George I Makhatadze

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9366988/publications.pdf

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	Energetics of Protein Structure. Advances in Protein Chemistry, 1995, 47, 307-425.	4.4	933
2	Protein interactions with urea and guanidinium chloride. Journal of Molecular Biology, 1992, 226, 491-505.	4.2	610
3	Contribution of Hydration to Protein Folding Thermodynamics. Journal of Molecular Biology, 1993, 232, 660-679.	4.2	406
4	Protein Stability and Surface Electrostatics:Â A Charged Relationshipâ€. Biochemistry, 2006, 45, 2761-2766.	2.5	285
5	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
6	Contribution of Surface Salt Bridges to Protein Stability: Guidelines for Protein Engineering. Journal of Molecular Biology, 2003, 327, 1135-1148.	4.2	216
7	Engineering a Thermostable Protein via Optimization of Chargeâ"Charge Interactions on the Protein Surfaceâ€. Biochemistry, 1999, 38, 16419-16423.	2.5	213
8	To charge or not to charge?. Trends in Biotechnology, 2001, 19, 132-135.	9.3	203
9	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
10	Thermodynamics of Protein Interactions with Urea and Guanidinium Hydrochloride. Journal of Physical Chemistry B, 1999, 103, 4781-4785.	2.6	177
11	Solvent isotope effect and protein stability. Nature Structural Biology, 1995, 2, 852-855.	9.7	172
12	Thermodynamics of ubiquitin unfolding. Proteins: Structure, Function and Bioinformatics, 1994, 18, 246-253.	2.6	170
13	Molecular Mechanism for the Preferential Exclusion of TMAO from Protein Surfaces. Journal of Physical Chemistry B, 2012, 116, 12095-12104.	2.6	162
14	Heat capacity changes upon burial of polar and nonpolar groups in proteins. Protein Science, 2008, 10, 1343-1352.	7.6	120
15	Anion binding to the ubiquitin molecule. Protein Science, 1998, 7, 689-697.	7.6	118
16	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
17	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
18	Energetics of Target Peptide Binding by Calmodulin Reveals Different Modes of Binding. Journal of Biological Chemistry, 2001, 276, 14083-14091.	3.4	107

#	Article	IF	Citations
19	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
20	Thermodynamics of bpti folding. Protein Science, 1993, 2, 2028-2036.	7.6	102
21	ProteinVolume: calculating molecular van der Waals and void volumes in proteins. BMC Bioinformatics, 2015, 16, 101.	2.6	84
22	Energetics of ribonuclease T1 structure. Biochemistry, 1994, 33, 3312-3319.	2.5	81
23	Heat capacity change for ribonuclease A folding. Protein Science, 1999, 8, 1500-1504.	7.6	77
24	Molecular determinant of the effects of hydrostatic pressure on protein folding stability. Nature Communications, 2017, 8, 14561.	12.8	75
25	Thermodynamics of barnase unfolding. Protein Science, 1994, 3, 669-676.	7.6	74
26	On the entropy of protein folding. Protein Science, 1996, 5, 507-510.	7.6	74
27	Heat capacities of amino acids, peptides and proteins. Biophysical Chemistry, 1998, 71, 133-156.	2.8	74
28	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
29	Temperature Dependence of the Thermodynamics of Helixâ€“Coil Transition. Journal of Molecular Biology, 2004, 335, 1029-1037.	4.2	70
30	Cold denaturation of ubiquitin. BBA - Proteins and Proteomics, 1999, 1429, 384-390.	2.1	69
31	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
32	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
33	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
34	Predictive Model of Linear Antimicrobial Peptides Active against Gram-Negative Bacteria. Journal of Chemical Information and Modeling, 2018, 58, 1141-1151.	5.4	57
35	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
36	Enzyme Activity in the Crowded Milieu. PLoS ONE, 2012, 7, e39418.	2.5	54

#	Article	IF	Citations
37	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
38	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
39	Interactions of the Cold Shock Protein CspB fromBacillus subtilis with Single-stranded DNA. Journal of Biological Chemistry, 2001, 276, 15511-15518.	3.4	51
40	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
41	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
42	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
43	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
44	Effects of Charge-to-Alanine Substitutions on the Stability of Ribosomal Protein L30e from Thermococcus celer. Biochemistry, 2005, 44, 16817-16825.	2.5	43
45	Thermodynamics Of Î±â€Helix Formation. Advances in Protein Chemistry, 2005, 72, 199-226.	4.4	42
46	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
47	Differential Scanning Calorimetry. , 2002, 173, 113-119.		41
48	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
49	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
50	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
51	Universal Convergence of the Specific Volume Changes of Globular Proteins upon Unfolding. Biochemistry, 2009, 48, 10846-10851.	2.5	36
52	Cooperativity of complex salt bridges. Protein Science, 2008, 17, 1285-1290.	7.6	35
53	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
54	Mechanism of Fibril Formation by a 39-Residue Peptide (PAPf39) from Human Prostatic Acidic Phosphatase. Biochemistry, 2009, 48, 11582-11591.	2.5	33

#	Article	IF	Citations
55	Conformational and thermodynamic properties of peptide binding to the human S100P protein. Protein Science, 2002, 11, 1367-1375.	7.6	31
56	Chapter 22 Use of Pressure Perturbation Calorimetry to Characterize the Volumetric Properties of Proteins. Methods in Enzymology, 2009, 466, 527-547.	1.0	31
57	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
58	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
59	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
60	Chapter 7 A Computational Approach for the Rational Design of Stable Proteins and Enzymes. Methods in Enzymology, 2009, 454, 175-211.	1.0	29
61	Thermodynamics of the Trpâ€cage miniprotein unfolding in urea. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1376-1381.	2.6	29
62	The Role of Cross-Chain Ionic Interactions for the Stability of Collagen Model Peptides. Biophysical Journal, 2013, 105, 1681-1688.	0.5	29
63	Cloning, overexpression, purification, and spectroscopic characterization of human S100P. Protein Science, 1998, 7, 211-215.	7.6	28
64	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
65	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
66	Protein Stabilization by the Rational Design of Surface Chargeâ€“Charge Interactions. Methods in Molecular Biology, 2009, 490, 261-283.	0.9	27
67	Removal of surface chargeâ€charge interactions from ubiquitin leaves the protein folded and very stable. Protein Science, 2002, 11, 174-177.	7.6	26
68	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
69	Isothermal Titration Calorimetry. , 2002, 173, 121-126.		24
70	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
71	Pressure Perturbation Calorimetry of Unfolded Proteins. Journal of Physical Chemistry B, 2010, 114, 16166-16170.	2.6	21
72	Protonation/deprotonation effects on the stability of the Trp-cage miniprotein. Physical Chemistry Chemical Physics, 2011, 13, 17056.	2.8	21

#	Article	IF	Citations
73	Non-linearity of the collagen triple helix in solution and implications for collagen function. Biochemical Journal, 2017, 474, 2203-2217.	3.7	21
74	Structural Characterization of Semen Coagulum-Derived SEM1(86â€“107) Amyloid Fibrils That Enhance HIV-1 Infection. Biochemistry, 2014, 53, 3267-3277.	2.5	17
75	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
76	Energetics of chargeâ€“charge interactions between residues adjacent in sequence. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3494-3499.	2.6	14
77	Molecular Determinants of Temperature Dependence of Protein Volume Change upon Unfolding. Journal of Physical Chemistry B, 2017, 121, 8300-8310.	2.6	13
78	Putting the Piezolyte Hypothesis under Pressure. Biophysical Journal, 2017, 113, 974-977.	0.5	13
79	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
80	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
81	Protein adaptation to high hydrostatic pressure: Computational analysis of the structural proteome. Proteins: Structure, Function and Bioinformatics, 2020, 88, 584-592.	2.6	12
82	Intramolecular diffusion controls aggregation of the PAPf39 peptide. Biophysical Chemistry, 2016, 216, 37-43.	2.8	11
83	Novel Interactions of the TRTK12 Peptide with S100 Protein Family Members: Specificity and Thermodynamic Characterization. Biochemistry, 2013, 52, 5844-5856.	2.5	10
84	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
85	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
86	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
87	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
88	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
89	Bacterial expression and purification of the amyloidogenic peptide PAPf39 for multidimensional NMR spectroscopy. Protein Expression and Purification, 2013, 88, 196-200.	1.3	5
90	Thermal expansivities of peptides, polypeptides and proteins as measured by pressure perturbation calorimetry. Methods, 2015, 76, 61-66.	3.8	5

#	Article	IF	Citations
91	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
92	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
93	From Protein Design to the Energy Landscape of a Cold Unfolding Protein. Journal of Physical Chemistry B, 2022, 126, 1212-1231.	2.6	3
94	Contribution of buried aspartic acid to the stability of the PDZ2 protein. Journal of Chemical Thermodynamics, 2012, 52, 64-68.	2.0	2
95	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
96	Effects of Hydrostatic Pressure on the Thermodynamics of CspB-Bs Interactions with the ssDNA Template. Biochemistry, 2021, 60, 3086-3097.	2.5	2