

# J Martin Scholtz

## List of Publications by Year in descending order

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72  
papers

10,709  
citations

66343

42  
h-index

85541

71  
g-index

78  
all docs

78  
docs citations

78  
times ranked

11483  
citing authors

#	ARTICLE	IF	CITATIONS
1	Denaturant $m$ values and heat capacity changes: Relation to changes in accessible surface areas of protein unfolding. <i>Protein Science</i> , 1995, 4, 2138-2148.	7.6	1,815
2	A Helix Propensity Scale Based on Experimental Studies of Peptides and Proteins. <i>Biophysical Journal</i> , 1998, 75, 422-427.	0.5	910
3	Parameters of helix-coil transition theory for alanine-based peptides of varying chain lengths in water. <i>Biopolymers</i> , 1991, 31, 1463-1470.	2.4	515
4	The Mechanism of alpha-Helix Formation by Peptides. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1992, 21, 95-118.	18.3	496
5	A summary of the measured $pK$ values of the ionizable groups in folded proteins. <i>Protein Science</i> , 2009, 18, 247-251.	7.6	386
6	Protein Ionizable Groups: $pK$ Values and Their Contribution to Protein Stability and Solubility. <i>Journal of Biological Chemistry</i> , 2009, 284, 13285-13289.	3.4	369
7	Contribution of hydrogen bonds to protein stability. <i>Protein Science</i> , 2014, 23, 652-661.	7.6	323
8	$pK$ values of the ionizable groups of proteins. <i>Protein Science</i> , 2006, 15, 1214-1218.	7.6	307
9	Protein structure, stability and solubility in water and other solvents. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2004, 359, 1225-1235.	4.0	305
10	The energetics of ion-pair and hydrogen-bonding interactions in a helical peptide. <i>Biochemistry</i> , 1993, 32, 9668-9676.	2.5	296
11	Contribution of Hydrophobic Interactions to Protein Stability. <i>Journal of Molecular Biology</i> , 2011, 408, 514-528.	4.2	295
12	Lessons in stability from thermophilic proteins. <i>Protein Science</i> , 2006, 15, 1569-1578.	7.6	289
13	Toward a Molecular Understanding of Protein Solubility: Increased Negative Surface Charge Correlates with Increased Solubility. <i>Biophysical Journal</i> , 2012, 102, 1907-1915.	0.5	289
14	Forces stabilizing proteins. <i>FEBS Letters</i> , 2014, 588, 2177-2184.	2.8	273
15	Interactions of Peptides with a Protein Pore. <i>Biophysical Journal</i> , 2005, 89, 1030-1045.	0.5	248
16	Amino Acid Contribution to Protein Solubility: Asp, Glu, and Ser Contribute more Favorably than the other Hydrophilic Amino Acids in RNase Sa. <i>Journal of Molecular Biology</i> , 2007, 366, 449-460.	4.2	211
17	Increasing protein stability by altering long-range coulombic interactions. <i>Protein Science</i> , 1999, 8, 1843-1849.	7.6	203
18	A neutral, water-soluble, .alpha.-helical peptide: the effect of ionic strength on the helix-coil equilibrium. <i>Journal of the American Chemical Society</i> , 1991, 113, 5102-5104.	13.7	151

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19	Helix Propensities Are Identical in Proteins and Peptides. <i>Biochemistry</i> , 1997, 36, 10923-10929.	2.5	149
20	Protein conformational stabilities can be determined from hydrogen exchange rates. <i>Nature Structural Biology</i> , 1999, 6, 910-912.	9.7	148
21	Organophosphorus Hydrolase Is a Remarkably Stable Enzyme That Unfolds through a Homodimeric Intermediate. <i>Biochemistry</i> , 1997, 36, 14366-14374.	2.5	142
22	Increasing Protein Conformational Stability by Optimizing $\beta^2$ -Turn Sequence. <i>Journal of Molecular Biology</i> , 2007, 373, 211-218.	4.2	138
23	The role of protein stability, solubility, and net charge in amyloid fibril formation. <i>Protein Science</i> , 2009, 12, 2374-2378.	7.6	134
24	Conformational Stability of the Escherichia coli HPr Protein: A Test of the Linear Extrapolation Method and a Thermodynamic Characterization of Cold Denaturation. <i>Biochemistry</i> , 1996, 35, 11369-11378.	2.5	129
25	Kinetics of amide proton exchange in helical peptides of varying chain lengths. Interpretation by the Lifson-Roig equation. <i>Biochemistry</i> , 1992, 31, 1263-1269.	2.5	125
26	Measuring and Increasing Protein Solubility. <i>Journal of Pharmaceutical Sciences</i> , 2008, 97, 4155-4166.	3.3	125
27	Effect of a single aspartate on helix stability at different positions in a neutral alanine-based peptide. <i>Protein Science</i> , 1993, 2, 1604-1611.	7.6	123
28	Helical peptides with three pairs of Asp-Arg and Glu-Arg residues in different orientations and spacings. <i>Protein Science</i> , 1993, 2, 80-85.	7.6	113
29	Energetics of Polar Side-Chain Interactions in Helical Peptides: A Salt Effects on Ion Pairs and Hydrogen Bonds. <i>Biochemistry</i> , 1998, 37, 33-40.	2.5	100
30	Charge-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). <i>Journal of Molecular Biology</i> , 2003, 325, 1077-1092.	4.2	96
31	Guanidine Hydrochloride Unfolding of Peptide Helices: Separation of Denaturant and Salt Effects. <i>Biochemistry</i> , 1996, 35, 7292-7297.	2.5	90
32	Increasing protein stability by improving beta-turns. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 491-498.	2.6	90
33	Single-Molecule Electrophoresis of $\beta^2$ -Hairpin Peptides by Electrical Recordings and Langevin Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2007, 111, 3332-3335.	2.6	82
34	Hydrogen Bonding of $\beta^2$ -Turn Structure Is Stabilized in D <sub>2</sub> O. <i>Journal of the American Chemical Society</i> , 2009, 131, 15188-15193.	13.7	79
35	Chapter 23 Solvent Denaturation of Proteins and Interpretations of the m Value. <i>Methods in Enzymology</i> , 2009, 466, 549-565.	1.0	70
36	Trifluoroethanol effects on helix propensity and electrostatic interactions in the helical peptide from ribonuclease T <sub>1</sub> . <i>Protein Science</i> , 1998, 7, 383-388.	7.6	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.	4.2	62
38	The Contribution of Polar Group Burial to Protein Stability Is Strongly Context-dependent. Journal of Biological Chemistry, 2003, 278, 31790-31795.	3.4	57
39	Charge-charge interactions in the denatured state influence the folding kinetics of ribonuclease Sa. Protein Science, 2005, 14, 1934-1938.	7.6	46
40	Osmolyte effects on helix formation in peptides and the stability of coiled-coils. Protein Science, 2002, 11, 2048-2051.	7.6	45
41	Peptide Sequence and Conformation Strongly Influence Tryptophan Fluorescence. Biophysical Journal, 2008, 94, 2280-2287.	0.5	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.	7.6	43
43	Urea denatured state ensembles contain extensive secondary structure that is increased in hydrophobic proteins. Protein Science, 2010, 19, 929-943.	7.6	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.	13.7	40
45	Hydrogen bonding increases packing density in the protein interior. Proteins: Structure, Function and Bioinformatics, 2005, 63, 278-282.	2.6	38
46	pK Values of Histidine Residues in Ribonuclease Sa: Effect of Salt and Net Charge. Journal of Molecular Biology, 2003, 325, 1093-1105.	4.2	37
47	Contribution of Single Tryptophan Residues to the Fluorescence and Stability of Ribonuclease Sa. Biophysical Journal, 2004, 87, 4036-4047.	0.5	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.	3.6	34
49	Conformational stability of HPr: The histidineâ€containing phosphocarrier protein from <i>Bacillus subtilis</i>. Protein Science, 1995, 4, 35-43.	7.6	33
50	Asp79 Makes a Large, Unfavorable Contribution to the Stability of RNase Sa. Journal of Molecular Biology, 2005, 354, 967-978.	4.2	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.	2.6	31
52	Influence of N-Cap Mutations on the Structure and Stability of Escherichia coli HPr. Biochemistry, 1996, 35, 11268-11277.	2.5	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.	2.6	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.	1.3	28

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55	Perchlorate-induced denaturation of ribonuclease A: Investigation of possible folding intermediates. <i>Biochemistry</i> , 1993, 32, 4604-4608.	2.5	27
56	A Thermodynamic Comparison of HPr Proteins from Extremophilic Organisms. <i>Biochemistry</i> , 2006, 45, 4084-4092.	2.5	27
57	Increasing protein stability: Importance of $\Delta C_p$ and the denatured state. <i>Protein Science</i> , 2010, 19, 1044-1052.	7.6	26
58	Hydrogen-Exchange Stabilities of RNase T1 and Variants with Buried and Solvent-Exposed Ala $\rightarrow$ Gly Mutations in the Helix. <i>Biochemistry</i> , 1999, 38, 16481-16490.	2.5	23
59	Tryptophan Fluorescence Reveals the Presence of Long-Range Interactions in the Denatured State of Ribonuclease Sa. <i>Biophysical Journal</i> , 2008, 94, 2288-2296.	0.5	23
60	Determining the Conformational Stability of a Protein Using Urea Denaturation Curves. <i>Methods in Molecular Biology</i> , 2009, 490, 41-55.	0.9	22
61	NMR study and molecular dynamics simulations of optimized $\beta^2$ -hairpin fragments of protein G. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 285-296.	2.6	20
62	An engineered leucine zipperposition mutant with an unusual three-state unfolding pathway. <i>Protein Science</i> , 2001, 10, 24-33.	7.6	19
63	Energetic Implications for Protein Phosphorylation. <i>Journal of Biological Chemistry</i> , 1996, 271, 28898-28902.	3.4	17
64	Investigation of a side-chain-side-chain hydrogen bond by mutagenesis, thermodynamics, and NMR spectroscopy. <i>Protein Science</i> , 1995, 4, 936-944.	7.6	17
65	The HPr Proteins from the Thermophile <i>Bacillus stearothermophilus</i> can form Domain-swapped Dimers. <i>Journal of Molecular Biology</i> , 2005, 346, 919-931.	4.2	15
66	Determining the Conformational Stability of a Protein from Urea and Thermal Unfolding Curves. <i>Current Protocols in Protein Science</i> , 2013, 71, Unit28.4.	2.8	15
67	$\beta$ -Helix Formation by Peptides in Water. , 1995, , 171-192.		12
68	Charge-charge interactions are the primary determinants of the pK values of the ionizable groups in Ribonuclease T1. <i>Biophysical Chemistry</i> , 2002, 101-102, 211-219.	2.8	10
69	Ribonuclease Sa Conformational Stability Studied by NMR-Monitored Hydrogen Exchange. <i>Biochemistry</i> , 2005, 44, 7644-7655.	2.5	9
70	A Partially Buried Site in Homologous HPr Proteins is Not Optimized for Stability. <i>Journal of Molecular Biology</i> , 2002, 321, 355-362.	4.2	6
71	The Side Chain of Aspartic Acid 69 Dictates the Folding Mechanism of <i>Bacillus subtilis</i> HPr. <i>Biochemistry</i> , 2004, 43, 1360-1368.	2.5	2
72	The effect of intrinsic factors on amyloid formation. <i>FASEB Journal</i> , 2009, 23, 850.3.	0.5	0