George I Makhatadze

List of Publications by Year
in descending order

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Version: 2024-02-01

96 papers	7,339 citations	66343 42 h-index	54911 84 g-index
120 all docs	120 docs citations	120 times ranked	5975 citing authors

#	Article	IF	Citations
1	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. Journal of Physical Chemistry B, 2022, 126, 1212-1231.	2.6	3
2	Effects of Hydrostatic Pressure on the Thermodynamics of CspB-Bs Interactions with the ssDNA Template. Biochemistry, 2021, 60, 3086-3097.	2.5	2
3	Evolutionary conservation and structural localizations suggest a physical trace of metabolismâ€™s progressive geochronological emergence. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3700-3719.	3.5	3
4	Protein adaptation to high hydrostatic pressure: Computational analysis of the structural proteome. Proteins: Structure, Function and Bioinformatics, 2020, 88, 584-592.	2.6	12
5	Sequence-independent recognition of the amyloid structural motif by GFP protein family. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22122-22127.	7.1	7
6	Strategy for Stabilization of CutA1 Proteins Due to Ionâ€“Ion Interactions at Temperatures of over 100 Â°C. Biochemistry, 2018, 57, 2649-2656.	2.5	7
7	Predictive Model of Linear Antimicrobial Peptides Active against Gram-Negative Bacteria. Journal of Chemical Information and Modeling, 2018, 58, 1141-1151.	5.4	57
8	Evidence for the principle of minimal frustration in the evolution of protein folding landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1627-E1632.	7.1	59
9	Reply to Candel et al.: Evidence for evolutionary conservation of folding kinetics in the thioredoxin protein family. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4124-E4124.	7.1	2
10	Non-linearity of the collagen triple helix in solution and implications for collagen function. Biochemical Journal, 2017, 474, 2203-2217.	3.7	21
11	Linking computation and experiments to study the role of chargeâ€“charge interactions in protein folding and stability. Physical Biology, 2017, 14, 013002.	1.8	8
12	Molecular determinant of the effects of hydrostatic pressure on protein folding stability. Nature Communications, 2017, 8, 14561.	12.8	75
13	Molecular Determinants of Temperature Dependence of Protein Volume Change upon Unfolding. Journal of Physical Chemistry B, 2017, 121, 8300-8310.	2.6	13
14	Putting the Piezolyte Hypothesis under Pressure. Biophysical Journal, 2017, 113, 974-977.	0.5	13
15	Intramolecular diffusion controls aggregation of the PAPf39 peptide. Biophysical Chemistry, 2016, 216, 37-43.	2.8	11
16	Influence of surface charge, binding site residues and glycosylation on Thielavia terrestris cutinase biochemical characteristics. Applied Microbiology and Biotechnology, 2016, 100, 4435-4446.	3.6	25
17	Applications of pressure perturbation calorimetry to study factors contributing to the volume changes upon protein unfolding. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 1036-1042.	2.4	5
18	Gallic Acid Is an Antagonist of Semen Amyloid Fibrils That Enhance HIV-1 Infection. Journal of Biological Chemistry, 2016, 291, 14045-14055.	3.4	12

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19	Modulation of folding energy landscape by chargeâ€“charge interactions: Linking experiments with computational modeling. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E259-66.	7.1	48
20	Thermal expansivities of peptides, polypeptides and proteins as measured by pressure perturbation calorimetry. Methods, 2015, 76, 61-66.	3.8	5
21	ProteinVolume: calculating molecular van der Waals and void volumes in proteins. BMC Bioinformatics, 2015, 16, 101.	2.6	84
22	Alterations of Nonconserved Residues Affect Protein Stability and Folding Dynamics through Chargeâ€“Charge Interactions. Journal of Physical Chemistry B, 2015, 119, 13103-13112.	2.6	22
23	Molecular Determinants of Expansivity of Native Globular Proteins: A Pressure Perturbation Calorimetry Study. Journal of Physical Chemistry B, 2014, 118, 6117-6122.	2.6	8
24	Structural Characterization of Semen Coagulum-Derived SEM1(86â€“107) Amyloid Fibrils That Enhance HIV-1 Infection. Biochemistry, 2014, 53, 3267-3277.	2.5	17
25	Structural and thermodynamic characterization of the recognition of the S100â€binding peptides TRTK12 and p53 by calmodulin. Protein Science, 2014, 23, 1247-1261.	7.6	6
26	Novel Interactions of the TRTK12 Peptide with S100 Protein Family Members: Specificity and Thermodynamic Characterization. Biochemistry, 2013, 52, 5844-5856.	2.5	10
27	Bacterial expression and purification of the amyloidogenic peptide PAPf39 for multidimensional NMR spectroscopy. Protein Expression and Purification, 2013, 88, 196-200.	1.3	5
28	The Role of Cross-Chain Ionic Interactions for the Stability of Collagen Model Peptides. Biophysical Journal, 2013, 105, 1681-1688.	0.5	29
29	Backtracking due to Residual Structure in the Unfolded State Changes the Folding of the Third Fibronectin Type III Domain from Tenascin-C. Journal of Physical Chemistry B, 2013, 117, 800-810.	2.6	12
30	Crystal and NMR structures of a Trp-cage mini-protein benchmark for computational fold prediction. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12521-12525.	7.1	31
31	Thermodynamic and Kinetic Analysis of Peptides Derived from CapZ, NDR, p53, HDM2, and HDM4 Binding to Human S100B. Biochemistry, 2012, 51, 7189-7201.	2.5	16
32	Core Sequence of PAPf39 Amyloid Fibrils and Mechanism of pH-Dependent Fibril Formation: The Role of Monomer Conformation. Biochemistry, 2012, 51, 10127-10136.	2.5	30
33	Molecular Mechanism for the Preferential Exclusion of TMAO from Protein Surfaces. Journal of Physical Chemistry B, 2012, 116, 12095-12104.	2.6	162
34	Electrostatic Contribution of Surface Charge Residues to the Stability of a Thermophilic Protein: Benchmarking Experimental and Predicted pKa Values. PLoS ONE, 2012, 7, e30296.	2.5	34
35	Enzyme Activity in the Crowded Milieu. PLoS ONE, 2012, 7, e39418.	2.5	54
36	Kinetic consequences of native state optimization of surfaceâ€exposed electrostatic interactions in the Fyn SH3 domain. Proteins: Structure, Function and Bioinformatics, 2012, 80, 858-870.	2.6	42

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37	Contribution of buried aspartic acid to the stability of the PDZ2 protein. Journal of Chemical Thermodynamics, 2012, 52, 64-68.	2.0	2
38	Protonation/deprotonation effects on the stability of the Trp-cage miniprotein. Physical Chemistry Chemical Physics, 2011, 13, 17056.	2.8	21
39	Statistical analysis of protein structures suggests that buried ionizable residues in proteins are hydrogen bonded or form salt bridges. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2027-2032.	2.6	27
40	Energetics of chargeâ€“charge interactions between residues adjacent in sequence. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3494-3499.	2.6	14
41	Thermodynamics of the Trpâ€cage miniprotein unfolding in urea. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1376-1381.	2.6	29
42	Pressure Perturbation Calorimetry of Unfolded Proteins. Journal of Physical Chemistry B, 2010, 114, 16166-16170.	2.6	21
43	Rational stabilization of enzymes by computational redesign of surface chargeâ€“charge interactions. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2601-2606.	7.1	201
44	Chapter 7 A Computational Approach for the Rational Design of Stable Proteins and Enzymes. Methods in Enzymology, 2009, 454, 175-211.	1.0	29
45	Mechanism of Fibril Formation by a 39-Residue Peptide (PAPf39) from Human Prostatic Acidic Phosphatase. Biochemistry, 2009, 48, 11582-11591.	2.5	33
46	Universal Convergence of the Specific Volume Changes of Globular Proteins upon Unfolding. Biochemistry, 2009, 48, 10846-10851.	2.5	36
47	Chapter 22 Use of Pressure Perturbation Calorimetry to Characterize the Volumetric Properties of Proteins. Methods in Enzymology, 2009, 466, 527-547.	1.0	31
48	Annexin I and Annexin II N-Terminal Peptides Binding to S100 Protein Family Members: Specificity and Thermodynamic Characterization. Biochemistry, 2009, 48, 2788-2798.	2.5	39
49	Protein Stabilization by the Rational Design of Surface Chargeâ€“Charge Interactions. Methods in Molecular Biology, 2009, 490, 261-283.	0.9	27
50	Cooperativity of complex salt bridges. Protein Science, 2008, 17, 1285-1290.	7.6	35
51	Heat capacity changes upon burial of polar and nonpolar groups in proteins. Protein Science, 2008, 10, 1343-1352.	7.6	120
52	Role of the Chargeâ€“Charge Interactions in Defining Stability and Halophilicity of the CspB Proteins. Journal of Molecular Biology, 2007, 366, 842-856.	4.2	62
53	Unfolding Thermodynamics of Trp-Cage, a 20 Residue Miniprotein, Studied by Differential Scanning Calorimetry and Circular Dichroism Spectroscopyâ€. Biochemistry, 2007, 46, 2876-2880.	2.5	115
54	Computational design of the Fyn SH3 domain with increased stability through optimization of surface chargeâ€“charge interactions. Protein Science, 2007, 16, 2694-2702.	7.6	56

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55	Calorimetric Evidence for a Two-State Unfolding of the Î²-Hairpin Peptide Trpzip4. Journal of the American Chemical Society, 2006, 128, 30-31.	13.7	49
56	Protein Stability and Surface Electrostatics:Â A Charged Relationshipâ€. Biochemistry, 2006, 45, 2761-2766.	2.5	285
57	How to improve nature: study of the electrostatic properties of the surface of Î±-lactalbumin. Protein Engineering, Design and Selection, 2005, 18, 425-433.	2.1	40
58	Enthalpy of helix-coil transition: Missing link in rationalizing the thermodynamics of helix-forming propensities of the amino acid residues. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1413-1418.	7.1	52
59	Thermodynamics Of Î±â€Helix Formation. Advances in Protein Chemistry, 2005, 72, 199-226.	4.4	42
60	Effects of Charge-to-Alanine Substitutions on the Stability of Ribosomal Protein L30e from Thermococcus celer. Biochemistry, 2005, 44, 16817-16825.	2.5	43
61	Temperature Dependence of the Thermodynamics of Helixâ€“Coil Transition. Journal of Molecular Biology, 2004, 335, 1029-1037.	4.2	70
62	Mechanism of Thermostabilization in a Designed Cold Shock Protein with Optimized Surface Electrostatic Interactions. Journal of Molecular Biology, 2004, 336, 929-942.	4.2	74
63	Noncharged amino acid residues at the solvent-exposed positions in the middle and at the C terminus of the Î±-helix have the same helical propensity. Protein Science, 2003, 12, 1169-1176.	7.6	29
64	Contribution of Surface Salt Bridges to Protein Stability: Guidelines for Protein Engineering. Journal of Molecular Biology, 2003, 327, 1135-1148.	4.2	216
65	Isothermal Titration Calorimetry. , 2002, 173, 121-126.		24
66	The enthalpy of the alanine peptide helix measured by isothermal titration calorimetry using metal-binding to induce helix formation. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1298-1302.	7.1	104
67	Differential Scanning Calorimetry. , 2002, 173, 113-119.		41
68	Conformational and thermodynamic properties of peptide binding to the human S100P protein. Protein Science, 2002, 11, 1367-1375.	7.6	31
69	Thermodynamic Consequences of Burial of Polar and Non-polar Amino Acid Residues in the Protein Interior. Journal of Molecular Biology, 2002, 320, 343-357.	4.2	110
70	Removal of surface chargeâ€charge interactions from ubiquitin leaves the protein folded and very stable. Protein Science, 2002, 11, 174-177.	7.6	26
71	Molecular Characterization and Tissue Distribution of a Novel Member of the S100 Family of EF-Hand Proteins,. Biochemistry, 2001, 40, 15538-15548.	2.5	53
72	To charge or not to charge?. Trends in Biotechnology, 2001, 19, 132-135.	9.3	203

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73	Energetics of Target Peptide Binding by Calmodulin Reveals Different Modes of Binding. Journal of Biological Chemistry, 2001, 276, 14083-14091.	3.4	107
74	Interactions of the Cold Shock Protein CspB fromBacillus subtilis with Single-stranded DNA. Journal of Biological Chemistry, 2001, 276, 15511-15518.	3.4	51
75	Major cold shock proteins, CspA from Escherichia coli and CspB from Bacillus subtilis, interact differently with single-stranded DNA templates. BBA - Proteins and Proteomics, 2000, 1479, 196-202.	2.1	46
76	Contribution of proton linkage to the thermodynamic stability of the major coldâ€shock protein of Escherichia coli CspA. Protein Science, 2000, 9, 387-394.	7.6	27
77	Interactions of the Major Cold Shock Protein of Bacillus subtilis CspB with Single-stranded DNA Templates of Different Base Composition. Journal of Biological Chemistry, 1999, 274, 33601-33608.	3.4	63
78	Heat capacity change for ribonuclease A folding. Protein Science, 1999, 8, 1500-1504.	7.6	77
79	Cold denaturation of ubiquitin. BBA - Proteins and Proteomics, 1999, 1429, 384-390.	2.1	69
80	Thermodynamics of Protein Interactions with Urea and Guanidinium Hydrochloride. Journal of Physical Chemistry B, 1999, 103, 4781-4785.	2.6	177
81	Thermal versus Guanidine-Induced Unfolding of Ubiquitin. An Analysis in Terms of the Contributions from Chargeâ^'Charge Interactions to Protein Stabilityâ€. Biochemistry, 1999, 38, 8138-8149.	2.5	243
82	Engineering a Thermostable Protein via Optimization of Chargeâ^'Charge Interactions on the Protein Surfaceâ€. Biochemistry, 1999, 38, 16419-16423.	2.5	213
83	MEARA Sequence Repeat of Human CstF-64 Polyadenylation Factor Is Helical in Solution. A Spectroscopic and Calorimetric Studyâ€. Biochemistry, 1999, 38, 12869-12875.	2.5	44
84	Cloning, overexpression, purification, and spectroscopic characterization of human S100P. Protein Science, 1998, 7, 211-215.	7.6	28
85	Anion binding to the ubiquitin molecule. Protein Science, 1998, 7, 689-697.	7.6	118
86	Heat capacities of amino acids, peptides and proteins. Biophysical Chemistry, 1998, 71, 133-156.	2.8	74
87	On the entropy of protein folding. Protein Science, 1996, 5, 507-510.	7.6	74
88	Solvent isotope effect and protein stability. Nature Structural Biology, 1995, 2, 852-855.	9.7	172
89	Energetics of Protein Structure. Advances in Protein Chemistry, 1995, 47, 307-425.	4.4	933
90	Thermodynamics of barnase unfolding. Protein Science, 1994, 3, 669-676.	7.6	74

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91	Effect of pH and phosphate ions on selfâ€association properties of the major coldâ€shock protein from Bacillus subtilis. Protein Science, 1994, 3, 2144-2147.	7.6	39
92	Thermodynamics of ubiquitin unfolding. Proteins: Structure, Function and Bioinformatics, 1994, 18, 246-253.	2.6	170
93	Energetics of ribonuclease T1 structure. Biochemistry, 1994, 33, 3312-3319.	2.5	81
94	Thermodynamics of bpti folding. Protein Science, 1993, 2, 2028-2036.	7.6	102
95	Contribution of Hydration to Protein Folding Thermodynamics. Journal of Molecular Biology, 1993, 232, 660-679.	4.2	406
96	Protein interactions with urea and guanidinium chloride. Journal of Molecular Biology, 1992, 226, 491-505.	4.2	610