J Martin Scholtz

List of Publications by Year
in descending order

72 papers	10,709 citations	66234 42 h-index	85405 71 g-index
78 all docs	78 docs citations	78 times ranked	11483 citing authors

#	Article	IF	Citations
1	Denaturant <i>m</i> values and heat capacity changes: Relation to changes in accessible surface areas of protein unfolding. Protein Science, 1995, 4, 2138-2148.	3.1	1,815
2	A Helix Propensity Scale Based on Experimental Studies of Peptides and Proteins. Biophysical Journal, 1998, 75, 422-427.	0.2	910
3	Parameters of helix-coil transition theory for alanine-based peptides of varying chain lengths in water. Biopolymers, 1991, 31, 1463-1470.	1.2	515
4	The Mechanism of alpha-Helix Formation by Peptides. Annual Review of Biophysics and Biomolecular Structure, 1992, 21, 95-118.	18.3	496
5	A summary of the measured p<i>K</i> values of the ionizable groups in folded proteins. Protein Science, 2009, 18, 247-251.	3.1	386
6	Protein Ionizable Groups: pK Values and Their Contribution to Protein Stability and Solubility. Journal of Biological Chemistry, 2009, 284, 13285-13289.	1.6	369
7	Contribution of hydrogen bonds to protein stability. Protein Science, 2014, 23, 652-661.	3.1	323
8	pK values of the ionizable groups of proteins. Protein Science, 2006, 15, 1214-1218.	3.1	307
9	Protein structure, stability and solubility in water and other solvents. Philosophical Transactions of the Royal Society B: Biological Sciences, 2004, 359, 1225-1235.	1.8	305
10	The energetics of ion-pair and hydrogen-bonding interactions in a helical peptide. Biochemistry, 1993, 32, 9668-9676.	1.2	296
11	Contribution of Hydrophobic Interactions to Protein Stability. Journal of Molecular Biology, 2011, 408, 514-528.	2.0	295
12	Lessons in stability from thermophilic proteins. Protein Science, 2006, 15, 1569-1578.	3.1	289
13	Toward a Molecular Understanding of Protein Solubility: Increased Negative Surface Charge Correlates with Increased Solubility. Biophysical Journal, 2012, 102, 1907-1915.	0.2	289
14	Forces stabilizing proteins. FEBS Letters, 2014, 588, 2177-2184.	1.3	273
15	Interactions of Peptides with a Protein Pore. Biophysical Journal, 2005, 89, 1030-1045.	0.2	248
16	Amino Acid Contribution to Protein Solubility: Asp, Glu, and Ser Contribute more Favorably than the other Hydrophilic Amino Acids in RNase Sa. Journal of Molecular Biology, 2007, 366, 449-460.	2.0	211
17	Increasing protein stability by altering longâ€range coulombic interactions. Protein Science, 1999, 8, 1843-1849.	3.1	203
18	A neutral, water-soluble, .alpha.-helical peptide: the effect of ionic strength on the helix-coil equilibrium. Journal of the American Chemical Society, 1991, 113, 5102-5104.	6.6	151

#	Article	IF	Citations
19	Helix Propensities Are Identical in Proteins and Peptidesâ€. Biochemistry, 1997, 36, 10923-10929.	1.2	149
20	Protein conformational stabilities can be determined from hydrogen exchange rates. Nature Structural Biology, 1999, 6, 910-912.	9.7	148
21	Organophosphorus Hydrolase Is a Remarkably Stable Enzyme That Unfolds through a Homodimeric Intermediateâ€. Biochemistry, 1997, 36, 14366-14374.	1.2	142
22	Increasing Protein Conformational Stability by Optimizing Î²-Turn Sequence. Journal of Molecular Biology, 2007, 373, 211-218.	2.0	138
23	The role of protein stability, solubility, and net charge in amyloid fibril formation. Protein Science, 2009, 12, 2374-2378.	3.1	134
24	Conformational Stability of the Escherichia coli HPr Protein:â€‰ Test of the Linear Extrapolation Method and a Thermodynamic Characterization of Cold Denaturation. Biochemistry, 1996, 35, 11369-11378.	1.2	129
25	Kinetics of amide proton exchange in helical peptides of varying chain lengths. Interpretation by the Lifson-Roig equation. Biochemistry, 1992, 31, 1263-1269.	1.2	125
26	Measuring and Increasing Protein Solubility. Journal of Pharmaceutical Sciences, 2008, 97, 4155-4166.	1.6	125
27	Effect of a single aspartate on helix stability at different positions in a neutral alanineâ€based peptide. Protein Science, 1993, 2, 1604-1611.	3.1	123
28	Helical peptides with three pairs of Aspâ€Arg and Gluâ€Arg residues in different orientations and spacings. Protein Science, 1993, 2, 80-85.	3.1	113
29	Energetics of Polar Side-Chain Interactions in Helical Peptides:Â Salt Effects on Ion Pairs and Hydrogen Bondsâ€. Biochemistry, 1998, 37, 33-40.	1.2	100
30	Chargeâ€"Charge Interactions are Key Determinants of the pK Values of Ionizable Groups in Ribonuclease Sa (pI=3.5) and a Basic Variant (pI=10.2). Journal of Molecular Biology, 2003, 325, 1077-1092.	2.0	96
31	Guanidine Hydrochloride Unfolding of Peptide Helices:â€‰ Separation of Denaturant and Salt Effects. Biochemistry, 1996, 35, 7292-7297.	1.2	90
32	Increasing protein stability by improving betaâ€turns. Proteins: Structure, Function and Bioinformatics, 2009, 77, 491-498.	1.5	90
33	Single-Molecule Electrophoresis of Î²-Hairpin Peptides by Electrical Recordings and Langevin Dynamics Simulations. Journal of Physical Chemistry B, 2007, 111, 3332-3335.	1.2	82
34	Hydrogen Bonding of Î²-Turn Structure Is Stabilized in D₂O. Journal of the American Chemical Society, 2009, 131, 15188-15193.	6.6	79
35	Chapter 23 Solvent Denaturation of Proteins and Interpretations of the m Value. Methods in Enzymology, 2009, 466, 549-565.	0.4	70
36	Trifluoroethanol effects on helix propensity and electrostatic interactions in the helical peptide from ribonuclease T₁. Protein Science, 1998, 7, 383-388.	3.1	65

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37	Hydrogen Bonding Markedly Reduces the pK of Buried Carboxyl Groups in Proteins. Journal of Molecular Biology, 2006, 362, 594-604.	2.0	62
38	The Contribution of Polar Group Burial to Protein Stability Is Strongly Context-dependent. Journal of Biological Chemistry, 2003, 278, 31790-31795.	1.6	57
39	Charge-charge interactions in the denatured state influence the folding kinetics of ribonuclease Sa. Protein Science, 2005, 14, 1934-1938.	3.1	46
40	Osmolyte effects on helix formation in peptides and the stability of coiled-coils. Protein Science, 2002, 11, 2048-2051.	3.1	45
41	Peptide Sequence and Conformation Strongly Influence Tryptophan Fluorescence. Biophysical Journal, 2008, 94, 2280-2287.	0.2	44
42	Phosphorylation of serineâ€46 in HPr, a key regulatory protein in bacteria, results in stabilization of its solution structure. Protein Science, 1995, 4, 2478-2486.	3.1	43
43	Urea denatured state ensembles contain extensive secondary structure that is increased in hydrophobic proteins. Protein Science, 2010, 19, 929-943.	3.1	41
44	Conformational Preferences of RNase AC-Peptide Derivatives Containing a Highly Constrained Analogue of Phenylalanine. Journal of the American Chemical Society, 1998, 120, 9435-9443.	6.6	40
45	Hydrogen bonding increases packing density in the protein interior. Proteins: Structure, Function and Bioinformatics, 2005, 63, 278-282.	1.5	38
46	pK Values of Histidine Residues in Ribonuclease Sa: Effect of Salt and Net Charge. Journal of Molecular Biology, 2003, 325, 1093-1105.	2.0	37
47	Contribution of Single Tryptophan Residues to the Fluorescence and Stability of Ribonuclease Sa. Biophysical Journal, 2004, 87, 4036-4047.	0.2	36
48	Carbodiimide EDC Induces Cross-Links That Stabilize RNase A C-Dimer against Dissociation: EDC Adducts Can Affect Protein Net Charge, Conformation, and Activity. Bioconjugate Chemistry, 2009, 20, 1459-1473.	1.8	34
49	Conformational stability of HPr: The histidineâ€containing phosphocarrier protein from <i>Bacillus subtilis</i>. Protein Science, 1995, 4, 35-43.	3.1	33
50	Asp79 Makes a Large, Unfavorable Contribution to the Stability of RNase Sa. Journal of Molecular Biology, 2005, 354, 967-978.	2.0	32
51	Factors That Influence Helical Preferences for Singly Charged Gas-Phase Peptide Ions: The Effects of Multiple Potential Charge-Carrying Sites. Journal of Physical Chemistry B, 2010, 114, 809-816.	1.2	31
52	Influence of N-Cap Mutations on the Structure and Stability of Escherichia coli HPr. Biochemistry, 1996, 35, 11268-11277.	1.2	30
53	Terminal ion pairs stabilize the second Î²-hairpin of the B1 domain of protein G. Proteins: Structure, Function and Bioinformatics, 2006, 63, 1005-1017.	1.5	29
54	pKa of Fentanyl Varies With Temperature: Implications for Acid-Base Management During Extremes of Body Temperature. Journal of Cardiothoracic and Vascular Anesthesia, 2005, 19, 759-762.	0.6	28

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55	Perchlorate-induced denaturation of ribonuclease A: Investigation of possible folding intermediates. Biochemistry, 1993, 32, 4604-4608.	1.2	27
56	A Thermodynamic Comparison of HPr Proteins from Extremophilic Organismsâ€. Biochemistry, 2006, 45, 4084-4092.	1.2	27
57	Increasing protein stability: Importance of Î”<i>C</i>_p and the denatured state. Protein Science, 2010, 19, 1044-1052.	3.1	26
58	Hydrogen-Exchange Stabilities of RNase T1 and Variants with Buried and Solvent-Exposed Ala â†' Gly Mutations in the Helixâ€. Biochemistry, 1999, 38, 16481-16490.	1.2	23
59	Tryptophan Fluorescence Reveals the Presence of Long-Range Interactions in the Denatured State of Ribonuclease Sa. Biophysical Journal, 2008, 94, 2288-2296.	0.2	23
60	Determining the Conformational Stability of a Protein Using Urea Denaturation Curves. Methods in Molecular Biology, 2009, 490, 41-55.	0.4	22
61	NMR study and molecular dynamics simulations of optimized Î²-hairpin fragments of protein G. Proteins: Structure, Function and Bioinformatics, 2007, 69, 285-296.	1.5	20
62	An engineered leucine zipperaposition mutant with an unusual three-state unfolding pathway. Protein Science, 2001, 10, 24-33.	3.1	19
63	Energetic Implications for Protein Phosphorylation. Journal of Biological Chemistry, 1996, 271, 28898-28902.	1.6	17
64	Investigation of a sideâ€chainâ€sideâ€chain hydrogen bond by mutagenesis, thermodynamics, and NMR spectroscopy. Protein Science, 1995, 4, 936-944.	3.1	17
65	The HPr Proteins from the Thermophile Bacillus stearothermophilus can form Domain-swapped Dimers. Journal of Molecular Biology, 2005, 346, 919-931.	2.0	15
66	Determining the Conformational Stability of a Protein from Urea and Thermal Unfolding Curves. Current Protocols in Protein Science, 2013, 71, Unit28.4.	2.8	15
67	Î±-Helix Formation by Peptides in Water. , 1995, , 171-192.		12
68	Chargeâ€"charge interactions are the primary determinants of the pK values of the ionizable groups in Ribonuclease T1. Biophysical Chemistry, 2002, 101-102, 211-219.	1.5	10
69	Ribonuclease Sa Conformational Stability Studied by NMR-Monitored Hydrogen Exchangeâ€. Biochemistry, 2005, 44, 7644-7655.	1.2	9
70	A Partially Buried Site in Homologous HPr Proteins is Not Optimized for Stability. Journal of Molecular Biology, 2002, 321, 355-362.	2.0	6
71	The Side Chain of Aspartic Acid 69 Dictates the Folding Mechanism ofBacillus subtilisHPrâ€. Biochemistry, 2004, 43, 1360-1368.	1.2	2
72	The effect of intrinsic factors on amyloid formation. FASEB Journal, 2009, 23, 850.3.	0.2	0