Dave Thirumalai

List of Publications by Year
in descending order

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277 papers	23,591 citations	6250 80 h-index	10152 140 g-index
317 all docs	317 docs citations	317 times ranked	11465 citing authors

#	Article	IF	Citations
1	A mathematical model for phenotypic heterogeneity in breast cancer with implications for therapeutic strategies. Journal of the Royal Society Interface, 2022, 19, 20210803.	1.5	9
2	The Asakuraâ€“Oosawa theory: Entropic forces in physics, biology, and soft matter. Journal of Chemical Physics, 2022, 156, 080401.	1.2	19
3	Plus and minus ends of microtubules respond asymmetrically to kinesin binding by a long-range directionally driven allosteric mechanism. Science Advances, 2022, 8, eabn0856.	4.7	3
4	Condensates in RNA repeat sequences are heterogeneously organized and exhibit reptation dynamics. Nature Chemistry, 2022, 14, 775-785.	6.6	25
5	Adhesion strength between cells regulate nonmonotonic growth by a biomechanical feedback mechanism. Biophysical Journal, 2022, 121, 3719-3729.	0.2	11
6	Mechanical feedback controls the emergence of dynamical memory in growing tissue monolayers. Journal of Chemical Physics, 2022, 156, .	1.2	8
7	Cooperativity and Folding Kinetics in a Multidomain Protein with Interwoven Chain Topology. ACS Central Science, 2022, 8, 763-774.	5.3	10
8	Role of water-bridged interactions in metal ion coupled protein allostery. PLoS Computational Biology, 2022, 18, e1010195.	1.5	4
9	Water-Mediated Interactions Determine Helix Formation of Peptides in Open Nanotubes. Journal of Physical Chemistry B, 2021, 125, 817-824.	1.2	1
10	Retardation of Folding Rates of Substrate Proteins in the Nanocage of GroEL. Biochemistry, 2021, 60, 460-464.	1.2	4
11	Molecular Transfer Model for pH Effects on Intrinsically Disordered Proteins: Theory and Applications. Journal of Chemical Theory and Computation, 2021, 17, 1944-1954.	2.3	8
12	Low Force Unfolding of a Single-Domain Protein by Parallel Pathways. Journal of Physical Chemistry B, 2021, 125, 1799-1805.	1.2	4
13	Shape changes and cooperativity in the folding of the central domain of the 16S ribosomal RNA. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
14	From Hi-C Contact Map to Three-Dimensional Organization of Interphase Human Chromosomes. Physical Review X, 2021, 11, .	2.8	12
15	On the Emergence of Orientational Order in Folded Proteins with Implications for Allostery. Symmetry, 2021, 13, 770.	1.1	5
16	Random First Order Transition Theory for Glassy Dynamics in a Single Condensed Polymer. Physical Review Letters, 2021, 126, 137801.	2.9	5
17	Asymmetry in histone rotation in forced unwrapping and force quench rewrapping in a nucleosome. Nucleic Acids Research, 2021, 49, 4907-4918.	6.5	8
18	Mechanical heterogeneity along single cell-cell junctions is driven by lateral clustering of cadherins during vertebrate axis elongation. ELife, 2021, 10, .	2.8	34

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19	Multiscale Coarse-Grained Model for the Stepping of Molecular Motors with Application to Kinesin. Journal of Chemical Theory and Computation, 2021, 17, 5358-5368.	2.3	3
20	Energy Landscape of Ubiquitin Is Weakly Multidimensional. Journal of Physical Chemistry B, 2021, 125, 8682-8689.	1.2	6
21	Effects of Gold Nanoparticles on the Stepping Trajectories of Kinesin. Journal of Physical Chemistry B, 2021, 125, 10432-10444.	1.2	4
22	Sequence Determines the Switch in the Fibril Forming Regions in the Low-Complexity FUS Protein and Its Variants. Journal of Physical Chemistry Letters, 2021, 12, 9026-9032.	2.1	19
23	Step-Wise Hydration of Magnesium by Four Water Molecules Precedes Phosphate Release in a Myosin Motor. Journal of Physical Chemistry B, 2021, 125, 1107-1117.	1.2	8
24	Theory and simulations of condensin mediated loop extrusion in DNA. Nature Communications, 2021, 12, 5865.	5.8	20
25	Temperature and Guanidine Hydrochloride Effects on the Folding Thermodynamics of WW Domain and Variants. Journal of Physical Chemistry B, 2021, 125, 11386-11391.	1.2	2
26	Autobiography of Dave Thirumalai. Journal of Physical Chemistry B, 2021, 125, 13834-13839.	1.2	0
27	Iterative annealing mechanism explains the functions of the GroEL and RNA chaperones. Protein Science, 2020, 29, 360-377.	3.1	32
28	Cooperation among Tumor Cell Subpopulations Leads to Intratumor Heterogeneity. Biophysical Reviews and Letters, 2020, 15, 99-119.	0.9	7
29	A FÃ¶rster Resonance Energy Transfer-Based Sensor of Steric Pressure on Membrane Surfaces. Journal of the American Chemical Society, 2020, 142, 20796-20805.	6.6	21
30	Spatially heterogeneous dynamics of cells in a growing tumor spheroid: comparison between theory and experiments. Soft Matter, 2020, 16, 5294-5304.	1.2	38
31	Differences in the free energies between the excited states of A Î² 40 and A Î² 42 monomers encode their aggregation propensities. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19926-19937.	3.3	49
32	Dramatic Shape Changes Occur as Cytochrome c Folds. Journal of Physical Chemistry B, 2020, 124, 8240-8248.	1.2	4
33	Charge Density of Cation Determines Inner versus Outer Shell Coordination to Phosphate in RNA. Journal of Physical Chemistry B, 2020, 124, 4114-4122.	1.2	15
34	Fragile-to-strong crossover, growing length scales, and dynamic heterogeneity in Wigner glasses. Physical Review E, 2020, 101, 032605.	0.8	4
35	Processivity and Velocity for Motors Stepping onÂPeriodic Tracks. Biophysical Journal, 2020, 118, 1537-1551.	0.2	6
36	Theoretical perspectives on biological machines. Reviews of Modern Physics, 2020, 92, .	16.4	60

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37	Self-generated persistent random forces drive phase separation in growing tumors. Journal of Chemical Physics, 2020, 153, 201101.	1.2	12
38	Myosin V executes steps of variable length via structurally constrained diffusion. ELife, 2020, 9, .	2.8	7
39	Cooperation Among Tumor Cell Subpopulations Leads to Intratumor Heterogeneity. , 2020, , 79-99.		0
40	Ion Condensation onto Ribozyme Is Site Specific and Fold Dependent. Biophysical Journal, 2019, 116, 2400-2410.	0.2	32
41	Conformational heterogeneity in human interphase chromosome organization reconciles the FISH and Hi-C paradox. Nature Communications, 2019, 10, 3894.	5.8	27
42	Processivity, Velocity, and Universal Characteristics of Nucleic Acid Unwinding by Helicases. Biophysical Journal, 2019, 117, 867-879.	0.2	6
43	Theory and simulations for RNA folding in mixtures of monovalent and divalent cations. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21022-21030.	3.3	55
44	Universal Nature of Collapsibility in the Context of Protein Folding and Evolution. Trends in Biochemical Sciences, 2019, 44, 675-687.	3.7	31
45	Giant Casimir Nonequilibrium Forces Drive Coil to Globule Transition in Polymers. Journal of Physical Chemistry Letters, 2019, 10, 2788-2793.	2.1	1
46	Symmetry, Rigidity, and Allosteric Signaling: From Monomeric Proteins to Molecular Machines. Chemical Reviews, 2019, 119, 6788-6821.	23.0	82
47	Origin of superdiffusive behavior in a class of nonequilibrium systems. Physical Review E, 2019, 99, 032401.	0.8	9
48	Sequence Effects on Size, Shape, and Structural Heterogeneity in Intrinsically Disordered Proteins. Journal of Physical Chemistry B, 2019, 123, 3462-3474.	1.2	125
49	Share, but unequally: a plausible mechanism for emergence and maintenance of intratumour heterogeneity. Journal of the Royal Society Interface, 2019, 16, 20180820.	1.5	18
50	How kinesin waits for ATP affects the nucleotide and load dependence of the stepping kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23091-23099.	3.3	16
51	Denaturants Alter the Flux through Multiple Pathways in the Folding of PDZ Domain. Journal of Physical Chemistry B, 2018, 122, 1408-1416.	1.2	8
52	Cell Growth Rate Dictates the Onset of Glass to Fluidlike Transition and Long Time Superdiffusion in an Evolving Cell Colony. Physical Review X, 2018, 8, .	2.8	33
53	Structure of APP-C991â€“99 and implications for role of extra-membrane domains in function and oligomerization. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 1698-1708.	1.4	38
54	Dynamics of Allosteric Transitions in Dynein. Structure, 2018, 26, 1664-1677.e5.	1.6	14

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55	Chain organization of human interphase chromosome determines the spatiotemporal dynamics of chromatin loci. PLoS Computational Biology, 2018, 14, e1006617.	1.5	71
56	Molecular Simulations of Ion Effects on the Thermodynamics of RNA Folding. Journal of Physical Chemistry B, 2018, 122, 11860-11867.	1.2	30
57	Synergy between intrinsically disordered domains and structured proteins amplifies membrane curvature sensing. Nature Communications, 2018, 9, 4152.	5.8	102
58	Frictional Effects on RNA Folding: Speed Limit and Kramers Turnover. Journal of Physical Chemistry B, 2018, 122, 11279-11288.	1.2	10
59	Forced-rupture of cell-adhesion complexes reveals abrupt switch between two brittle states. Journal of Chemical Physics, 2018, 148, 123332.	1.2	7
60	Charge fluctuation effects on the shape of flexible polyampholytes with applications to intrinsically disordered proteins. Journal of Chemical Physics, 2018, 149, 163323.	1.2	54
61	Monovalent ions modulate the flux through multiple folding pathways of an RNA pseudoknot. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7313-E7322.	3.3	24
62	Signalling networks and dynamics of allosteric transitions in bacterial chaperonin GroEL: implications for iterative annealing of misfolded proteins. Philosophical Transactions of the Royal Society B: Biological Sciences, 2018, 373, 20170182.	1.8	18
63	Interface Residues That Drive Allosteric Transitions Also Control the Assembly of <scp>l</scp>-Lactate Dehydrogenase. Journal of Physical Chemistry B, 2018, 122, 11195-11205.	1.2	8
64	Interphase human chromosome exhibits out of equilibrium glassy dynamics. Nature Communications, 2018, 9, 3161.	5.8	127
65	Regulatory element in fibrin triggers tension-activated transition from catch to slip bonds. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8575-8580.	3.3	23
66	Sequence-Dependent Three Interaction Site Model for Single- and Double-Stranded DNA. Journal of Chemical Theory and Computation, 2018, 14, 3763-3779.	2.3	46
67	Phenomenological and microscopic theories for catch bonds. Journal of Structural Biology, 2017, 197, 50-56.	1.3	50
68	Collapse Precedes Folding in Denaturant-Dependent Assembly of Ubiquitin. Journal of Physical Chemistry B, 2017, 121, 995-1009.	1.2	37
69	Thermodynamics of Helixâ€“Coil Transitions of Polyalanine in Open Carbon Nanotubes. Journal of Physical Chemistry Letters, 2017, 8, 494-499.	2.1	3
70	Protein collapse is encoded in the folded state architecture. Soft Matter, 2017, 13, 3622-3638.	1.2	28
71	Kinematics of the lever arm swing in myosin VI. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4389-E4398.	3.3	16
72	Chromatin Is Stretched but Intact When the Nucleus Is Squeezed through Constrictions. Biophysical Journal, 2017, 112, 411-412.	0.2	1

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73	Ultrasensitivity of Water Exchange Kinetics to the Size of Metal Ion. Journal of the American Chemical Society, 2017, 139, 12334-12337.	6.6	43
74	Optimal information transfer in enzymatic networks: A field theoretic formulation. Physical Review E, 2017, 96, 012406.	0.8	6
75	Molecular chaperones maximize the native state yield on biological times by driving substrates out of equilibrium. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E10919-E10927.	3.3	36
76	Theory and computations in biology: Kamalâ€™s legacy. Physical Biology, 2017, 14, 010401.	0.8	0
77	Parsing the roles of neck-linker docking and tethered head diffusion in the stepping dynamics of kinesin. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9838-E9845.	3.3	33
78	Ripping RNA by Force Using Gaussian Network Models. Journal of Physical Chemistry B, 2017, 121, 3515-3522.	1.2	2
79	Noise Control in Gene Regulatory Networks with Negative Feedback. Journal of Physical Chemistry B, 2016, 120, 6166-6177.	1.2	15
80	Salt Effects on the Thermodynamics of a Frameshifting RNA Pseudoknot under Tension. Journal of Molecular Biology, 2016, 428, 2847-2859.	2.0	27
81	Impact of membrane lipid composition on the structure and stability of the transmembrane domain of amyloid precursor protein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5281-7.	3.3	74
82	Discrete Step Sizes of Molecular Motors Lead to Bimodal Non-Gaussian Velocity Distributions under Force. Physical Review Letters, 2016, 117, 078101.	2.9	25
83	Directly measuring single-molecule heterogeneity using force spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3852-61.	3.3	32
84	Reply to Alberti: Are in vitro folding experiments relevant in vivo?. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3192-E3192.	3.3	0
85	Force-dependent switch in protein unfolding pathways and transition-state movements. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E715-24.	3.3	59
86	Folding PDZ2 Domain Using the Molecular Transfer Model. Journal of Physical Chemistry B, 2016, 120, 8090-8101.	1.2	21
87	Importance of Hydrodynamic Interactions in the Stepping Kinetics of Kinesin. Journal of Physical Chemistry B, 2016, 120, 2071-2075.	1.2	15
88	Confinement-Induced Glassy Dynamics in a Model for Chromosome Organization. Physical Review Letters, 2015, 115, 198102.	2.9	69
89	Colloquium: Random first order transition theory concepts in biology and physics. Reviews of Modern Physics, 2015, 87, 183-209.	16.4	117
90	Using Simulations and Kinetic Network Models to Reveal the Dynamics and Functions of Riboswitches. Methods in Enzymology, 2015, 553, 235-258.	0.4	9

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91	Protein folding guides disulfide bond formation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11241-11246.	3.3	105
92	Unexpected Swelling of Stiff DNA in a Polydisperse Crowded Environment. Journal of the American Chemical Society, 2015, 137, 10970-10978.	6.6	35
93	Effects of Macromolecular Crowding on the Collapse of Biopolymers. Physical Review Letters, 2015, 114, 068303.	2.9	109
94	Helicase Processivity and Not the Unwinding Velocity Exhibits Universal Increase with Force. Biophysical Journal, 2015, 109, 220-230.	0.2	20
95	How do metal ions direct ribozyme folding?. Nature Chemistry, 2015, 7, 793-801.	6.6	110
96	Dissecting Ubiquitin Folding Using the Self-Organized Polymer Model. Journal of Physical Chemistry B, 2015, 119, 11358-11370.	1.2	45
97	Sequence-resolved free energy profiles of stress-bearing vimentin intermediate filaments. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11359-11364.	3.3	17
98	Entropy and enthalpy of interaction between amino acid side chains in nanopores. Journal of Chemical Physics, 2014, 141, 22D523.	1.2	4
99	Cellular Signaling Networks Function as Generalized Wiener-Kolmogorov Filters to Suppress Noise. Physical Review X, 2014, 4, .	2.8	19
100	Development and Applications of Coarseâ€Grained Models for RNA. Israel Journal of Chemistry, 2014, 54, 1358-1373.	1.0	5
101	Evidence of Disorder in Biological Molecules from Single Molecule Pulling Experiments. Physical Review Letters, 2014, 112, 138101.	2.9	26
102	Membraneâ€“Protein Interactions Are Key to Understanding Amyloid Formation. Journal of Physical Chemistry Letters, 2014, 5, 633-635.	2.1	25
103	Structural Heterogeneity in Transmembrane Amyloid Precursor Protein Homodimer Is a Consequence of Environmental Selection. Journal of the American Chemical Society, 2014, 136, 9619-9626.	6.6	40
104	Plasticity of hydrogen bond networks regulates mechanochemistry of cell adhesion complexes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9048-9053.	3.3	46
105	Propensity to Form Amyloid Fibrils Is Encoded as Excitations in the Free Energy Landscape of Monomeric Proteins. Journal of Molecular Biology, 2014, 426, 2653-2666.	2.0	55
106	Entropic stabilization of the folded states of RNA due to macromolecular crowding. Biophysical Reviews, 2013, 5, 225-232.	1.5	24
107	Protein folding: from theory to practice. Current Opinion in Structural Biology, 2013, 23, 22-29.	2.6	52
108	Design principles governing the motility of myosin V. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4059-E4068.	3.3	46

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109	From mechanical folding trajectories to intrinsic energy landscapes of biopolymers. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4500-4505.	3.3	80
110	Coarse-Grained Model for Predicting RNA Folding Thermodynamics. Journal of Physical Chemistry B, 2013, 117, 4901-4911.	1.2	140
111	Manifestation of random first-order transition theory in Wigner glasses. Physical Review E, 2013, 88, 042308.	0.8	10
112	Generalized iterative annealing model for the action of RNA chaperones. Journal of Chemical Physics, 2013, 139, 121924.	1.2	15
113	On the origin of the unusual behavior in the stretching of single-stranded DNA. Journal of Chemical Physics, 2012, 136, 235103.	1.2	33
114	Multiple barriers in forced rupture of protein complexes. Journal of Chemical Physics, 2012, 137, 055103.	1.2	24
115	Denaturant-dependent folding of GFP. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17832-17838.	3.3	71
116	Role of Water in Protein Aggregation and Amyloid Polymorphism. Accounts of Chemical Research, 2012, 45, 83-92.	7.6	301
117	Theory of the Molecular Transfer Model for Proteins with Applications to the Folding of the src-SH3 Domain. Journal of Physical Chemistry B, 2012, 116, 6707-6716.	1.2	46
118	Random First-Order Phase Transition Theory of the Structural Glass Transition. , 2012, , 223-236.		7
119	Chain Length Determines the Folding Rates of RNA. Biophysical Journal, 2012, 102, L11-L13.	0.2	47
120	Hidden complexity in the isomerization dynamics of Holliday junctions. Nature Chemistry, 2012, 4, 907-914.	6.6	85
121	Effects of pH on Proteins: Predictions for Ensemble and Single-Molecule Pulling Experiments. Journal of the American Chemical Society, 2012, 134, 979-987.	6.6	85
122	Dissecting the Kinematics of the Kinesin Step. Structure, 2012, 20, 628-640.	1.6	73
123	Folding of Human Telomerase RNA Pseudoknot Using Ion-Jump and Temperature-Quench Simulations. Journal of the American Chemical Society, 2011, 133, 20634-20643.	6.6	47
124	Crowding Promotes the Switch from Hairpin to Pseudoknot Conformation in Human Telomerase RNA. Journal of the American Chemical Society, 2011, 133, 11858-11861.	6.6	86
125	Capturing the essence of folding and functions of biomolecules using coarse-grained models. Nature Communications, 2011, 2, 487.	5.8	222
126	Toward a Molecular Theory of Early and Late Events in Monomer to Amyloid Fibril Formation. Annual Review of Physical Chemistry, 2011, 62, 437-463.	4.8	249

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127	Hydrophobic and Ionic-Interactions in Bulk and Confined Water with Implications for Collapse and Folding of Proteins. Journal of Statistical Physics, 2011, 145, 276-292.	0.5	8
128	Compaction and Tensile Forces Determine the Accuracy of Folding Landscape Parameters from Single Molecule Pulling Experiments. Physical Review Letters, 2011, 106, 138102.	2.9	33
129	Collapse kinetics and chevron plots from simulations of denaturant-dependent folding of globular proteins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7787-7792.	3.3	85
130	Rigor to Post-Rigor Transition in Myosin V: Link between the Dynamics and the Supporting Architecture. Structure, 2010, 18, 471-481.	1.6	60
131	Myosin VI: How Do Charged Tails Exert Control?. Structure, 2010, 18, 1393-1394.	1.6	4
132	Factors Governing Fibrillogenesis of Polypeptide Chains Revealed by Lattice Models. Physical Review Letters, 2010, 105, 218101.	2.9	104
133	Promoter melting triggered by bacterial RNA polymerase occurs in three steps. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12523-12528.	3.3	61
134	Dry amyloid fibril assembly in a yeast prion peptide is mediated by long-lived structures containing water wires. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21459-21464.	3.3	82
135	Theoretical Perspectives on Protein Folding. Annual Review of Biophysics, 2010, 39, 159-183.	4.5	183
136	Theory of Biopolymer Stretching at High Forces. Macromolecules, 2010, 43, 4394-4400.	2.2	35
137	Crowding Effects on the Structural Transitions in a Flexible Helical Homopolymer. Physical Review Letters, 2009, 102, 118101.	2.9	32
138	Assembly mechanisms of RNA pseudoknots are determined by the stabilities of constituent secondary structures. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17349-17354.	3.3	100
139	Water-mediated interactions between hydrophobic and ionic species in cylindrical nanopores. Journal of Chemical Physics, 2009, 130, 094502.	1.2	12
140	How accurate are polymer models in the analysis of FÃ¶rster resonance energy transfer experiments on proteins?. Journal of Chemical Physics, 2009, 130, 124903.	1.2	89
141	On the accuracy of inferring energetic coupling between distant sites in protein families from evolutionary imprints: Illustrations using lattice model. Proteins: Structure, Function and Bioinformatics, 2009, 77, 823-831.	1.5	32
142	Charge states rather than propensity for Î²-structure determine enhanced fibrillogenesis in wild-type Alzheimer's Î²-amyloid peptide compared to E22Q Dutch mutant. Protein Science, 2009, 11, 1639-1647.	3.1	69
143	Transmembrane Structures of Amyloid Precursor Protein Dimer Predicted by Replica-Exchange Molecular Dynamics Simulations. Journal of the American Chemical Society, 2009, 131, 3438-3439.	6.6	79
144	Structures of Î²-Amyloid Peptide 1â^'40, 1â^'42, and 1â^'55â€"the 672â^'726 Fragment of APPâ€"in a Membrane Environment with Implications for Interactions with Î³-Secretase. Journal of the American Chemical Society, 2009, 131, 17843-17852.	6.6	95

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145	Molecular Origin of Constant m-Values, Denatured State Collapse, and Residue-Dependent Transition Midpoints in Globular Proteins. Biochemistry, 2009, 48, 3743-3754.	1.2	56
146	Influence of Preformed Asp23â˜'Lys28 Salt Bridge on the Conformational Fluctuations of Monomers and Dimers of AÎ² Peptides with Implications for Rates of Fibril Formation. Journal of Physical Chemistry B, 2009, 113, 1162-1172.	1.2	147
147	Allostery Wiring Diagrams in the Transitions that Drive the GroEL Reaction Cycle. Journal of Molecular Biology, 2009, 387, 390-406.	2.0	77
148	Metal Ion Dependence of Cooperative Collapse Transitions in RNA. Journal of Molecular Biology, 2009, 393, 753-764.	2.0	86
149	Coupling between Normal Modes Drives Protein Conformational Dynamics: Illustrations Using Allosteric Transitions in Myosin II. Biophysical Journal, 2009, 96, 2128-2137.	0.2	47
150	Crowding Effects on the Mechanical Stability and Unfolding Pathways of Ubiquitin. Journal of Physical Chemistry B, 2009, 113, 359-368.	1.2	27
151	Identifying natural substrates for chaperonins using a sequence-based approach. Protein Science, 2009, 14, 193-201.	3.1	22
152	Collapse transition in proteins. Physical Chemistry Chemical Physics, 2009, 11, 83-93.	1.3	125
153	Allosteric Transitions in Biological Nanomachines are Described by Robust Normal Modes of Elastic Networks. Current Protein and Peptide Science, 2009, 10, 128-132.	0.7	43
154	Kinetic Model for the Coupling between Allosteric Transitions in GroEL and Substrate Protein Folding and Aggregation. Journal of Molecular Biology, 2008, 377, 1279-1295.	2.0	28
155	Structures and Free-Energy Landscapes of the Wild Type and Mutants of the AÎ²21â€“30 Peptide Are Determined by an Interplay between Intrapeptide Electrostatic and Hydrophobic Interactions. Journal of Molecular Biology, 2008, 379, 815-829.	2.0	71
156	Interactions between amino acid side chains in cylindrical hydrophobic nanopores with applications to peptide stability. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17636-17641.	3.3	47
157	Multiple Probes are Required to Explore and Control the Rugged Energy Landscape of RNA Hairpins. Journal of the American Chemical Society, 2008, 130, 1538-1539.	6.6	73
158	Effects of denaturants and osmolytes on proteins are accurately predicted by the molecular transfer model. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13403-13408.	3.3	182
159	Factors Governing Helix Formation in Peptides Confined to Carbon Nanotubes. Nano Letters, 2008, 8, 3702-3708.	4.5	38
160	Relative Stability of Helices Determines the Folding Landscape of Adenine Riboswitch Aptamers. Journal of the American Chemical Society, 2008, 130, 14080-14081.	6.6	80
161	Force-dependent hopping rates of RNA hairpins can be estimated from accurate measurement of the folding landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9604-9609.	3.3	74
162	Urea denaturation by stronger dispersion interactions with proteins than water implies a 2-stage unfolding. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16928-16933.	3.3	470

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163	Minimal Models for Proteins and RNA: From Folding to Function. Progress in Molecular Biology and Translational Science, 2008, 84, 203-250.	0.9	38
164	Intermediates and Transition States in Protein Folding. , 2007, 350, 277-304.		9
165	Measuring the energy landscape roughness and the transition state location of biomolecules using single molecule mechanical unfolding experiments. Journal of Physics Condensed Matter, 2007, 19, 113101.	0.7	83
166	Monomer adds to preformed structured oligomers of Abeta-peptides by a two-stage dock-lock mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 111-116.	3.3	344
167	Revealing the bifurcation in the unfolding pathways of GFP by using single-molecule experiments and simulations. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20268-20273.	3.3	145
168	Allosteric Communication in Dihydrofolate Reductase: Signaling Network and Pathways for Closed to Occluded Transition and Back. Journal of Molecular Biology, 2007, 374, 250-266.	2.0	69
169	Charge Density of Divalent Metal Cations Determines RNA Stability. Journal of the American Chemical Society, 2007, 129, 2676-2682.	6.6	169
170	Stretching Homopolymers. Macromolecules, 2007, 40, 7343-7353.	2.2	39
171	Interactions between Hydrophobic and Ionic Solutes in Aqueous Guanidinium Chloride and Urea Solutions:Â Lessons for Protein Denaturation Mechanism. Journal of the American Chemical Society, 2007, 129, 7346-7353.	6.6	324
172	Mechanical Unfolding of RNA: From Hairpins to Structures with Internal Multiloops. Biophysical Journal, 2007, 92, 731-743.	0.2	83
173	Allosteric Transitions in the Chaperonin GroEL are Captured by a Dominant Normal Mode that is Most Robust to Sequence Variations. Biophysical Journal, 2007, 93, 2289-2299.	0.2	111
174	Dynamics of Asp23â^'Lys28 Salt-Bridge Formation in Aî²10-35Monomers. Journal of the American Chemical Society, 2006, 128, 16159-16168.	6.6	200
175	Forced-Unfolding and Force-Quench Refolding of RNA Hairpins. Biophysical Journal, 2006, 90, 3410-3427.	0.2	91
176	Nanoporeâ€"Protein Interactions Dramatically Alter Stability and Yield of the Native State in Restricted Spaces. Journal of Molecular Biology, 2006, 357, 632-643.	2.0	85
177	Counterion Charge Density Determines the Position and Plasticity of RNA Folding Transition States. Journal of Molecular Biology, 2006, 359, 446-454.	2.0	59
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