.	2.0	200
169	Can Non-Mechanical Proteins Withstand Force? Stretching Barnase by Atomic Force Microscopy and Molecular Dynamics Simulation. Biophysical Journal, 2001, 81, 2344-2356.	0.2	234
170	Molecular Dynamics and NMR Study of the Î±(1â†'4) and Î±(1â†'6) Glycosidic Linkages:Â Maltose and Isomaltose. Journal of Physical Chemistry B, 2001, 105, 4742-4751.	1.2	61