Daniel P Raleigh

List of Publications by Year
in descending order

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240 papers	13,695 citations	15504 65 h-index	30087 103 g-index
248 all docs	248 docs citations	248 times ranked	9914 citing authors

#	Article	IF	Citations
1	Rotational resonance in solid state NMR. Chemical Physics Letters, 1988, 146, 71-76.	2.6	579
2	Histone H2B ubiquitylation disrupts local and higher-order chromatin compaction. Nature Chemical Biology, 2011, 7, 113-119.	8.0	392
3	De Novo Design of Helical Bundles as Models for Understanding Protein Folding and Function. Accounts of Chemical Research, 2000, 33, 745-754.	15.6	311
4	Two-dimensional IR spectroscopy and isotope labeling defines the pathway of amyloid formation with residue-specific resolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6614-6619.	7.1	277
5	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometryâ€“mass spectrometry. Nature Chemistry, 2015, 7, 73-81.	13.6	255
6	The Flavanol (â^')-Epigallocatechin 3-Gallate Inhibits Amyloid Formation by Islet Amyloid Polypeptide, Disaggregates Amyloid Fibrils, and Protects Cultured Cells against IAPP-Induced Toxicity. Biochemistry, 2010, 49, 8127-8133.	2.5	241
7	Mechanism of IAPP amyloid fibril formation involves an intermediate with a transient Î²-sheet. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19285-19290.	7.1	224
8	Protein folding: Defining a â€œstandardâ€•set of experimental conditions and a preliminary kinetic data set of two-state proteins. Protein Science, 2005, 14, 602-616.	7.6	207
9	Rational Modification of Protein Stability by the Mutation of Charged Surface Residuesâ€. Biochemistry, 2000, 39, 872-879.	2.5	197
10	Effects of Sequential Proline Substitutions on Amyloid Formation by Human Amylin20-29â€. Biochemistry, 1999, 38, 1811-1818.	2.5	192
11	A critical assessment of the role of helical intermediates in amyloid formation by natively unfolded proteins and polypeptides. Protein Engineering, Design and Selection, 2009, 22, 453-459.	2.1	177
12	Islet Amyloid Polypeptide: Structure, Function, and Pathophysiology. Journal of Diabetes Research, 2016, 2016, 1-18.	2.3	177
13	A role for helical intermediates in amyloid formation by natively unfolded polypeptides?. Physical Biology, 2009, 6, 015005.	1.8	170
14	Islet amyloid: From fundamental biophysics to mechanisms of cytotoxicity. FEBS Letters, 2013, 587, 1106-1118.	2.8	166
15	De novo protein design: from molten globules to native-like states. Current Opinion in Structural Biology, 1993, 3, 601-610.	5.7	163
16	Toxic oligomers and islet beta cell death: guilty by association or convicted by circumstantial evidence?. Diabetologia, 2010, 53, 1046-1056.	6.3	160
17	Two-dimensional infrared spectroscopy reveals the complex behaviour of an amyloid fibril inhibitor. Nature Chemistry, 2012, 4, 355-360.	13.6	158
18	Ion Mobility Spectrometryâ€“Mass Spectrometry Defines the Oligomeric Intermediates in Amylin Amyloid Formation and the Mode of Action of Inhibitors. Journal of the American Chemical Society, 2014, 136, 660-670.	13.7	158

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19	A Single-Point Mutation Converts the Highly Amyloidogenic Human Islet Amyloid Polypeptide into a Potent Fibrillization Inhibitor. Journal of the American Chemical Society, 2007, 129, 11300-11301.	13.7	156
20	Islet amyloid deposition limits the viability of human islet grafts but not porcine islet grafts. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4305-4310.	7.1	154
21	The Role of His-18 in Amyloid Formation by Human Islet Amyloid Polypeptideâ€. Biochemistry, 2005, 44, 16284-16291.	2.5	150
22	Ionic Strength Effects on Amyloid Formation by Amylin Are a Complicated Interplay among Debye Screening, Ion Selectivity, and Hofmeister Effects. Biochemistry, 2012, 51, 8478-8490.	2.5	134
23	Analysis of amylin cleavage products provides new insights into the amyloidogenic region of human amylin. Journal of Molecular Biology, 1999, 294, 1375-1385.	4.2	131
24	pKaValues and the pH Dependent Stability of the N-Terminal Domain of L9 as Probes of Electrostatic Interactions in the Denatured State. Differentiation between Local and Nonlocal Interactionsâ€. Biochemistry, 1999, 38, 4896-4903.	2.5	128
25	Islet amyloid polypeptide toxicity and membrane interactions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19279-19284.	7.1	128
26	Time-resolved studies define the nature of toxic IAPP intermediates, providing insight for anti-amyloidosis therapeutics. ELife, 2016, 5, .	6.0	126
27	Aromatic Interactions Are Not Required for Amyloid Fibril Formation by Islet Amyloid Polypeptide but Do Influence the Rate of Fibril Formation and Fibril Morphologyâ€. Biochemistry, 2007, 46, 3255-3261.	2.5	124
28	Dynamic NMR Line-Shape Analysis Demonstrates that the Villin Headpiece Subdomain Folds on the Microsecond Time Scale. Journal of the American Chemical Society, 2003, 125, 6032-6033.	13.7	122
29	Analysis of the Inhibition and Remodeling of Islet Amyloid Polypeptide Amyloid Fibers by Flavanols. Biochemistry, 2012, 51, 2670-2683.	2.5	122
30	Role of Aromatic Interactions in Amyloid Formation by Peptides Derived from Human Amylinâ€. Biochemistry, 2004, 43, 15901-15908.	2.5	117
31	Residue Specific Resolution of Protein Folding Dynamics Using Isotope-Edited Infrared Temperature Jump Spectroscopyâ€. Biochemistry, 2007, 46, 3279-3285.	2.5	115
32	2DIR Spectroscopy of Human Amylin Fibrils Reflects Stable Î²-Sheet Structure. Journal of the American Chemical Society, 2011, 133, 16062-16071.	13.7	114
33	Morin hydrate inhibits amyloid formation by islet amyloid polypeptide and disaggregates amyloid fibers. Protein Science, 2012, 21, 373-382.	7.6	112
34	Incorporation of Pseudoproline Derivatives Allows the Facile Synthesis of Human IAPP, a Highly Amyloidogenic and Aggregation-Prone Polypeptide. Organic Letters, 2005, 7, 693-696.	4.6	111
35	Role of Aromatic Interactions in Amyloid Formation by Islet Amyloid Polypeptide. Biochemistry, 2013, 52, 333-342.	2.5	111
36	Global analysis of the effects of temperature and denaturant on the folding and unfolding kinetics of the N-terminal domain of the protein L9 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 284, 1661-1670.	4.2	110

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37	Islet Amyloid Polypeptide Membrane Interactions: Effects of Membrane Composition. Biochemistry, 2017, 56, 376-390.	2.5	109
38	Thermodynamics and Kinetics of Non-native Interactions in Protein Folding: A Single Point Mutant Significantly Stabilizes the N-terminal Domain of L9 by Modulating Non-native Interactions in the Denatured State. Journal of Molecular Biology, 2004, 338, 827-837.	4.2	105
39	Low levels of asparagine deamidation can have a dramatic effect on aggregation of amyloidogenic peptides: Implications for the study of amyloid formation. Protein Science, 2009, 11, 342-349.	7.6	104
40	Aggregation of islet amyloid polypeptide: from physical chemistry to cell biology. Current Opinion in Structural Biology, 2013, 23, 82-89.	5.7	104
41	A de Novo Designed Protein Mimics the Native State of Natural Proteins. Journal of the American Chemical Society, 1995, 117, 7558-7559.	13.7	102
42	Rescuing a destabilized protein fold through backbone cyclization. Journal of Molecular Biology, 2001, 308, 1045-1062.	4.2	98
43	The Î²-cell assassin: IAPP cytotoxicity. Journal of Molecular Endocrinology, 2017, 59, R121-R140.	2.5	97
44	Strategies for Extracting Structural Information from 2D IR Spectroscopy of Amyloid: Application to Islet Amyloid Polypeptide. Journal of Physical Chemistry B, 2009, 113, 15679-15691.	2.6	95
45	Rational design of potent domain antibody inhibitors of amyloid fibril assembly. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19965-19970.	7.1	93
46	Destabilization of Human IAPP Amyloid Fibrils by Proline Mutations Outside of the Putative Amyloidogenic Domain: Is There a Critical Amyloidogenic Domain in Human IAPP?. Journal of Molecular Biology, 2006, 355, 274-281.	4.2	92
47	Local control of peptide conformation: Stabilization ofcis proline peptide bonds by aromatic proline interactions. Biopolymers, 1998, 45, 381-394.	2.4	89
48	Deamidation Accelerates Amyloid Formation and Alters Amylin Fiber Structure. Journal of the American Chemical Society, 2012, 134, 12658-12667.	13.7	88
49	Rifampicin Does Not Prevent Amyloid Fibril Formation by Human Islet Amyloid Polypeptide but Does Inhibit Fibril Thioflavin-T Interactions: Implications for Mechanistic Studies of Î²-Cell Death. Biochemistry, 2008, 47, 6016-6024.	2.5	84
50	A de novo designed protein shows a thermally induced transition from a native to a molten globule-like state. Journal of the American Chemical Society, 1992, 114, 10079-10081.	13.7	83
51	Effect of modulating unfolded state structure on the folding kinetics of the villin headpiece subdomain. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16662-16667.	7.1	82
52	Azidohomoalanine: A Conformationally Sensitive IR Probe of Protein Folding, Protein Structure, and Electrostatics. Angewandte Chemie - International Edition, 2010, 49, 7473-7475.	13.8	81
53	Global analysis of the thermal and chemical denaturation of the Nâ€terminal domain of the ribosomal protein L9 in H₂O and D₂O. Determination of the thermodynamic parameters, Î”HÂ°, Î”SÂ°, and Î”CÂ°_p, and evaluation of solvent isotope effects. Protein Science, 1998, 7, 2405-2412.	7.6	77
54	Submillisecond folding of the peripheral subunit-binding domain 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 293, 763-768.	4.2	76

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55	Efficient Microwave-Assisted Synthesis of Human Islet Amyloid Polypeptide Designed to Facilitate the Specific Incorporation of Labeled Amino Acids. Organic Letters, 2010, 12, 4848-4851.	4.6	76
56	Exploiting the Right Side of the Ramachandran Plot:Â Substitution of Glycines byd-Alanine Can Significantly Increase Protein Stability. Journal of the American Chemical Society, 2004, 126, 13194-13195.	13.7	75
57	Interpretation of p-Cyanophenylalanine Fluorescence in Proteins in Terms of Solvent Exposure and Contribution of Side-Chain Quenchers: A Combined Fluorescence, IR and Molecular Dynamics Study. Biochemistry, 2009, 48, 9040-9046.	2.5	75
58	Sensitivity of Amyloid Formation by Human Islet Amyloid Polypeptide to Mutations at Residue 20. Journal of Molecular Biology, 2012, 421, 282-295.	4.2	75
59	Experiments and simulations show how long-range contacts can form in expanded unfolded proteins with negligible secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2123-2128.	7.1	74
60	Structure and Stability of the N-Terminal Domain of the Ribosomal Protein L9:â€‰ Evidence for Rapid Two-State Folding. Biochemistry, 1998, 37, 1025-1032.	2.5	73
61	Surface Salt Bridges, Double-Mutant Cycles, and Protein Stability:Â an Experimental and Computational Analysis of the Interaction of the Asp 23 Side Chain with the N-Terminus of the N-Terminal Domain of the Ribosomal Protein L9â€. Biochemistry, 2003, 42, 7050-7060.	2.5	72
62	Recovery and purification of highly aggregation-prone disulfide-containing peptides: Application to islet amyloid polypeptide. Analytical Biochemistry, 2006, 351, 181-186.	2.4	72
63	The Ability of Rodent Islet Amyloid Polypeptide To Inhibit Amyloid Formation by Human Islet Amyloid Polypeptide Has Important Implications for the Mechanism of Amyloid Formation and the Design of Inhibitors. Biochemistry, 2010, 49, 872-881.	2.5	72
64	Peptide Models Provide Evidence for Significant Structure in the Denatured State of a Rapidly Folding Protein:Â The Villin Headpiece Subdomainâ€. Biochemistry, 2004, 43, 3264-3272.	2.5	71
65	Mutational Analysis Demonstrates that Specific Electrostatic Interactions can Play a Key Role in the Denatured State Ensemble of Proteins. Journal of Molecular Biology, 2005, 353, 174-185.	4.2	69
66	Two-dimensional Infrared Spectroscopy Provides Evidence of an Intermediate in the Membrane-catalyzed Assembly of Diabetic Amyloid. Journal of Physical Chemistry B, 2009, 113, 2498-2505.	2.6	68
67	Defining the Molecular Basis of Amyloid Inhibitors: Human Islet Amyloid Polypeptideâ€“Insulin Interactions. Journal of the American Chemical Society, 2014, 136, 12912-12919.	13.7	67
68	Temperature-dependent Dynamics of the Villin Headpiece Helical Subdomain, An Unusually Small Thermostable Protein. Journal of Molecular Biology, 2002, 320, 841-854.	4.2	66
69	De novo protein design: what are we learning?. Current Opinion in Structural Biology, 1991, 1, 984-993.	5.7	65
70	Î¦-Values beyond the Ribosomally Encoded Amino Acids:Â Kinetic and Thermodynamic Consequences of Incorporating Trifluoromethyl Amino Acids in a Globular Protein. Journal of the American Chemical Society, 2003, 125, 9286-9287.	13.7	65
71	Residue-Specific, Real-Time Characterization of Lag-Phase Species and Fibril Growth During Amyloid Formation: A Combined Fluorescence and IR Study of p-Cyanophenylalanine Analogs of Islet Amyloid Polypeptide. Journal of Molecular Biology, 2010, 400, 878-888.	4.2	65
72	Characterizing a Partially Folded Intermediate of the Villin Headpiece Domain Under Non-denaturing Conditions: Contribution of His41 to the pH-dependent Stability of the N-terminal Subdomain. Journal of Molecular Biology, 2006, 355, 1078-1094.	4.2	63

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73	Stereological analysis of the human testis after vasectomy indicates impairment of spermatogenic efficiency with increasing obstructive interval. Fertility and Sterility, 2004, 81, 1595-1603.	1.0	61
74	A Free Energy Barrier Caused by the Refolding of an Oligomeric Intermediate Controls the Lag Time of Amyloid Formation by hIAPP. Journal of the American Chemical Society, 2017, 139, 16748-16758.	13.7	60
75	Analysis of the Amyloidogenic Potential of Pufferfish (Takifugu rubripes) Islet Amyloid Polypeptide Highlights the Limitations of Thioflavin-T Assays and the Difficulties in Defining Amyloidogenicity. Biochemistry, 2016, 55, 510-518.	2.5	59
76	RAGE binds preamyloid IAPP intermediates and mediates pancreatic Î² cell proteotoxicity. Journal of Clinical Investigation, 2018, 128, 682-698.	8.2	58
77	Multistate Folding of the Villin Headpiece Domain. Journal of Molecular Biology, 2006, 355, 1066-1077.	4.2	55
78	Peptide models of local and long-range interactions in the molten globule state of human Î±-lactalbumin. Journal of Molecular Biology, 1998, 283, 279-291.	4.2	52
79	Defining the core structure of the Î±-lactalbumin molten globule state 1 1Edited by C. R. Matthews. Journal of Molecular Biology, 1999, 294, 213-221.	4.2	52
80	Azido Homoalanine is a Useful Infrared Probe for Monitoring Local Electrostatistics and Side-Chain Solvation in Proteins. Journal of Physical Chemistry Letters, 2011, 2, 2158-2162.	4.6	52
81	The Protein Folding Transition State: What Are φ-Values Really Telling Us?. Protein and Peptide Letters, 2005, 12, 117-122.	0.9	52
82	Ph-dependent interactions and the stability and folding kinetics of the N-terminal domain of L9. electrostatic interactions are only weakly formed in the transition state for folding 1 1Edited by C. R. Matthews. Journal of Molecular Biology, 2000, 299, 1091-1100.	4.2	50
83	Rapid Cooperative Two-state Folding of a Miniature Î±â€“Î² Protein and Design of a Thermostable Variant. Journal of Molecular Biology, 2003, 326, 1261-1270.	4.2	50
84	Fine Structure Analysis of a Protein Folding Transition State; Distinguishing Between Hydrophobic Stabilization and Specific Packing. Journal of Molecular Biology, 2005, 354, 693-705.	4.2	50
85	Amyloid Formation by Pro-Islet Amyloid Polypeptide Processing Intermediates:â€‰ Examination of the Role of Protein Heparan Sulfate Interactions and Implications for Islet Amyloid Formation in Type 2 Diabetes. Biochemistry, 2007, 46, 12091-12099.	2.5	50
86	Use of the Novel Fluorescent Amino Acid p-Cyanophenylalanine Offers a Direct Probe of Hydrophobic Core Formation during the Folding of the N-Terminal Domain of the Ribosomal Protein L9 and Provides Evidence for Two-State Folding. Biochemistry, 2007, 46, 12308-12313.	2.5	50
87	Mutational Analysis of the Ability of Resveratrol To Inhibit Amyloid Formation by Islet Amyloid Polypeptide: Critical Evaluation of the Importance of Aromaticâ€“Inhibitor and Histidineâ€“Inhibitor Interactions. Biochemistry, 2015, 54, 666-676.	2.5	50
88	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12301-12310.	7.1	50
89	Energetically significant networks of coupled interactions within an unfolded protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12079-12084.	7.1	49
90	Insights into the consequences of co-polymerisation in the early stages of IAPP and AÎ² peptide assembly from mass spectrometry. Analyst, The, 2015, 140, 6990-6999.	3.5	48

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91	Molecular Signature for Receptor Engagement in the Metabolic Peptide Hormone Amylin. ACS Pharmacology and Translational Science, 2018, 1, 32-49.	4.9	48
92	An exceptionally stable helix from the ribosomal protein L9: implications for protein folding and stability. Journal of Molecular Biology, 1997, 270, 640-647.	4.2	47
93	Denatured State Effects and the Origin of Nonclassical Ï† Values in Protein Folding. Journal of the American Chemical Society, 2006, 128, 16492-16493.	13.7	47
94	The Unfolded State of the Villin Headpiece Helical Subdomain: Computational Studies of the Role of Locally Stabilized Structure. Journal of Molecular Biology, 2006, 360, 1094-1107.	4.2	46
95	A Simple and Economical Method for the Production of ¹³C,¹⁸O-Labeled Fmoc-Amino Acids with High Levels of Enrichment:â€‰ Applications to Isotope-Edited IR Studies of Proteins. Organic Letters, 2007, 9, 4935-4937.	4.6	46
96	The Sulfated Triphenyl Methane Derivative Acid Fuchsin Is a Potent Inhibitor of Amyloid Formation by Human Islet Amyloid Polypeptide and Protects against the Toxic Effects of Amyloid Formation. Journal of Molecular Biology, 2010, 400, 555-566.	4.2	46
97	Combination of Kinetically Selected Inhibitorsin TransLeads to Highly Effective Inhibition of Amyloid Formation. Journal of the American Chemical Society, 2010, 132, 14340-14342.	13.7	45
98	Rational modification of protein stability by targeting surface sites leads to complicated results. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11337-11342.	7.1	44
99	Characterization of the Heparin Binding Site in the N-Terminus of Human Pro-Islet Amyloid Polypeptide:â€‰ Implications for Amyloid Formation. Biochemistry, 2006, 45, 9228-9237.	2.5	43
100	The Fluorescent Amino Acid pâ€Cyanophenylalanine Provides an Intrinsic Probe of Amyloid Formation. ChemBioChem, 2008, 9, 1372-1374.	2.6	43
101	Differential Ordering of the Protein Backbone and Side Chains during Protein Folding Revealed by Site-Specific Recombinant Infrared Probes. Journal of the American Chemical Society, 2011, 133, 20335-20340.	13.7	42
102	Raising the Speed Limit for Î²-Hairpin Formation. Journal of the American Chemical Society, 2012, 134, 14476-14482.	13.7	42
103	15NR1ÏMeasurements Allow the Determination of Ultrafast Protein Folding Rates. Journal of the American Chemical Society, 2000, 122, 5387-5388.	13.7	41
104	Electrostatic interactions in the denatured state ensemble: Their effect upon protein folding and protein stability. Archives of Biochemistry and Biophysics, 2008, 469, 20-28.	3.0	41
105	NMR Characterization of a Peptide Model Provides Evidence for Significant Structure in the Unfolded State of the Villin Headpiece Helical Subdomain. Biochemistry, 2006, 45, 6940-6946.	2.5	40
106	Solution Structure and Folding Characteristics of the C-Terminal SH3 Domain of c-Crk-II,. Biochemistry, 2006, 45, 8874-8884.	2.5	40
107	A peptide model for proline isomerism in the unfolded state of staphylococcal nuclease. Journal of Molecular Biology, 1992, 228, 338-342.	4.2	39
108	Calcium Binding Peptides from Î±-Lactalbumin:Â Implications for Protein Folding and Stabilityâ€. Biochemistry, 1997, 36, 4607-4615.	2.5	39

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109	Structure of Hexadienoyl-CoA Bound to Enoyl-CoA Hydratase Determined by Transferred Nuclear Overhauser Effect Measurements:Â Mechanistic Predictions Based on the X-ray Structure of 4-(Chlorobenzoyl)-CoA Dehalogenaseâ€. Biochemistry, 1997, 36, 2211-2220.	2.5	39
110	Cooperative folding of a protein mini domain: the peripheral subunit-binding domain of the pyruvate dehydrogenase multienzyme complex 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 276, 479-489.	4.2	39
111	pH-dependent Stability and Folding Kinetics of a Protein with an Unusual Î±â€“Î² Topology: The C-terminal Domain of the Ribosomal Protein L9. Journal of Molecular Biology, 2002, 318, 571-582.	4.2	39
112	Analysis of the pH-dependent Folding and Stability of Histidine Point Mutants Allows Characterization of the Denatured State and Transition State for Protein Folding. Journal of Molecular Biology, 2005, 345, 163-173.	4.2	39
113	The Cold Denatured State Is Compact but Expands at Low Temperatures: Hydrodynamic Properties of the Cold Denatured State of the C-terminal Domain of L9. Journal of Molecular Biology, 2007, 368, 256-262.	4.2	39
114	Beyond the Decoupling Approximation in the Model Free Approach for the Interpretation of NMR Relaxation of Macromolecules in Solution. Journal of the American Chemical Society, 2003, 125, 8400-8404.	13.7	38
115	Electrostatic Interactions in the Denatured State and in the Transition State for Protein Folding: Effects of Denatured State Interactions on the Analysis of Transition State Structure. Journal of Molecular Biology, 2006, 359, 1437-1446.	4.2	38
116	Modulation of p-Cyanophenylalanine Fluorescence by Amino Acid Side Chains and Rational Design of Fluorescence Probes of Î±-Helix Formation. Biochemistry, 2010, 49, 6290-6295.	2.5	38
117	The Cold Denatured State of the C-terminal Domain of Protein L9 Is Compact and Contains Both Native and Non-native Structure. Journal of the American Chemical Society, 2010, 132, 4669-4677.	13.7	38
118	Thermodynamic genetics of the folding of the B1 immunoglobulin-binding domain from streptococcal protein G. Proteins: Structure, Function and Bioinformatics, 1995, 21, 11-21.	2.6	37
119	Folding Intermediate in the Villin Headpiece Domain Arises from Disruption of a N-Terminal Hydrogen-Bonded Network. Journal of the American Chemical Society, 2007, 129, 3056-3057.	13.7	37
120	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. Chemical Science, 2017, 8, 5030-5040.	7.4	37
121	Conformational analysis of a set of peptides corresponding to the entire primary sequence of the N-terminal domain of the ribosomal protein L9: evidence for stable native-like secondary structure in the unfolded state 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 287, 395-407.	4.2	36
122	Rationally Designed, Nontoxic, Nonamyloidogenic Analogues of Human Islet Amyloid Polypeptide with Improved Solubility. Biochemistry, 2014, 53, 5876-5884.	2.5	36
123	Neprilysin Impedes Islet Amyloid Formation by Inhibition of Fibril Formation Rather Than Peptide Degradation. Journal of Biological Chemistry, 2010, 285, 18177-18183.	3.4	35
124	Design and Optimization of Anti-amyloid Domain Antibodies Specific for Î²-Amyloid and Islet Amyloid Polypeptide. Journal of Biological Chemistry, 2016, 291, 2858-2873.	3.4	35
125	Analysis of Core Packing in a Cooperatively Folded Miniature Protein: The Ultrafast Folding Villin Headpiece Helical Subdomain. Biochemistry, 2009, 48, 4607-4616.	2.5	34
126	Changes in glucosylceramide structure affect virulence and membrane biophysical properties of Cryptococcus neoformans. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 2224-2233.	2.6	34

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127	Synthesis and Purification of Amyloidogenic Peptides. Analytical Biochemistry, 2001, 288, 76-82.	2.4	33
128	The Unfolded State of NTL9 Is Compact in the Absence of Denaturantâ€. Biochemistry, 2006, 45, 10110-10116.	2.5	33
129	Enhancement of the effect of small anisotropies in magic-angle spinning nuclear magnetic resonance. Journal of the Chemical Society Faraday Transactions I, 1988, 84, 3691.	1.0	32
130	Ester to Amide Switch Peptides Provide a Simple Method for Preparing Monomeric Islet Amyloid Polypeptide under Physiologically Relevant Conditions and Facilitate Investigations of Amyloid Formation. Journal of the American Chemical Society, 2010, 132, 4052-4053.	13.7	32
131	Phosphorus-31 magnetic resonance imaging of hydroxyapatite: A model for bone imaging. Magnetic Resonance in Medicine, 1992, 25, 1-11.	3.0	31
132	Contribution to Stability and Folding of a Buried Polar Residue at the CARM1 Methylation Site of the KIX Domain of CBPâ€. Biochemistry, 2003, 42, 7044-7049.	2.5	31
133	Design of a Hyperstable Protein by Rational Consideration of Unfolded State Interactions. Journal of the American Chemical Society, 2006, 128, 3144-3145.	13.7	31
134	Cooperative Cold Denaturation: The Case of the C-Terminal Domain of Ribosomal Protein L9. Biochemistry, 2013, 52, 2402-2409.	2.5	31
135	Local Interactions Drive the Formation of Nonnative Structure in the Denatured State of Human Î±-Lactalbumin:â€‰ A High Resolution Structural Characterization of a Peptide Model in Aqueous Solution,. Biochemistry, 1999, 38, 7380-7387.	2.5	30
136	Direct Characterization of the Folded, Unfolded and Urea-denatured States of the C-terminal Domain of the Ribosomal Protein L9. Journal of Molecular Biology, 2005, 349, 839-846.	4.2	30
137	Tuning protein autoinhibition by domain destabilization. Nature Structural and Molecular Biology, 2011, 18, 550-555.	8.2	30
138	Mutational Analysis of Preamyloid Intermediates: The Role of His-Tyr Interactions in Islet Amyloid Formation. Biophysical Journal, 2014, 106, 1520-1527.	0.5	30
139	Domain-Specific Incorporation of Noninvasive Optical Probes into Recombinant Proteins. Journal of the American Chemical Society, 2004, 126, 14004-14012.	13.7	29
140	Rational Design, Structural and Thermodynamic Characterization of a Hyperstable Variant of the Villin Headpiece Helical Subdomain. Biochemistry, 2007, 46, 7497-7505.	2.5	29
141	The Denatured State Ensemble Contains Significant Local and Long-Range Structure under Native Conditions: Analysis of the N-Terminal Domain of Ribosomal Protein L9. Biochemistry, 2013, 52, 2662-2671.	2.5	29
142	Characterizing septum inhibition in Mycobacterium tuberculosis for novel drug discovery. Tuberculosis, 2008, 88, 420-429.	1.9	28
143	The Unfolded State of the C-Terminal Domain of the Ribosomal Protein L9 Contains Both Native and Non-Native Structure. Biochemistry, 2009, 48, 4707-4719.	2.5	28
144	Nucleobindin 1 Is a Calcium-regulated Guanine Nucleotide Dissociation Inhibitor of GÎ±i1. Journal of Biological Chemistry, 2010, 285, 31647-31660.	3.4	28

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145	A Structural Basis for the Regulation of an H-NOX-Associated Cyclic-di-GMP Synthase/Phosphodiesterase Enzyme by Nitric Oxide-Bound H-NOX. Biochemistry, 2014, 53, 2126-2135.	2.5	28
146	High Pressure ZZ-Exchange NMR Reveals Key Features of Protein Folding Transition States. Journal of the American Chemical Society, 2016, 138, 15260-15266.	13.7	28
147	General Strategy for the Bioorthogonal Incorporation of Strongly Absorbing, Solvation-Sensitive Infrared Probes into Proteins. Journal of Physical Chemistry B, 2014, 118, 7946-7953.	2.6	27
148	Neprilysin Is Required for Angiotensin-(1â€“7)â€™s Ability to Enhance Insulin Secretion via Its Proteolytic Activity to Generate Angiotensin-(1â€“2). Diabetes, 2017, 66, 2201-2212.	0.6	27
149	Cyclic Ion Mobilityâ€“Collision Activation Experiments Elucidate Protein Behavior in the Gas Phase. Journal of the American Society for Mass Spectrometry, 2021, 32, 1545-1552.	2.8	27
150	Folding of the Multidomain Ribosomal Protein L9:Â The Two Domains Fold Independently with Remarkably Different Ratesâ€. Biochemistry, 1999, 38, 5643-5650.	2.5	26
151	Effects of varying the local propensity to form secondary structure on the stability and folding kinetics of a rapid folding mixed Î±/Î² protein: characterization of a truncation mutant of the N-terminal domain of the ribosomal protein L9 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 289, 167-174.	4.2	26
152	Amyloid Formation in Heterogeneous Environments: Islet Amyloid Polypeptide Glycosaminoglycan Interactions. Journal of Molecular Biology, 2013, 425, 492-505.	4.2	26
153	Crystallization of a designed peptide from a molten globule ensemble. Folding & Design, 1996, 1, 57-64.	4.5	25
154	Ionic-Strength-Dependent Effects in Protein Folding:â€‰ Analysis of Rate Equilibrium Free-Energy Relationships and Their Interpretation. Biochemistry, 2007, 46, 14206-14214.	2.5	25
155	Native like structure in the unfolded state of the villin headpiece helical subdomain, an ultrafast folding protein. Protein Science, 2009, 18, 1692-1701.	7.6	25
156	Temperature Dependence of Water Interactions with the Amide Carbonyls of Î±-Helices. Biochemistry, 2012, 51, 5293-5299.	2.5	25
157	Analysis of the Ability of Pramlintide To Inhibit Amyloid Formation by Human Islet Amyloid Polypeptide Reveals a Balance between Optimal Recognition and Reduced Amyloidogenicity. Biochemistry, 2015, 54, 6704-6711.	2.5	25
158	Human Islet Amyloid Polypeptide N-Terminus Fragment Self-Assembly: Effect of Conserved Disulfide Bond on Aggregation Propensity. Journal of the American Society for Mass Spectrometry, 2016, 27, 1010-1018.	2.8	25
159	Nativelike Structure and Stability in a Truncation Mutant of a Protein Minidomain:Â The Peripheral Subunit-Binding Domainâ€. Biochemistry, 1999, 38, 4128-4136.	2.5	24
160	Stereospecificity of the Reaction Catalyzed by Enoyl-CoA Hydratase. Journal of the American Chemical Society, 2000, 122, 3987-3994.	13.7	24
161	Characterization of Large Peptide Fragments Derived from the N-Terminal Domain of the Ribosomal Protein L9:Â Definition of the Minimum Folding Motif and Characterization of Local Electrostatic Interactionsâ€. Biochemistry, 2002, 41, 13360-13369.	2.5	24
162	An analysis of sideband suppression techniques in magic-angle sample spinning NMR. Journal of Magnetic Resonance, 1987, 72, 238-250.	0.5	23

#	Article	IF	Citations
163	Reconciling the Solution and X-ray Structures of the Villin Headpiece Helical Subdomain:Â Molecular Dynamics Simulations and Double Mutant Cycles Reveal a Stabilizing Cationâ˜Ï€ Interactionâ€. Biochemistry, 2007, 46, 3624-3634.	2.5	23
164	Positioning the Intracellular Salt Potassium Glutamate in the Hofmeister Series by Chemical Unfolding Studies of NTL9. Biochemistry, 2016, 55, 2251-2259.	2.5	23
165	A protein dissection study demonstrates that two specific hydrophobic clusters play a key role in stabilizing the core structure of the molten globule state of human ?-lactalbumin. Proteins: Structure, Function and Bioinformatics, 2001, 42, 237-242.	2.6	22
166	Partially folded equilibrium intermediate of the villin headpiece HP67 defined by 13C relaxation dispersion. Journal of Biomolecular NMR, 2009, 45, 85-98.	2.8	22
167	On the global architecture of initiation factor IF3: a comparative study of the linker regions from the Escherichia coli protein and the Bacillus stearothermophilus protein. Journal of Molecular Biology, 1998, 278, 871-878.	4.2	21
168	The failure of simple empirical relationships to predict the viscosity of mixed aqueous solutions of guanidine hydrochloride and glucose has important implications for the study of protein folding. Protein Science, 2000, 9, 1601-1603.	7.6	21
169	Slow Folding of a Three-Helix Protein via a Compact Intermediate. Biochemistry, 2005, 44, 627-634.	2.5	21
170	The Low-pH Unfolded State of the C-Terminal Domain of the Ribosomal Protein L9 Contains Significant Secondary Structure in the Absence of Denaturant but Is No More Compact Than the Low-pH Urea Unfolded State. Biochemistry, 2008, 47, 9565-9573.	2.5	21
171	Ï•-Value Analysis for Ultrafast Folding Proteins by NMR Relaxation Dispersion. Journal of the American Chemical Society, 2010, 132, 450-451.	13.7	21
172	Nucleobindin 1 Caps Human Islet Amyloid Polypeptide Protofibrils to Prevent Amyloid Fibril Formation. Journal of Molecular Biology, 2012, 421, 378-389.	4.2	21
173	Size-Dependent Relationships between Protein Stability and Thermal Unfolding Temperature Have Important Implications for Analysis of Protein Energetics and High-Throughput Assays of Proteinâ€“Ligand Interactions. Journal of Physical Chemistry B, 2018, 122, 5278-5285.	2.6	21
174	Experimental and Computational Analysis of Protein Stabilization by Gly-to-<scp>d</scp>-Ala Substitution: A Convolution of Native State and Unfolded State Effects. Journal of the American Chemical Society, 2016, 138, 15682-15689.	13.7	20
175	General Amyloid Inhibitors? A Critical Examination of the Inhibition of IAPP Amyloid Formation by Inositol Stereoisomers. PLoS ONE, 2014, 9, e104023.	2.5	20
176	Rational and Computational Design of Stabilized Variants of Cyanovirin-N That Retain Affinity and Specificity for Glycan Ligands. Biochemistry, 2011, 50, 10698-10712.	2.5	19
177	Inhibition of Glycosaminoglycan-Mediated Amyloid Formation by Islet Amyloid Polypeptide and proIAPP Processing Intermediates. Journal of Molecular Biology, 2011, 406, 491-502.	4.2	19
178	Analysis of electrostatic interactions in the denatured state ensemble of the Nâ€terminal domain of L9 under native conditions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3500-3510.	2.6	19
179	Analysis of Baboon IAPP Provides Insight into Amyloidogenicity and Cytotoxicity of Human IAPP. Biophysical Journal, 2020, 118, 1142-1151.	0.5	19
180	A Role for the C-Terminus of Calcitonin in Aggregation and Gel Formation: A Comparative Study of C-Terminal Fragments of Human and Salmon Calcitonin. Biochemical and Biophysical Research Communications, 1998, 245, 344-348.	2.1	18

#	Article	IF	Citations
181	The Ability of Insulin To Inhibit the Formation of Amyloid by Pro-Islet Amyloid Polypeptide Processing Intermediates Is Significantly Reduced in the Presence of Sulfated Glycosaminoglycans. Biochemistry, 2014, 53, 2605-2614.	2.5	18
182	Analysis of the Role of the Conserved Disulfide in Amyloid Formation by Human Islet Amyloid Polypeptide in Homogeneous and Heterogeneous Environments. Biochemistry, 2018, 57, 3065-3074.	2.5	17
183	Amyloidogenicity, Cytotoxicity, and Receptor Activity of Bovine Amylin: Implications for Xenobiotic Transplantation and the Design of Nontoxic Amylin Variants. ACS Chemical Biology, 2018, 13, 2747-2757.	3.4	17
184	Conformational analysis of peptide fragments derived from the peripheral subunit-binding domain from the pyruvate dehydrogenase multienzyme complex ofBacillus stearothermophilus: Evidence for nonrandom structure in the unfolded state. , 1999, 49, 29-40.		15
185	pH-dependent stability of the human ?-lactalbumin molten globule state: Contrasting roles of the 6?120 disulfide and the ?-subdomain at low and neutral pH. Proteins: Structure, Function and Bioinformatics, 2003, 52, 193-202.	2.6	14
186	Mutational Analysis of the Folding Transition State of the C-Terminal Domain of Ribosomal Protein L9:â€‰ A Protein with an Unusual Î²-Sheet Topology. Biochemistry, 2007, 46, 1013-1021.	2.5	14
187	Biophysical and Functional Analyses Suggest That Adenovirus E4-ORF3 Protein Requires Higher-order Multimerization to Function against Promyelocytic Leukemia Protein Nuclear Bodies. Journal of Biological Chemistry, 2012, 287, 22573-22583.	3.4	14
188	Denatured State Ensembles with the Same Radii of Gyration Can Form Significantly Different Long-Range Contacts. Biochemistry, 2014, 53, 39-47.	2.5	14
189	Heterogeneity in the Folding of Villin Headpiece Subdomain HP36. Journal of Physical Chemistry B, 2018, 122, 11640-11648.	2.6	14
190	Evolutionary Adaptation and Amyloid Formation: Does the Reduced Amyloidogenicity and Cytotoxicity of Ursine Amylin Contribute to the Metabolic Adaption of Bears and Polar Bears?. Israel Journal of Chemistry, 2017, 57, 750-761.	2.3	13
191	Solution structure of a peptide model of a region important for the folding of ?-lactalbumin provides evidence for the formation of nonnative structure in the denatured state. , 2000, 38, 189-196.		12
192	pH Jump Studies of the Folding of the Multidomain Ribosomal Protein L9:Â The Structural Organization of the N-Terminal Domain Does Not Affect the Anomalously Slow Folding of the C-Terminal Domainâ€. Biochemistry, 2000, 39, 4955-4962.	2.5	12
193	A Comparative Study of Peptide Models of the Î±-Domain of Î±-Lactalbumin, Lysozyme, and Î±-Lactalbumin/Lysozyme Chimeras Allows the Elucidation of Critical Factors That Contribute to the Ability to Form Stable Partially Folded States. Biochemistry, 2001, 40, 2138-2147.	2.5	12
194	Efficient high level expression of peptides and proteins as fusion proteins with the N-terminal domain of L9: Application to the villin headpiece helical subdomain. Protein Expression and Purification, 2006, 47, 234-240.	1.3	12
195	A Critical Assessment of Putative Gatekeeper Interactions in the Villin Headpiece Helical Subdomain. Journal of Molecular Biology, 2010, 401, 274-285.	4.2	12
196	Matrix Metalloproteinase-9 Protects Islets from Amyloid-induced Toxicity. Journal of Biological Chemistry, 2015, 290, 30475-30485.	3.4	12
197	Sterol Structure Strongly Modulates Membraneâ€“Islet Amyloid Polypeptide Interactions. Biochemistry, 2018, 57, 1868-1879.	2.5	12
198	Scaffold Hopping Transformations Using Auxiliary Restraints for Calculating Accurate Relative Binding Free Energies. Journal of Chemical Theory and Computation, 2021, 17, 3710-3726.	5.3	12

#	Article	IF	Citations
199	Protein unfolded states populated at high and ambient pressure are similarly compact. Biophysical Journal, 2021, 120, 2592-2598.	0.5	12
200	On the Relationship Between Protein Stability and Folding Kinetics: A Comparative Study of the N-terminal Domains of RNase HI, E. coli and Bacillus stearothermophilus L9. Journal of Molecular Biology, 2001, 312, 569-577.	4.2	11
201	Temperature-Dependent Hammond Behavior in a Protein-Folding Reaction: Analysis of Transition-State Movement and Ground-State Effects. Journal of Molecular Biology, 2008, 378, 699-706.	4.2	11
202	Detection of Helical Intermediates During Amyloid Formation by Intrinsically Disordered Polypeptides and Proteins. Methods in Molecular Biology, 2016, 1345, 55-66.	0.9	11
203	Experimental Characterization of the Denatured State Ensemble of Proteins. Methods in Molecular Biology, 2009, 490, 339-351.	0.9	11
204	A Non-perturbing Probe of Coiled Coil Formation Based on Electron Transfer Mediated Fluorescence Quenching. Biochemistry, 2016, 55, 3685-3691.	2.5	10
205	Low concentration IL-1Î² promotes islet amyloid formation by increasing hIAPP release from humanised mouse islets in vitro. Diabetologia, 2020, 63, 2385-2395.	6.3	10
206	Stereospecific1H and13C NMR Assignments of Crotonyl CoA and Hexadienoyl CoA:Â Conformational Analysis and Comparison with Proteinâ^'CoA Complexes. Journal of the American Chemical Society, 1998, 120, 9988-9994.	13.7	9
207	pH Dependent Thermodynamic and Amide Exchange Studies of theC-Terminal Domain of the Ribosomal Protein L9:Â Implications for Unfolded State Structureâ€. Biochemistry, 2006, 45, 8499-8506.	2.5	9
208	Azidohomoalanine: A Conformationally Sensitive IR Probe of Protein Folding, Protein Structure, and Electrostatics. Angewandte Chemie, 2010, 122, 7635-7637.	2.0	9
209	Aspirin, Diabetes, and Amyloid: Re-examination of the Inhibition of Amyloid Formation by Aspirin and Ketoprofen. ACS Chemical Biology, 2014, 9, 1632-1637.	3.4	9
210	The Unfolded State of the C-Terminal Domain of L9 Expands at Low but Not at Elevated Temperatures. Biophysical Journal, 2018, 115, 655-663.	0.5	9
211	Dissecting the Energetics of Intrinsically Disordered Proteins via a Hybrid Experimental and Computational Approach. Journal of Physical Chemistry B, 2019, 123, 10394-10402.	2.6	9
212	Pressure-Temperature Analysis of the Stability ofÂthe CTL9 Domain Reveals Hidden Intermediates. Biophysical Journal, 2019, 116, 445-453.	0.5	9
213	Analysis of Proline Substitutions Reveals the Plasticity and Sequence Sensitivity of Human IAPP Amyloidogenicity and Toxicity. Biochemistry, 2020, 59, 742-754.	2.5	9
214	The dye SYPRO orange binds to amylin amyloid fibrils but not preâ€fibrillar intermediates. Protein Science, 2016, 25, 1834-1840.	7.6	8
215	Selenomethionine, p-cyanophenylalanine pairs provide a convenient, sensitive, non-perturbing fluorescent probe of local helical structure. Chemical Communications, 2016, 52, 2055-2058.	4.1	8
216	Amyloidogenicity and cytotoxicity of des-Lys-1 human amylin provides insight into amylin self-assembly and highlights the difficulties of defining amyloidogenicity. Protein Engineering, Design and Selection, 2019, 32, 87-93.	2.1	8

#	Article	IF	Citations
217	The Cold-Unfolded State Is Expanded but Contains Long- and Medium-Range Contacts and Is Poorly Described by Homopolymer Models. Biochemistry, 2020, 59, 3290-3299.	2.5	8
218	The effect of experimental imperfections on TOSS spectra. Journal of Magnetic Resonance, 1990, 89, 1-9.	0.5	7
219	Amide proton exchange measurements as a probe of the stability and dynamics of the nâ€terminal domain of the ribosomal protein L9: Comparison with the intact protein. Protein Science, 1998, 7, 1994-1997.	7.6	7
220	Protein Dissection Experiments Reveal Key Differences in the Equilibrium Folding of Î±-Lactalbumin and the Calcium Binding Lysozymesâ€. Biochemistry, 2004, 43, 9961-9967.	2.5	7
221	Kinetic Isotope Effects Reveal the Presence of Significant Secondary Structure in the Transition State for the Folding of the N-terminal Domain of L9. Journal of Molecular Biology, 2007, 370, 349-355.	4.2	7
222	Guilt by Association: The Physical Chemistry and Biology of Protein Aggregation. Journal of Physical Chemistry Letters, 2014, 5, 2012-2014.	4.6	7
223	Analysis of Amylin Consensus Sequences Suggests That Human Amylin Is Not Optimized to Minimize Amyloid Formation and Provides Clues to Factors That Modulate Amyloidogenicity. ACS Chemical Biology, 2020, 15, 1408-1416.	3.4	7
224	A comparative study of the Î±-subdomains of bovine and human Î±-lactalbumin reveals key differences that correlate with molten globule stability. Protein Science, 2009, 14, 89-96.	7.6	5
225	Competition between Intradomain and Interdomain Interactions: A Buried Salt Bridge Is Essential for Villin Headpiece Folding and Actin Binding. Biochemistry, 2011, 50, 3706-3712.	2.5	5
226	The N-Terminal Domain of Ribosomal Protein L9 Folds via a Diffuse and Delocalized Transition State. Biophysical Journal, 2017, 112, 1797-1806.	0.5	5
227	The triphenylmethane dye brilliant blue G is only moderately effective at inhibiting amyloid formation by human amylin or at disaggregating amylin amyloid fibrils, but interferes with amyloid assays; Implications for inhibitor design. PLoS ONE, 2019, 14, e0219130.	2.5	5
228	Analysis of Prairie Vole Amylin Reveals the Importance of the N-Terminus and Residue 22 in Amyloidogenicity and Cytotoxicity. Biochemistry, 2020, 59, 471-478.	2.5	5
229	Conformational analysis of the interdomain linker of the central homology region of chloroplast initiation factor IF3 supports a structural model of two compact domains connected by a flexible tether. FEBS Letters, 1998, 433, 153-156.	2.8	4
230	Local interactions and the role of the 6-120 disulfide bond in Î±-lactalbumin: implications for formation of the molten globule state. BBA - Proteins and Proteomics, 2000, 1476, 9-19.	2.1	4
231	Selenomethionine Quenching of Tryptophan Fluorescence Provides a Simple Probe of Protein Structure. Biochemistry, 2017, 56, 1085-1094.	2.5	4
232	Differential effects of serine side chain interactions in amyloid formation by islet amyloid polypeptide. Protein Science, 2020, 29, 555-563.	7.6	4
233	Preparation of Asymmetric Vesicles with Trapped CsCl Avoids Osmotic Imbalance, Non-Physiological External Solutions, and Minimizes Leakage. Langmuir, 2021, 37, 11611-11617.	3.5	4
234	In Vitro Studies of Membrane Permeability Induced by Amyloidogenic Polypeptides Using Large Unilamellar Vesicles. Methods in Molecular Biology, 2016, 1345, 283-290.	0.9	3

#	Article	IF	Citations
235	Quantitative Analysis of Protein Unfolded State Energetics: Experimental and Computational Studies Demonstrate That Non-Native Side-Chain Interactions Stabilize Local Native Backbone Structure. Journal of Physical Chemistry B, 2021, 125, 3269-3277.	2.6	3
236	The Fluorescent Dye 1,6-Diphenyl-1,3,5-hexatriene Binds to Amyloid Fibrils Formed by Human Amylin and Provides a New Probe of Amylin Amyloid Kinetics. Biochemistry, 2021, 60, 1964-1970.	2.5	3
237	NMR Studies of Methanogens: What Good Is a Cyclic Pyrophosphate?. Annals of the New York Academy of Sciences, 1987, 508, 16-32.	3.8	1
238	Multiple-frequency decoupling in magic-angle-spinning NMR of paramagnetic solids. Journal of Magnetic Resonance, 1992, 97, 162-170.	0.5	1
239	Local control of peptide conformation: Stabilization of cis proline peptide bonds by aromatic proline interactions. , 1998, 45, 381.		1
240	Conformational analysis of peptide fragments derived from the peripheral subunit-binding domain from the pyruvate dehydrogenase multienzyme complex of Bacillus stearothermophilus: Evidence for nonrandom structure in the unfolded state. Biopolymers, 1999, 49, 29.	2.4	1