

HEAT CAPACITY IN PROTEINS

Annual Review of Physical Chemistry

56, 521-548

DOI: [10.1146/annurev.physchem.56.092503.141202](https://doi.org/10.1146/annurev.physchem.56.092503.141202)

Citation Report

#	ARTICLE	IF	CITATIONS
3	Hydration Changes in the Association of Hoechst 33258 with DNA. <i>Biochemistry</i> , 2005, 44, 16988-16997.	1.2	50
4	Thermodynamics of Nucleotide Binding to Actomyosin V and VI: A Positive Heat Capacity Change Accompanies Strong ADP Binding. <i>Biochemistry</i> , 2005, 44, 10238-10249.	1.2	51
5	Explanation of the Stability of Thermophilic Proteins Based on Unique Micromorphology. <i>Biophysical Journal</i> , 2006, 90, 4204-4212.	0.2	31
6	Micellization of Bovine β -Casein Studied by Isothermal Titration Microcalorimetry and Cryogenic Transmission Electron Microscopy. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 5555-5561.	2.4	113
7	Thermodynamics of Tryptophan-Mediated Activation of the trpRNA-Binding Attenuation Protein. <i>Biochemistry</i> , 2006, 45, 7844-7853.	1.2	23
8	Thermodynamics of Statherin Adsorption onto Hydroxyapatite. <i>Biochemistry</i> , 2006, 45, 5576-5586.	1.2	74
9	Arginine Methylation in a β -Hairpin Peptide: Implications for Arginine Interactions, Cp, and the Cold Denatured State. <i>Journal of the American Chemical Society</i> , 2006, 128, 12735-12742.	6.6	79
10	Heat Capacity Changes Associated with DNA Duplex Formation: A Salt- and Sequence-Dependent Effects. <i>Biochemistry</i> , 2006, 45, 604-616.	1.2	47
11	Thermodynamic Characterization of Binding of <i>Oxytricha nova</i> Single Strand Telomere DNA with the Alpha Protein N-terminal Domain. <i>Journal of Molecular Biology</i> , 2006, 359, 1217-1234.	2.0	17
12	Thermodynamic and Kinetic Characterization of Ligand Binding to the Purine Riboswitch Aptamer Domain. <i>Journal of Molecular Biology</i> , 2006, 359, 754-768.	2.0	246
13	The Alkali Molten Globule State of Horse Ferricytochrome c: Observation of Cold Denaturation. <i>Journal of Molecular Biology</i> , 2006, 364, 483-495.	2.0	34
14	Amino acid substitutions affecting protein dynamics in eglin C do not affect heat capacity change upon unfolding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 295-300.	1.5	4
15	Protein stability and dynamics in the pressure-temperature plane. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 346-354.	1.1	83
16	Mechanistic Studies of Ubiquitin C-Terminal Hydrolase L1. <i>Biochemistry</i> , 2006, 45, 2443-2452.	1.2	34
17	Phase transition in polypeptides: a step towards the understanding of protein folding. <i>European Physical Journal D</i> , 2006, 40, 363-367.	0.6	24
19	Heat capacity changes associated with nucleic acid folding. <i>Biopolymers</i> , 2006, 82, 38-58.	1.2	96
20	Structural Reorganization and the Cooperative Binding of Single-stranded Telomere DNA in <i>Sterkiella nova</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 40124-40134.	1.6	13
21	Positive and Negative Design in Stability and Thermal Adaptation of Natural Proteins. <i>PLoS Computational Biology</i> , 2007, 3, e52.	1.5	116

#	ARTICLE	IF	CITATIONS
22	Thermodynamical properties of reaction intermediates during apoplastocyanin folding in time domain. <i>Journal of Chemical Physics</i> , 2007, 127, 175103.	1.2	31
23	Comparative modeling of the conformational stability of chymotrypsin inhibitor 2 protein mutants using amino acid sequence autocorrelation (AASA) and amino acid 3D autocorrelation (AA3DA) vectors and ensembles of Bayesian-regularized genetic neural networks. <i>Molecular Simulation</i> , 2007, 33, 1045-1056.	0.9	4
24	Thermodynamic characterization of specific interactions between the human Lon protease and G-quartet DNA. <i>Nucleic Acids Research</i> , 2007, 36, 1273-1287.	6.5	45
25	Enhancing Recombinant Protein Quality and Yield by Protein Stability Profiling. <i>Journal of Biomolecular Screening</i> , 2007, 12, 418-428.	2.6	76
26	An ultraviolet photoacoustic spectroscopy study of the interaction between Lys49 α -phospholipase A2 and amphiphilic molecules. <i>Biochemical and Biophysical Research Communications</i> , 2007, 353, 889-894.	1.0	3
27	Rigidification of a Flexible Protease Inhibitor Variant upon Binding to Trypsin. <i>Journal of Molecular Biology</i> , 2007, 366, 230-243.	2.0	31
28	Structural and Thermodynamic Insights into the Assembly of the Heteromeric Pyridoxal Phosphate Synthase from <i>Plasmodium falciparum</i> . <i>Journal of Molecular Biology</i> , 2007, 374, 732-748.	2.0	17
29	The Thermodynamic Solvate Difference Rule: α Solvation Parameters and Their Use in Interpretation of the Role of Bound Solvent in Condensed-Phase Solvates. <i>Inorganic Chemistry</i> , 2007, 46, 9768-9778.	1.9	46
30	Binding of a Single Zinc Ion to One Subunit of Copper α Zinc Superoxide Dismutase Apoprotein Substantially Influences the Structure and Stability of the Entire Homodimeric Protein. <i>Journal of the American Chemical Society</i> , 2007, 129, 4575-4583.	6.6	97
31	Thermodynamic Characterization of the Protein α Protein Interaction in the Heteromeric <i>Bacillus subtilis</i> Pyridoxalphosphate Synthase. <i>Biochemistry</i> , 2007, 46, 5131-5139.	1.2	36
32	Conformational Dynamics and the Energetics of Protein α Ligand Interactions: α Role of Interdomain Loop in Human Cytochrome P450 Reductase. <i>Biochemistry</i> , 2007, 46, 8244-8255.	1.2	29
33	Ligand Binding and Protein Dynamics in Lactate Dehydrogenase. <i>Biophysical Journal</i> , 2007, 93, 1474-1483.	0.2	64
34	Applications of isothermal titration calorimetry in RNA biochemistry and biophysics. <i>Biopolymers</i> , 2007, 87, 293-301.	1.2	98
35	Thermostable variants of the recombinant xylanase a from <i>Bacillus subtilis</i> produced by directed evolution show reduced heat capacity changes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1280-1293.	1.5	72
36	Energetics of protein homodimerization: Effects of water sequestering on the formation of β -lactoglobulin dimer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 1475-1487.	1.5	50
37	Thermodynamic characterization of interleukin-8 monomer binding to CXCR1 receptor N-terminal domain. <i>FEBS Journal</i> , 2007, 274, 241-251.	2.2	40
38	Is there a relationship between protein thermal stability and the denaturation heat capacity change?. <i>Journal of Thermal Analysis and Calorimetry</i> , 2008, 93, 429-438.	2.0	10
39	Photoacoustic spectroscopy of aromatic amino acids in proteins. <i>European Biophysics Journal</i> , 2008, 37, 205-212.	1.2	7

#	ARTICLE	IF	CITATIONS
40	Thermodynamics of Tâ€cell receptorâ€™ peptide/MHC interactions: progress and opportunities. <i>Journal of Molecular Recognition</i> , 2008, 21, 275-287.	1.1	61
41	Heat capacity changes associated with guanine quadruplex formation: An isothermal titration calorimetry study. <i>Biopolymers</i> , 2008, 89, 302-309.	1.2	40
42	Thermodynamics and mechanism of cutinase stabilization by trehalose. <i>Biopolymers</i> , 2008, 89, 538-547.	1.2	31
43	Conformational constraint in protein ligand design and the inconsistency of binding entropy. <i>Biopolymers</i> , 2008, 89, 653-667.	1.2	69
44	Î±-helixâ€™ random coil phase transition: analysis of ab initio theory predictions. <i>European Physical Journal D</i> , 2008, 46, 227-240.	0.6	19
45	Ab initio theory of helixâ€™ coil phase transition. <i>European Physical Journal D</i> , 2008, 46, 215-225.	0.6	17
46	Structural mobility of the monomeric Câ€™terminal domain of the HIVâ€™1 capsid protein. <i>FEBS Journal</i> , 2008, 275, 3299-3311.	2.2	23
47	The Cardiac Ca ²⁺ -Sensitive Regulatory Switch, a System in Dynamic Equilibrium. <i>Biophysical Journal</i> , 2008, 95, 4772-4789.	0.2	16
48	Calculation of Protein Heat Capacity from Replica-Exchange Molecular Dynamics Simulations with Different Implicit Solvent Models. <i>Journal of Physical Chemistry B</i> , 2008, 112, 15064-15073.	1.2	35
49	Solvent Electrostriction-Driven Peptide Folding Revealed by Quasi-Gaussian Entropy Theory and Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2008, 112, 11155-11163.	1.2	9
50	Analysis of the Thermodynamics of Binding of an SH3 Domain to Proline-rich Peptides using a Chimeric Fusion Protein. <i>Journal of Molecular Biology</i> , 2008, 377, 117-135.	2.0	17
51	Thermodynamic analysis reveals that GTP binding affects the interaction between the Î±- and Î³-subunits of translation initiation factor 2. <i>Biochemical and Biophysical Research Communications</i> , 2008, 371, 596-599.	1.0	3
52	Determination of the thermodynamics of carbonic anhydrase acid-unfolding by titration calorimetry. <i>Journal of Proteomics</i> , 2008, 70, 1043-1047.	2.4	8
53	Stability and kinetics of G-quadruplex structures. <i>Nucleic Acids Research</i> , 2008, 36, 5482-5515.	6.5	644
54	Proteometric modelling of protein conformational stability using amino acid sequence autocorrelation vectors and genetic algorithm-optimised support vector machines. <i>Molecular Simulation</i> , 2008, 34, 857-872.	0.9	3
55	Energetics and Role of the Hydrophobic Interaction during Photoreaction of the BLUF Domain of AppA. <i>Journal of Physical Chemistry B</i> , 2008, 112, 1494-1501.	1.2	14
56	Heat Capacity, Configurational Entropy, and the Role of Ionic Interactions in Protein Thermostability. <i>Biotechnology and Biotechnological Equipment</i> , 2008, 22, 612-619.	0.5	6
57	Structural Flexibility in Hydrated Proteins. <i>Journal of Physical Chemistry B</i> , 2008, 112, 10071-10075.	1.2	6

#	ARTICLE	IF	CITATIONS
58	Determination of Protein Denaturation and Glass Transition Temperatures Using High-Frequency Time Domain Reflectometry. <i>Journal of Physical Chemistry B</i> , 2008, 112, 15903-15906.	1.2	7
59	Kinetic Analysis of Interaction of BRCA1 Tandem Breast Cancer C-Terminal Domains with Phosphorylated Peptides Reveals Two Binding Conformations. <i>Biochemistry</i> , 2008, 47, 9866-9879.	1.2	15
60	Protein's unfolding and the glass transition: a common thermodynamic signature.. <i>AIP Conference Proceedings</i> , 2008, , .	0.3	1
61	Impact of the Oxidized Guanine Lesion Spiroiminodihydantoin on the Conformation and Thermodynamic Stability of a 15-mer DNA Duplex. <i>Biochemistry</i> , 2008, 47, 2584-2591.	1.2	23
62	The pretranslocation ribosome is targeted by GTP-bound EF-G in partially activated form. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15678-15683.	3.3	36
63	FSH and TSH binding to their respective receptors: similarities, differences and implication for glycoprotein hormone specificity. <i>Journal of Molecular Endocrinology</i> , 2008, 41, 145-164.	1.1	27
64	Dynamical transition, hydrophobic interface, and the temperature dependence of electrostatic fluctuations in proteins. <i>Physical Review E</i> , 2008, 78, 061901.	0.8	21
65	Conformational changes and flexibility in T-cell receptor recognition of peptide-MHC complexes. <i>Biochemical Journal</i> , 2008, 415, 183-196.	1.7	99
66	Conformational energies and entropies of peptides, and the peptide-protein binding problem. <i>Physical Biology</i> , 2009, 6, 036014.	0.8	10
67	Structural Basis for p300 Taz2-p53 TAD1 Binding and Modulation by Phosphorylation. <i>Structure</i> , 2009, 17, 202-210.	1.6	126
69	The Thermodynamic Influence of Trapped Water Molecules on a Protein-Ligand Interaction. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 5207-5210.	7.2	36
70	Phase transitions in polypeptides: analysis of energy fluctuations. <i>European Physical Journal D</i> , 2009, 51, 25-32.	0.6	15
71	Ligand-Induced Changes in the Structure and Dynamics of Escherichia coli Peptide Deformylase. <i>Biochemistry</i> , 2009, 48, 7595-7607.	1.2	10
72	Binding Mechanism of an SH3 Domain Studied by NMR and ITC. <i>Journal of the American Chemical Society</i> , 2009, 131, 4355-4367.	6.6	99
73	Protein Cold Denaturation as Seen From the Solvent. <i>Journal of the American Chemical Society</i> , 2009, 131, 1025-1036.	6.6	76
74	Thermodynamic Analysis Reveals a Temperature-dependent Change in the Catalytic Mechanism of <i>Bacillus stearothermophilus</i> Tyrosyl-tRNA Synthetase. <i>Journal of Biological Chemistry</i> , 2009, 284, 4179-4190.	1.6	24
75	Thermodynamics of GTP and GDP Binding to Bacterial Initiation Factor 2 Suggests Two Types of Structural Transitions. <i>Journal of Molecular Biology</i> , 2009, 394, 621-626.	2.0	23
76	Two Distinct Motifs within the p53 Transactivation Domain Bind to the Taz2 Domain of p300 and Are Differentially Affected by Phosphorylation. <i>Biochemistry</i> , 2009, 48, 1244-1255.	1.2	63

#	ARTICLE	IF	CITATIONS
77	Heat capacity changes in carbohydrates and protein-carbohydrate complexes. <i>Biochemical Journal</i> , 2009, 420, 239-247.	1.7	12
78	Densities, Specific Heat Capacities, Apparent and Partial Molar Volumes and Heat Capacities of Glycine in Aqueous Solutions of Formamide, Acetamide, and N,N-Dimethylacetamide at T=298.15 K and Ambient Pressure. <i>Journal of Solution Chemistry</i> , 2010, 39, 877-896.	0.6	28
79	Survey of the year 2008: applications of isothermal titration calorimetry. <i>Journal of Molecular Recognition</i> , 2010, 23, 395-413.	1.1	59
80	Post-mortem calorimetric and biochemical profiles of Chinook salmon (<i>Oncorhynchus tshawytscha</i>) white muscle following rested and exhausted harvesting. <i>Thermochimica Acta</i> , 2010, 499, 133-143.	1.2	9
81	Hydrophobic interaction chromatography of proteins: Thermodynamic analysis of conformational changes. <i>Journal of Chromatography A</i> , 2010, 1217, 184-190.	1.8	63
82	Thermodynamics of radicicol binding to human Hsp90 alpha and beta isoforms. <i>Biophysical Chemistry</i> , 2010, 152, 153-163.	1.5	23
83	New concept for quantification of similarity relates entropy and energy of objects: First and Second Law entangled, group behavior of micro black holes expected. <i>Journal of Systems Chemistry</i> , 2010, 1, 2.	1.7	2
84	Structural and thermodynamic analysis of the GFP:GFP nanobody complex. <i>Protein Science</i> , 2010, 19, 2389-2401.	3.1	317
85	Conformational changes in polypeptides and proteins. <i>International Journal of Quantum Chemistry</i> , 2010, 110, 257-269.	1.0	3
86	Human telomeric G-quadruplex: thermodynamic and kinetic studies of telomeric quadruplex stability. <i>FEBS Journal</i> , 2010, 277, 1098-1106.	2.2	119
87	A chemically modified Î±-amylase with a molten-globule state has entropically driven enhanced thermal stability. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 769-780.	1.0	33
88	Thermodynamic Analysis of the CSL-Notch Interaction. <i>Journal of Biological Chemistry</i> , 2010, 285, 6681-6692.	1.6	40
89	Picomole-scale characterization of protein stability and function by quantitative cysteine reactivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4908-4913.	3.3	24
90	Pressure Perturbation Calorimetry and the Thermodynamics of Noncovalent Interactions in Water: Comparison of Protein-Protein, Protein-Ligand, and Cyclodextrin-Adamantane Complexes. <i>Journal of Physical Chemistry B</i> , 2010, 114, 16228-16235.	1.2	40
91	Analyzing Protein Folding Cooperativity by Differential Scanning Calorimetry and NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2010, 132, 6214-6222.	6.6	34
92	A Complete Thermodynamic Characterization of Electrostatic and Hydrophobic Associations in the Temperature Range 0 to 100 Å°C from Explicit-Solvent Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 1293-1306.	2.3	25
93	Assessing Energetic Contributions to Binding from a Disordered Region in a Protein-Protein Interaction. <i>Biochemistry</i> , 2010, 49, 9256-9268.	1.2	17
94	Evidence, from Simulations, of a Single State with Residual Native Structure at the Thermal Denaturation Midpoint of a Small Globular Protein. <i>Journal of the American Chemical Society</i> , 2010, 132, 9444-9452.	6.6	31

#	ARTICLE	IF	CITATIONS
95	Comparison of Entropic Contributions to Binding in a "Hydrophilic" versus "Hydrophobic" Ligand-Protein Interaction. <i>Journal of the American Chemical Society</i> , 2010, 132, 8682-8689.	6.6	46
96	Energetic Effects of Magnesium in the Recognition of Adenosine Nucleotides by the F ₁ -ATPase F ₂ Subunit. <i>Biochemistry</i> , 2010, 49, 5258-5268.	1.2	22
97	Protein Heat Capacity: An Anomaly that Maybe Never Was. <i>Journal of Physical Chemistry Letters</i> , 2010, 1, 3298-3304.	2.1	62
98	Half-Solidity of Tetrahedral-like Al ₅₅ Clusters. <i>ACS Nano</i> , 2010, 4, 1092-1098.	7.3	14
99	The hydrophobic effect and its role in cold denaturation. <i>Cryobiology</i> , 2010, 60, 91-99.	0.3	164
100	Predicting solvation energies for kinetic modeling. <i>Annual Reports on the Progress of Chemistry Section C</i> , 2010, 106, 211.	4.4	59
101	Microtubule and MAPs. <i>Methods in Cell Biology</i> , 2010, 95, 449-480.	0.5	12
102	Peptide-Mediated Constructs of Quantum Dot Nanocomposites for Enzymatic Control of Nonradiative Energy Transfer. <i>Nano Letters</i> , 2011, 11, 1530-1539.	4.5	38
103	Antibiotic Selection by the Promiscuous Aminoglycoside Acetyltransferase-(3)-IIIb Is Thermodynamically Achieved through the Control of Solvent Rearrangement. <i>Biochemistry</i> , 2011, 50, 9309-9317.	1.2	10
104	A Direct Comparison of the MM-GB/SA Scoring Procedure and Free-Energy Perturbation Calculations Using Carbonic Anhydrase as a Test Case: Strengths and Pitfalls of Each Approach. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 2296-2306.	2.3	23
105	Structural Transitions of Translation Initiation Factor IF2 upon GDPNP and GDP Binding in Solution. <i>Biochemistry</i> , 2011, 50, 9779-9787.	1.2	10
107	Energetics of SecA Dimerization. <i>Journal of Molecular Biology</i> , 2011, 408, 87-98.	2.0	29
109	Fluctuation theory of molecular association and conformational equilibria. <i>Journal of Chemical Physics</i> , 2011, 135, 014502.	1.2	20
110	The Nucleotide Exchange Factor Ric-8A Is a Chaperone for the Conformationally Dynamic Nucleotide-Free State of G α i1. <i>PLoS ONE</i> , 2011, 6, e23197.	1.1	52
111	Role of Packing, Hydration, and Fluctuations on Thermostability. , 2011, , 21-46.		0
112	Assembly and Solution Structure of the Core Retromer Protein Complex. <i>Traffic</i> , 2011, 12, 56-71.	1.3	76
113	The Contribution of Entropy, Enthalpy, and Hydrophobic Desolvation to Cooperativity in Repeat-Protein Folding. <i>Structure</i> , 2011, 19, 349-360.	1.6	67
114	Partition Function of a Polypeptide. , 2011, , 55-67.		0

#	ARTICLE	IF	CITATIONS
115	Phase Transitions in Polypeptides. , 2011, , 69-99.		0
116	NMR-based structural biology of proteins in supercooled water. Journal of Structural and Functional Genomics, 2011, 12, 1-7.	1.2	14
117	A miniaturized technique for assessing protein thermodynamics and function using fast determination of quantitative cysteine reactivity. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1034-1047.	1.5	26
118	Indefinite noncooperative self-association of chicken deoxy hemoglobin D. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1499-1512.	1.5	5
119	Structure of Sir2Tm bound to a propionylated peptide. Protein Science, 2011, 20, 131-139.	3.1	21
120	Strategies for the Thermodynamic Characterization of Linked Binding/Local Folding Reactions Within the Native State. Methods in Enzymology, 2011, 492, 253-282.	0.4	14
121	Relationships between ligand binding sites, protein architecture and correlated paths of energy and conformational fluctuations. Physical Biology, 2011, 8, 056003.	0.8	20
122	Mechanism of the hydrophobic effect in the biomolecular recognition of arylsulfonamides by carbonic anhydrase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17889-17894.	3.3	304
123	Entropy-enthalpy transduction caused by conformational shifts can obscure the forces driving protein-ligand binding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20006-20011.	3.3	109
124	Interaction of water with the G-quadruplex loop contributes to the binding energy of G-quadruplex to protein. Molecular BioSystems, 2012, 8, 2766.	2.9	17
125	Influence of Fluorination on the Thermodynamics of Protein Folding. Journal of the American Chemical Society, 2012, 134, 13027-13034.	6.6	38
126	Core-Binding Factor \hat{I}^2 Increases the Affinity between Human Cullin 5 and HIV-1 Vif within an E3 Ligase Complex. Biochemistry, 2012, 51, 8702-8704.	1.2	26
127	Thermodynamics of Coupled Folding in the Interaction of Archaeal RNase P Proteins RPP21 and RPP29. Biochemistry, 2012, 51, 926-935.	1.2	13
128	The Distal C-Terminal Region of the KcsA Potassium Channel Is a pH-Dependent Tetramerization Domain. Journal of Molecular Biology, 2012, 418, 237-247.	2.0	9
129	Electronic specific heat of an \hat{I}^3 -helical polypeptide and its biochemical variants. Chemical Physics Letters, 2012, 542, 123-127.	1.2	3
130	Thermodynamics of Ligand Binding to a Heterogeneous RNA Population in the Malachite Green Aptamer. Biochemistry, 2012, 51, 565-572.	1.2	24
131	Trivalent chromium and aluminum affect the thermostability and conformation of collagen very differently. Journal of Inorganic Biochemistry, 2012, 117, 124-130.	1.5	24
132	Analysis of RNA Folding and Ligand Binding by Conventional and High-Throughput Calorimetry. Methods in Molecular Biology, 2012, 905, 145-174.	0.4	8

#	ARTICLE	IF	CITATIONS
133	Spectroscopic Methods of Analysis. <i>Methods in Molecular Biology</i> , 2012, , .	0.4	7
134	Synthetic Polymer Nanoparticleâ€“Polysaccharide Interactions: A Systematic Study. <i>Journal of the American Chemical Society</i> , 2012, 134, 2681-2690.	6.6	91
135	Thermodynamics of Aryl-Dihydroxyphenyl-Thiadiazole Binding to Human Hsp90. <i>PLoS ONE</i> , 2012, 7, e36899.	1.1	27
136	Temperatureâ€“dependent study reveals that dynamics of hydrophobic residues plays an important functional role in the mitochondrial Tim9â€“Tim10 complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 602-615.	1.5	6
137	Thermal coefficients of the methyl groups within ubiquitin. <i>Protein Science</i> , 2012, 21, 562-570.	3.1	18
138	Thermophilic proteins: insight and perspective from in silico experiments. <i>Chemical Society Reviews</i> , 2012, 41, 1665-1676.	18.7	68
139	In-depth biophysical analysis of interactions between therapeutic antibodies and the extracellular domain of the epidermal growth factor receptor. <i>Analytical Biochemistry</i> , 2012, 421, 138-151.	1.1	13
140	Structureâ€“activity relationships for the binding of polymyxins with human Î±-1-acid glycoprotein. <i>Biochemical Pharmacology</i> , 2012, 84, 278-291.	2.0	40
141	Van â€“t Hoff global analyses of variable temperature isothermal titration calorimetry data. <i>Thermochimica Acta</i> , 2012, 527, 148-157.	1.2	19
142	Applications of isothermal titration calorimetry in pure and applied researchâ€“survey of the literature from 2010. <i>Journal of Molecular Recognition</i> , 2012, 25, 32-52.	1.1	155
143	Probing Protein Surface with a Solvent Mimetic Carbene Coupled to Detection by Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 30-42.	1.2	10
144	The Binding of Benzoarylsulfonamide Ligands to Human Carbonic Anhydrase is Insensitive to Formal Fluorination of the Ligand. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 7714-7717.	7.2	47
146	Multimeric Complexes among Ankyrin-Repeat and SOCS-box Protein 9 (ASB9), ElonginBC, and Cullin 5: Insights into the Structure and Assembly of ECS-type Cullin-RING E3 Ubiquitin Ligases. <i>Biochemistry</i> , 2013, 52, 5236-5246.	1.2	24
147	Molecular Dynamics Perspective on the Protein Thermal Stability: A Case Study Using SAICAR Synthetase. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2448-2461.	2.5	29
149	The Role of Allosteric Coupling on Thermal Activation of Thermo-TRP Channels. <i>Biophysical Journal</i> , 2013, 104, 2160-2169.	0.2	67
150	How Conformational Flexibility Stabilizes the Hyperthermophilic Elongation Factor G-Domain. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13775-13785.	1.2	34
151	Enthalpic Signature of Methonium Desolvation Revealed in a Synthetic Hostâ€“Guest System Based on Cucurbit[7]uril. <i>Journal of the American Chemical Society</i> , 2013, 135, 6084-6091.	6.6	9
152	Entropyâ€“enthalpy compensation of biomolecular systems in aqueous phase: a dry perspective. <i>Monatshefte FÃ¼r Chemie</i> , 2013, 144, 59-65.	0.9	19

#	ARTICLE	IF	CITATIONS
153	Structure of Phosphorylated SF1 Bound to U2AF65 in an Essential Splicing Factor Complex. <i>Structure</i> , 2013, 21, 197-208.	1.6	55
154	Binding thermodynamics of a glutamate transporter homolog. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 634-640.	3.6	89
155	Energetics of oligomeric protein folding and association. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 44-64.	1.4	47
156	Homotropic Cooperativity from the Activation Pathway of the Allosteric Ligand-Responsive Regulatory <i>trp</i> RNA-Binding Attenuation Protein. <i>Biochemistry</i> , 2013, 52, 8855-8865.	1.2	4
157	Binding of a perfluorinated surfactant to β -lactoglobulin in aqueous solutions. <i>Food Hydrocolloids</i> , 2013, 30, 241-248.	5.6	6
158	Solvation thermodynamics and heat capacity of polar and charged solutes in water. <i>Journal of Chemical Physics</i> , 2013, 138, 115101.	1.2	21
159	Thermodynamics In Multiphase Biocatalysis. , 2013, , 311-336.		0
160	An Overview on the Thermodynamic Techniques used in Food Chemistry. <i>Modern Chemistry & Applications</i> , 2014, 02, .	0.2	2
161	Criteria for Selecting PEGylation Sites on Proteins for Higher Thermodynamic and Proteolytic Stability. <i>Journal of the American Chemical Society</i> , 2014, 136, 17547-17560.	6.6	54
162	Peptide-dependent Conformational Fluctuation Determines the Stability of the Human Leukocyte Antigen Class I Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 24680-24690.	1.6	37
163	Thermodynamic Characterization of the Unfolding of the Prion Protein. <i>Biophysical Journal</i> , 2014, 106, 410-420.	0.2	26
165	Infinitely Dilute Partial Molar Properties of Proteins from Computer Simulation. <i>Journal of Physical Chemistry B</i> , 2014, 118, 12844-12854.	1.2	11
166	Folding thermodynamics of protein-like oligomers with heterogeneous backbones. <i>Chemical Science</i> , 2014, 5, 3325-3330.	3.7	36
167	A monovalent cation acts as structural and catalytic cofactor in translational <i>GTP</i> ases. <i>EMBO Journal</i> , 2014, 33, 2547-2563.	3.5	29
168	Dynamic Inhomogeneity in the Photodynamics of Cyanobacterial Phytochrome Cph1. <i>Biochemistry</i> , 2014, 53, 2818-2826.	1.2	65
169	Allosteric Regulation in Phosphofructokinase from the Extreme Thermophile <i>Thermus thermophilus</i> . <i>Biochemistry</i> , 2014, 53, 270-278.	1.2	14
170	Cold Denaturation of β -Synuclein Amyloid Fibrils. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7799-7804.	7.2	72
171	Solvent Reorganization Plays a Temperature-Dependent Role in Antibiotic Selection by a Thermostable Aminoglycoside Nucleotidyltransferase-4. <i>Biochemistry</i> , 2014, 53, 5544-5550.	1.2	4

#	ARTICLE	IF	CITATIONS
172	Temperature and pressure effects on C112S azurin: Volume, expansivity, and flexibility changes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1787-1798.	1.5	8
173	Role of Ordered Proteins in the Folding-Upon-Binding of Intrinsically Disordered Proteins. <i>Journal of Physical Chemistry Letters</i> , 2014, 5, 833-838.	2.1	21
174	Thermodynamic properties and entropy scaling law for diffusivity in soft spheres. <i>Physical Review E</i> , 2014, 90, 012106.	0.8	26
175	Fluorinated Proteins: From Design and Synthesis to Structure and Stability. <i>Accounts of Chemical Research</i> , 2014, 47, 2878-2886.	7.6	147
176	The Complex Energy Landscape of the Protein IscU. <i>Biophysical Journal</i> , 2015, 109, 1019-1025.	0.2	14
177	Rigidity versus flexibility: the dilemma of understanding protein thermal stability. <i>FEBS Journal</i> , 2015, 282, 3899-3917.	2.2	206
178	- Implicit Solvation Methods in the Study of Ligand-Protein Interactions. , 2015, , 266-291.		0
179	The inverted free energy landscape of an intrinsically disordered peptide by simulations and experiments. <i>Scientific Reports</i> , 2015, 5, 15449.	1.6	118
180	Revealing the peptide presenting process of human leukocyte antigen through the analysis of fluctuation. <i>Biophysics (Nagoya-shi, Japan)</i> , 2015, 11, 103-106.	0.4	0
181	Destabilization of the dimer interface is a common consequence of diverse ALS-associated mutations in metal free SOD1. <i>Protein Science</i> , 2015, 24, 2081-2089.	3.1	40
182	Thermodynamics of Δ^2 dissociation from a fibril: Enthalpy, entropy, and volumetric properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1963-1972.	1.5	6
183	Zinc as chaperone-mimicking agent for retardation of amyloid Δ^2 peptide fibril formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5407-5412.	3.3	102
184	Thermodynamic implications of high Δ^2 of thermoTRP channels in living cells. <i>Biophysics (Nagoya-shi, Japan)</i> , 2015, 11, 33-38.	0.4	35
185	On the molecular basis of the high affinity binding of basic amino acids to LAOBP, a periplasmic binding protein from <i>Salmonella typhimurium</i> . <i>Journal of Molecular Recognition</i> , 2015, 28, 108-116.	1.1	10
186	Disorder-To-Order Transition of MAGI-1 PDZ1 C-Terminal Extension upon Peptide Binding: Thermodynamic and Dynamic Insights. <i>Biochemistry</i> , 2015, 54, 1327-1337.	1.2	10
187	A New General Model for Predicting Melting Thermodynamics of Complementary and Mismatched B-Form Duplexes Containing Locked Nucleic Acids: Application to Probe Design for Digital PCR Detection of Somatic Mutations. <i>Biochemistry</i> , 2015, 54, 1338-1352.	1.2	10
188	Global ITC fitting methods in studies of protein allostery. <i>Methods</i> , 2015, 76, 149-161.	1.9	36
189	Isothermal titration calorimetry of ion-coupled membrane transporters. <i>Methods</i> , 2015, 76, 171-182.	1.9	21

#	ARTICLE	IF	CITATIONS
190	Biophysical analysis of thermosensitive TRP channels with a special focus on the cold receptor TRPM8. <i>Temperature</i> , 2015, 2, 188-200.	1.7	15
191	Particle and Energy Pair and Triplet Correlations in Liquids and Liquid Mixtures from Experiment and Simulation. <i>Journal of Physical Chemistry B</i> , 2015, 119, 7761-7777.	1.2	15
192	Free energetics of carbon nanotube association in aqueous inorganic NaCl salt solutions: Temperature effects using all-atom molecular dynamics simulations. <i>Journal of Computational Chemistry</i> , 2015, 36, 1196-1212.	1.5	2
193	Thermodynamics and solvent linkage of macromolecule-ligand interactions. <i>Methods</i> , 2015, 76, 51-60.	1.9	17
194	Defining a Two-pronged Structural Model for PB1 (Phox/Bem1p) Domain Interaction in Plant Auxin Responses. <i>Journal of Biological Chemistry</i> , 2015, 290, 12868-12878.	1.6	31
195	Biophysical Studies on Interactions and Assembly of Full-size E3 Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2015, 290, 4178-4191.	1.6	24
196	Thermodynamics of Rev-RNA Interactions in HIV-1 Rev-RRE Assembly. <i>Biochemistry</i> , 2015, 54, 6545-6554.	1.2	16
197	The impact of Hydrogen peroxide on structure, stability and functional properties of Human R12C mutant α -crystallin: The imperative insights into pathomechanism of the associated congenital cataract incidence. <i>Free Radical Biology and Medicine</i> , 2015, 89, 819-830.	1.3	25
198	Prediction of the optimal set of contacts to fold the smallest knotted protein. <i>Journal of Physics Condensed Matter</i> , 2015, 27, 354109.	0.7	19
199	Bacterial Thymidylate Synthase Binds Two Molecules of Substrate and Cofactor without Cooperativity. <i>Journal of the American Chemical Society</i> , 2015, 137, 14260-14263.	6.6	18
200	DNA nanoswitches: a quantitative platform for gel-based biomolecular interaction analysis. <i>Nature Methods</i> , 2015, 12, 123-126.	9.0	71
201	Role of Internal Water on Protein Thermal Stability: The Case of Homologous G Domains. <i>Journal of Physical Chemistry B</i> , 2015, 119, 8939-8949.	1.2	21
202	Insights into Protein-Ligand Interactions: Mechanisms, Models, and Methods. <i>International Journal of Molecular Sciences</i> , 2016, 17, 144.	1.8	885
203	Water anomalous thermodynamics, attraction, repulsion, and hydrophobic hydration. <i>Journal of Chemical Physics</i> , 2016, 144, 164501.	1.2	14
204	Water Determines the Structure and Dynamics of Proteins. <i>Chemical Reviews</i> , 2016, 116, 7673-7697.	23.0	645
205	Theoretical-computational characterization of the temperature-dependent folding thermodynamics of α ² -hairpin peptide. <i>Chemical Physics Letters</i> , 2016, 659, 247-251.	1.2	1
206	Shedding light on the extra thermal stability of thermophilic proteins. <i>Biopolymers</i> , 2016, 105, 856-863.	1.2	33
207	Protein-protein interactions at high concentrations. Isothermal titration calorimetry determination of human serum albumin-lysozyme interaction enthalpy at several pH values. <i>Thermochimica Acta</i> , 2016, 641, 39-42.	1.2	2

#	ARTICLE	IF	CITATIONS
208	Forces Driving Chaperone Action. <i>Cell</i> , 2016, 166, 369-379.	13.5	89
209	Allosterism and Structure in Thermally Activated Transient Receptor Potential Channels. <i>Annual Review of Biophysics</i> , 2016, 45, 371-398.	4.5	51
210	Cataract-causing mutation S228P promotes β B1-crystallin aggregation and degradation by separating two interacting loops in C-terminal domain. <i>Protein and Cell</i> , 2016, 7, 501-515.	4.8	32
211	Inherent conformational flexibility of F ₁ -ATPase β -subunit. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2016, 1857, 1392-1402.	0.5	7
212	Biomimetic fiber mesh scaffolds based on gelatin and hydroxyapatite nano-rods: Designing intrinsic skills to attain bone repair abilities. <i>Colloids and Surfaces B: Biointerfaces</i> , 2016, 145, 382-391.	2.5	24
213	Thermodynamic Basis of Selectivity in the Interactions of Tissue Inhibitors of Metalloproteinases N-domains with Matrix Metalloproteinases-1, -3, and -14. <i>Journal of Biological Chemistry</i> , 2016, 291, 11348-11358.	1.6	7
214	Effect of Base-Pairing Partner on the Thermodynamic Stability of the Diastereomeric Spiroiminodihydantoin Lesion. <i>Chemical Research in Toxicology</i> , 2016, 29, 279-284.	1.7	5
215	On the Temperature Dependence of Enzyme-Catalyzed Rates. <i>Biochemistry</i> , 2016, 55, 1681-1688.	1.2	233
216	Thermal and conformational stability of insulin in the presence of imidazolium-based ionic liquids. <i>Journal of Thermal Analysis and Calorimetry</i> , 2016, 123, 2591-2598.	2.0	26
217	Combined Isothermal Titration and Differential Scanning Calorimetry Define Three-State Thermodynamics of β ALS-Associated Mutant Apo SOD1 Dimers and an Increased Population of Folded Monomer. <i>Biochemistry</i> , 2016, 55, 519-533.	1.2	18
218	Heat Capacity Changes and Disorder-to-Order Transitions in Allosteric Activation. <i>Biochemistry</i> , 2016, 55, 243-252.	1.2	4
219	Principles and equations for measuring and interpreting protein stability: From monomer to tetramer. <i>Biochimie</i> , 2016, 121, 29-37.	1.3	13
220	Defying the activity-stability trade-off in enzymes: taking advantage of entropy to enhance activity and thermostability. <i>Critical Reviews in Biotechnology</i> , 2017, 37, 309-322.	5.1	130
221	Analysis of self-assembly of S-layer protein slp-B53 from <i>Lysinibacillus sphaericus</i> . <i>European Biophysics Journal</i> , 2017, 46, 77-89.	1.2	19
222	Extraction of Thermodynamic Parameters of Protein Unfolding Using Parallelized Differential Scanning Fluorimetry. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 553-558.	2.1	54
223	Oligomerization affects the kinetics and thermodynamics of the interaction of a Bowman-Birk inhibitor with proteases. <i>Archives of Biochemistry and Biophysics</i> , 2017, 618, 9-14.	1.4	10
224	A look at ligand binding thermodynamics in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 363-377.	2.5	61
225	The impact of different mutations at Arg54 on structure, chaperone-like activity and oligomerization state of human β A-crystallin: The pathomechanism underlying congenital cataract-causing mutations R54L, R54P and R54C. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 604-618.	1.1	25

#	ARTICLE	IF	CITATIONS
226	Mechanistic Models Fit to Variable Temperature Calorimetric Data Provide Insights into Cooperativity. <i>Biophysical Journal</i> , 2017, 112, 1328-1338.	0.2	5
227	Melting Proteins: Evidence for Multiple Stable Structures upon Thermal Denaturation of Native Ubiquitin from Ion Mobility Spectrometry-Mass Spectrometry Measurements. <i>Journal of the American Chemical Society</i> , 2017, 139, 6306-6309.	6.6	86
228	Bacterial protease uses distinct thermodynamic signatures for substrate recognition. <i>Scientific Reports</i> , 2017, 7, 2848.	1.6	14
229	Crystal Structure of the Cul2-Rbx1-EloBC-VHL Ubiquitin Ligase Complex. <i>Structure</i> , 2017, 25, 901-911.e3.	1.6	105
230	Evolutionary drivers of thermoadaptation in enzyme catalysis. <i>Science</i> , 2017, 355, 289-294.	6.0	147
231	Temperature and osmotic stress dependence of the thermodynamics for binding linker histone H1 O , its carboxyl domain (H1 O -C) or globular domain (H1 O -G) to B-DNA. <i>Biochemistry and Biophysics Reports</i> , 2017, 12, 158-165.	0.7	1
232	Isothermal titration calorimetry and vesicle leakage assays highlight the differential behaviors of tau repeat segments upon interaction with anionic lipid membranes. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 1504-1509.	1.0	8
233	Elucidation of potential sites for antibody engineering by fluctuation editing. <i>Scientific Reports</i> , 2017, 7, 9597.	1.6	15
234	Entropy in molecular recognition by proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6563-6568.	3.3	139
235	SCoop: an accurate and fast predictor of protein stability curves as a function of temperature. <i>Bioinformatics</i> , 2017, 33, 3415-3422.	1.8	82
236	Volumetric and calorimetric properties of aqueous ionene solutions. <i>Journal of Molecular Liquids</i> , 2017, 228, 126-132.	2.3	1
237	Allosteric modulation of protein-protein interactions by individual lipid binding events. <i>Nature Communications</i> , 2017, 8, 2203.	5.8	65
238	Probing the Nanoscopic Thermodynamic Fingerprint of Paramagnetic Ligands Interacting with Amphiphilic Macromolecules. <i>Polymers</i> , 2017, 9, 324.	2.0	6
239	Thermal adaptation of mesophilic and thermophilic FtsZ assembly by modulation of the critical concentration. <i>PLoS ONE</i> , 2017, 12, e0185707.	1.1	9
240	Effect of peptide linker length and composition on immobilization and catalysis of leucine zipper enzyme fusion proteins. <i>AIChE Journal</i> , 2018, 64, 2934-2946.	1.8	15
241	Structural and thermodynamic insights into β -1,2-glucooligosaccharide capture by a solute-binding protein in <i>Listeria innocua</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 8812-8828.	1.6	19
242	Dynamical origins of heat capacity changes in enzyme-catalysed reactions. <i>Nature Communications</i> , 2018, 9, 1177.	5.8	64
243	Global versus local mechanisms of temperature sensing in ion channels. <i>Pflugers Archiv European Journal of Physiology</i> , 2018, 470, 733-744.	1.3	23

#	ARTICLE	IF	CITATIONS
244	Paclitaxel inhibited lysozyme fibrillation by increasing colloidal stability through formation of α -off-pathway α -oligomers. <i>International Journal of Biological Macromolecules</i> , 2018, 111, 870-879.	3.6	8
245	A surface plasmon resonance assay for characterisation and epitope mapping of anti-GLP-1 antibodies. <i>Journal of Molecular Recognition</i> , 2018, 31, e2711.	1.1	3
246	Hyperthermostable cube-shaped assembly in water. <i>Communications Chemistry</i> , 2018, 1, .	2.0	22
247	Unresolved Issues that Remain in Molecular Self-Assembly. <i>Bulletin of the Chemical Society of Japan</i> , 2018, 91, 957-978.	2.0	54
248	Thermodynamic study of aptamers binding to their target proteins. <i>Biochimie</i> , 2018, 145, 91-97.	1.3	47
249	Importance of the positively charged residue at position 54 to the chaperoning function, conformational stability and amyloidogenic nature of human β -crystallin. <i>Journal of Biochemistry</i> , 2018, 163, 187-199.	0.9	5
250	Novel physical chemistry approaches in biophysical researches with advanced application of lasers: Detection and manipulation. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 335-357.	1.1	8
251	Interfacial structural crossover and hydration thermodynamics of charged C_{60} in water. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 27069-27081.	1.3	6
252	Wetting of the Protein Active Site Leads to Non-Marcusian Reaction Kinetics. <i>Journal of Physical Chemistry B</i> , 2018, 122, 10490-10495.	1.2	11
253	The characteristics of molten globule states and folding pathways strongly depend on the sequence of a protein. <i>Molecular Physics</i> , 2018, 116, 3173-3180.	0.8	12
254	The forkhead domain hinge-loop plays a pivotal role in DNA binding and transcriptional activity of FOXO2. <i>Biological Chemistry</i> , 2018, 399, 881-893.	1.2	5
255	Emergence of a Negative Activation Heat Capacity during Evolution of a Designed Enzyme. <i>Journal of the American Chemical Society</i> , 2019, 141, 11745-11748.	6.6	42
256	Structural insight into the fungal β -glucosidases and their interactions with organics. <i>International Journal of Biological Macromolecules</i> , 2019, 138, 1019-1028.	3.6	6
257	Shift from Entropic Cu^{2+} Binding to Enthalpic Cu^{+} Binding Determines the Reduction Thermodynamics of Blue Copper Proteins. <i>Journal of the American Chemical Society</i> , 2019, 141, 14329-14339.	6.6	10
258	Does Fungicide α -Dodine Unfold Protein like Kosmo-Chaotropic Agent?. <i>Journal of Physical Chemistry B</i> , 2019, 123, 8240-8246.	1.2	2
259	Carbonic Anhydrase as Drug Target. , 2019, , .		8
260	Solution thermochemistry of concanavalin A tetramer conformers measured by variable-temperature ESI-IMS-MS. <i>International Journal of Mass Spectrometry</i> , 2019, 443, 93-100.	0.7	24
261	Inhibitor Binding to Carbonic Anhydrases by Isothermal Titration Calorimetry. , 2019, , 79-95.		0

#	ARTICLE	IF	CITATIONS
262	Stopping of porous projectiles in granular targets. <i>Monthly Notices of the Royal Astronomical Society: Letters</i> , 2019, 487, L13-L17.	1.2	4
263	Understanding the Contributions of Conformational Changes, Thermodynamics, and Kinetics of RNA–Small Molecule Interactions. <i>ACS Chemical Biology</i> , 2019, 14, 824-838.	1.6	29
264	Observation of Protein Thermodynamics in Ice by Passive Millimeter-Wave Microscopy. <i>Journal of Infrared, Millimeter, and Terahertz Waves</i> , 2019, 40, 585-594.	1.2	2
266	ITC Measurement for High-Affinity Aptamers Binding to Their Target Proteins. <i>Methods in Molecular Biology</i> , 2019, 1964, 119-128.	0.4	5
267	Febrile temperatures increase in vitro antibody affinity for malarial and dengue antigens. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007239.	1.3	13
268	Mechanism of Solvent Control of Protein Dynamics. <i>Physical Review Letters</i> , 2019, 122, 058101.	2.9	35
269	Echo dephasing and heat capacity from constrained and unconstrained dynamics of triiodothyronine nuclear receptor protein. <i>Journal of Biological Physics</i> , 2019, 45, 107-125.	0.7	3
270	Cooperative energetic effects elicited by the yeast Shwachman-Diamond syndrome protein (Sdo1) and guanine nucleotides modulate the complex conformational landscape of the elongation factor-like 1 (Efl1) GTPase. <i>Biophysical Chemistry</i> , 2019, 247, 13-24.	1.5	8
271	Insight into the Hydration of Cationic Surfactants: A Thermodynamic and Dielectric Study of Functionalized Quaternary Ammonium Chlorides. <i>Langmuir</i> , 2019, 35, 3759-3772.	1.6	20
272	GroEL Allostery Illuminated by a Relationship between the Hill Coefficient and the MWC Model. <i>Biophysical Journal</i> , 2019, 117, 1915-1921.	0.2	10
273	Does poly(ionic liquid) modulate the non-covalent interactions of chicken egg white lysozyme? Elucidation of biomolecular interactions between biomolecules and macromolecular solvents. <i>New Journal of Chemistry</i> , 2019, 43, 16759-16766.	1.4	7
274	Insight into impact of choline-based ionic liquids on bovine β -lactoglobulin structural analysis: Unexpected high thermal stability of protein. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 1-10.	3.6	27
275	Hydration differences between the major and minor grooves of DNA revealed from heat capacity measurements. <i>European Biophysics Journal</i> , 2019, 48, 131-138.	1.2	6
276	Thermodynamic stability of myoglobin-poly(ethylene glycol) bioconjugates: A calorimetric study. <i>Thermochimica Acta</i> , 2019, 671, 26-31.	1.2	19
277	Differential Scanning Calorimetry of Native Silk Feedstock. <i>Macromolecular Bioscience</i> , 2019, 19, 1800228.	2.1	11
278	Metal binding and conformational studies of the calcium binding domain of NADPH oxidase 5 reveal its similarity and difference to calmodulin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2352-2368.	2.0	4
279	Following Structural Changes by Thermal Denaturation Using Trapped Ion Mobility Spectrometry–Mass Spectrometry. <i>Journal of Physical Chemistry B</i> , 2020, 124, 6257-6265.	1.2	11
280	Cryo vs Thermo: Duality of Ethylene Glycol on the Stability of Proteins. <i>Journal of Physical Chemistry B</i> , 2020, 124, 10077-10088.	1.2	11

#	ARTICLE	IF	CITATIONS
281	A thermodynamic evaluation of antibody-surface interactions in multimodal cation exchange chromatography. <i>Journal of Chromatography A</i> , 2020, 1628, 461479.	1.8	7
282	Evidence for Many Unique Solution Structures for Chymotrypsin Inhibitor 2: A Thermodynamic Perspective Derived from vT-ESI-IMS-MS Measurements. <i>Journal of the American Chemical Society</i> , 2020, 142, 17372-17383.	6.6	26
283	Hidden Conformational States and Strange Temperature Optima in Enzyme Catalysis. <i>Biochemistry</i> , 2020, 59, 3844-3855.	1.2	16
284	The study of EGFR-ligand complex electron property relationship with biological activity. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 375-388.	2.0	1
285	Harnessing Environmental Ca ²⁺ for Extracellular Protein Thermostabilization. <i>Biochemistry</i> , 2020, 59, 3725-3740.	1.2	2
286	Thermodynamic Basis for Conformational Coupling in an ATP-Binding Cassette Exporter. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 7946-7953.	2.1	13
287	Regulation of chaperone function by coupled folding and oligomerization. <i>Science Advances</i> , 2020, 6, .	4.7	24
288	Computer simulations explain the anomalous temperature optimum in a cold-adapted enzyme. <i>Nature Communications</i> , 2020, 11, 2644.	5.8	35
289	Peptide cargo tunes a network of correlated motions in human leucocyte antigens. <i>FEBS Journal</i> , 2020, 287, 3777-3793.	2.2	6
290	Protein thermal stability. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 170, 239-272.	0.9	11
291	A Disorder-to-Order Transition Mediates RNA Binding of the <i>Caenorhabditis elegans</i> Protein MEX-5. <i>Biophysical Journal</i> , 2020, 118, 2001-2014.	0.2	4
292	The Unfolding Journey of Superoxide Dismutase 1 Barrels under Crowding: Atomistic Simulations Shed Light on Intermediate States and Their Interactions with Crowders. <i>Journal of Physical Chemistry Letters</i> , 2020, 11, 4206-4212.	2.1	18
293	Optimization strategy of single-digit nanomolar cross-class inhibitors of mammalian and protozoa cysteine proteases. <i>Bioorganic Chemistry</i> , 2020, 101, 104039.	2.0	7
294	Regulation of Photocycle Kinetics of Photoactive Yellow Protein by Modulating Flexibility of the β -Turn. <i>Journal of Physical Chemistry B</i> , 2020, 124, 1452-1459.	1.2	0
295	The congenital cataract-causing mutations P20R and A171T are associated with important changes in the amyloidogenic feature, structure and chaperone-like activity of human β -crystallin. <i>Biopolymers</i> , 2020, 111, e23350.	1.2	12
296	CL-FEP: An End-State Free Energy Perturbation Approach. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1396-1410.	2.3	8
297	Interplay between aggregation number, micelle charge and hydration of cationic surfactants. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 9998-10009.	1.3	10
298	Synthesis, anti-bacterial evaluation, DFT study and molecular docking as a potential 3-chymotrypsin-like protease (3CLpro) of SARS-CoV-2 inhibitors of a novel Schiff bases. <i>Journal of Molecular Structure</i> , 2021, 1228, 129454.	1.8	28

#	ARTICLE	IF	CITATIONS
299	Origin of heat capacity increment in DNA folding: The hydration effect. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129774.	1.1	9
300	The concept of protein folding/unfolding and its impacts on human health. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 126, 227-278.	1.0	2
301	Design of intrinsically disordered proteins that undergo phase transitions with lower critical solution temperatures. <i>APL Materials</i> , 2021, 9, .	2.2	29
303	<i>Danio rerio</i> Oocytes for Eukaryotic In-Cell NMR. <i>Biochemistry</i> , 2021, 60, 451-459.	1.2	11
304	Hydrolysis of Aliphatic Bis- ϵ -nitriles in the Presence of a Polar Super Aryl-Extended Calix[4]pyrrole Container. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 10359-10365.	7.2	16
305	Investigation of the LCST-Thermoresponsive Behavior of Novel Oligo(Ethylene Glycol)-Modified Pentafluorostyrene Homopolymers. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 2711.	1.3	9
306	Mathematical model for the thermal enhancement of radiation response: thermodynamic approach. <i>Scientific Reports</i> , 2021, 11, 5503.	1.6	11
307	Hydrolysis of Aliphatic Bis- ϵ -nitriles in the Presence of a Polar Super Aryl-Extended Calix[4]pyrrole Container. <i>Angewandte Chemie</i> , 2021, 133, 10447-10453.	1.6	2
308	Spectrally Silent Protein Reaction Dynamics Revealed by Time-Resolved Thermodynamics and Diffusion Techniques. <i>Accounts of Chemical Research</i> , 2021, 54, 2238-2248.	7.6	11
310	Probing coupled conformational transitions of intrinsically disordered proteins in their interactions with target proteins. <i>Analytical Biochemistry</i> , 2021, 619, 114126.	1.1	3
311	Uncovering Differences in Hydration Free Energies and Structures for Model Compound Mimics of Charged Side Chains of Amino Acids. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4148-4161.	1.2	41
312	Fundamentals to function: Quantitative and scalable approaches for measuring protein stability. <i>Cell Systems</i> , 2021, 12, 547-560.	2.9	13
313	Statistical Inference for Ergodic Algorithmic Model (EAM), Applied to Hydrophobic Hydration Processes. <i>Entropy</i> , 2021, 23, 700.	1.1	2
314	Anion solvation enhanced by positive supercharging mutations preserves thermal stability of an antibody in a wide pH range. <i>Biochemical and Biophysical Research Communications</i> , 2021, 563, 54-59.	1.0	4
315	HSA nanoparticles in drug recognition: mechanistic insights with naproxen, diclofenac and methimazole. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, , 1-13.	2.0	2
316	Competing stress-dependent oligomerization pathways regulate self-assembly of the periplasmic protease-chaperone DegP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
317	Evolution of dynamical networks enhances catalysis in a designer enzyme. <i>Nature Chemistry</i> , 2021, 13, 1017-1022.	6.6	60
318	Folding in Place: Design of β^2 -Strap Motifs to Stabilize the Folding of Hairpins with Long Loops. <i>Journal of Organic Chemistry</i> , 2021, 86, 13535-13547.	1.7	5

#	ARTICLE	IF	CITATIONS
319	Quantification of Conformational Entropy Unravels Effect of Disordered Flanking Region in Coupled Folding and Binding. <i>Journal of the American Chemical Society</i> , 2021, 143, 14540-14550.	6.6	22
320	Molecular Recognition in Water Using Macrocyclic Synthetic Receptors. <i>Chemical Reviews</i> , 2021, 121, 2445-2514.	23.0	158
321	Protein Folding. , 2007, , 303-343.		7
322	Cryoradiolysis and Cryospectroscopy for Studies of Heme-Oxygen Intermediates in Cytochromes P450. <i>Methods in Molecular Biology</i> , 2012, 875, 375-391.	0.4	10
323	Specific heat at constant pressure from first principles: contributions from fully anharmonic vibrations. <i>Materials Research Express</i> , 2019, 6, 125924.	0.8	2
325	Ligand-Induced Protein Mobility in Complexes of Carbonic Anhydrase II and Benzenesulfonamides with Oligoglycine Chains. <i>PLoS ONE</i> , 2013, 8, e57629.	1.1	2
326	A Simple Lattice Model That Captures Protein Folding, Aggregation and Amyloid Formation. <i>PLoS ONE</i> , 2014, 9, e85185.	1.1	66
327	Heat conduction by thyroid hormone receptors. <i>AIMS Biophysics</i> , 2018, 5, 245-256.	0.3	5
331	Kinetic and Thermodynamic Analyses of RNA-Protein Interactions. <i>Methods in Molecular Biology</i> , 2020, 2106, 137-150.	0.4	1
332	Investigation of Protein-Lipid Interactions Using Native Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2022, 2349, 41-64.	0.4	4
333	The effects of temperature on streptavidin-biotin binding using affinity isothermal titration calorimetry. <i>AIMS Biophysics</i> , 2020, 7, 236-247.	0.3	7
335	Quantitative multivalent binding model of the structure, size distribution and composition of the casein micelles of cow milk. <i>International Dairy Journal</i> , 2022, 126, 105292.	1.5	19
336	Myopathy-associated G154S mutation causes important changes in the conformational stability, amyloidogenic properties, and chaperone-like activity of human β -crystallin. <i>Biophysical Chemistry</i> , 2022, 282, 106744.	1.5	4
337	SAXS Reveals the Stabilization Effects of Modified Sugars on Model Proteins. <i>Life</i> , 2022, 12, 123.	1.1	3
338	Biophysical and <i>in silico</i> characterization of NrtA: a protein-based host for aqueous nitrate and nitrite recognition. <i>Chemical Communications</i> , 2022, 58, 965-968.	2.2	4
339	Investigation on the effect of nonpolar amino acids as macromolecular crowders on the stability of globular proteins. <i>Chemical Thermodynamics and Thermal Analysis</i> , 2022, 6, 100044.	0.7	1
340	In-Cell Structural Biology by NMR: The Benefits of the Atomic Scale. <i>Chemical Reviews</i> , 2022, 122, 9497-9570.	23.0	55
341	Heat and cold denaturation of yeast frataxin: The effect of pressure. <i>Biophysical Journal</i> , 2022, 121, 1502-1511.	0.2	3

#	ARTICLE	IF	CITATIONS
342	Applications of Time-Resolved Thermodynamics for Studies on Protein Reactions. <i>J</i> , 2022, 5, 186-197.	0.6	0
343	Initial heat analysis in dissociation isothermal titration calorimetry: An analytical tool for thermodynamic dissection of biomolecular condensates. <i>Biochemical and Biophysical Research Communications</i> , 2022, 605, 127-133.	1.0	0
344	Variable-Temperature Native Mass Spectrometry for Studies of Protein Folding, Stabilities, Assembly, and Molecular Interactions. <i>Annual Review of Biophysics</i> , 2022, 51, 63-77.	4.5	18
345	Î±Î±-hub coregulator structure and flexibility determine transcription factor binding and selection in regulatory interactomes. <i>Journal of Biological Chemistry</i> , 2022, 298, 101963.	1.6	5
346	Electro-magneto-chemical synthesis and characterization of thermally reduced graphene oxide: Influence of magnetic field and cyclic thermal loading on microstructural properties. <i>Journal of Solid State Chemistry</i> , 2022, 312, 123219.	1.4	11
348	Structural and ITC Characterization of Peptideâ€Protein Binding: Thermodynamic Consequences of Cyclization Constraints, a Case Study on Vascular Endothelial Growth Factor Ligands. <i>Chemistry - A European Journal</i> , 2022, 28, .	1.7	4
350	Yoda1â€™s energetic footprint on Piezo1 channels and its modulation by voltage and temperature. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	19
351	A general theory for temperature dependence in biology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	34
352	Altered Conformational Landscape upon Sensing Guanine Nucleotides in a Disease Mutant of Elongation Factor-like 1 (EFL1) GTPase. <i>Biomolecules</i> , 2022, 12, 1141.	1.8	0
353	Cucurbit[n]urils (n = 7, 8) can strongly bind neutral hydrophilic molecules in water. <i>Science China Chemistry</i> , 2022, 65, 1733-1740.	4.2	9
354	A computational study of potential therapeutics for COVID-19 invoking conceptual density functional theory. <i>Structural Chemistry</i> , 2022, 33, 2195-2204.	1.0	6
355	Thermodynamics for the Self-Assembly of Alkylated Peptides. <i>Langmuir</i> , 2022, 38, 11801-11809.	1.6	0
356	Analytical Method for Experimental Validation of Computer-Designed Antibody. <i>Methods in Molecular Biology</i> , 2023, , 409-433.	0.4	1
357	Ultrasound-assisted diffusion of waxy starch cryogel on frozen-stored pork meat. <i>LWT - Food Science and Technology</i> , 2022, 171, 114139.	2.5	2
358	Electrochemical exfoliation and characterizations of low-defect, large-scale thermally reduced graphene oxide via pencil core. <i>International Journal of Modern Physics B</i> , 2023, 37, .	1.0	1
359	Temperature dependent mechanical unfolding and refolding of a protein studied by thermo-regulated optical tweezers. <i>Biophysical Journal</i> , 2023, 122, 513-521.	0.2	1
361	Plant defensins as a model to study the thermostability of surface hydrophobic clusters: The <i>Pisum sativum</i> defensin 2 (Psd2). <i>Journal of Magnetic Resonance Open</i> , 2023, 16-17, 100106.	0.5	0
362	Therapeutic Potential of B₁₂N₁₂-X (X = Au, Os, and Pt) Nanostructured as Effective Fluorouracil (5Fu) Drug Delivery Materials. <i>ACS Applied Bio Materials</i> , 2023, 6, 1146-1160.	2.3	23

#	ARTICLE	IF	CITATIONS
363	Complex Physical Properties of an Adaptive, Self-Organizing Biological System. <i>Biophysica</i> , 2023, 3, 231-251.	0.6	0
364	Modeling the role of charged residues in thermophilic proteins by rotamer and dynamic cross correlation analysis. <i>Journal of Molecular Modeling</i> , 2023, 29, .	0.8	1
372	Comment on: "Computer Simulations Reveal an Entirely Entropic Activation Barrier for the Chemical Step in a Designer Enzyme" <i>ACS Catalysis</i> , 2023, 13, 10527-10530.	5.5	2