Daniel P Raleigh

List of Publications by Year
in descending order

240 papers	13,695 citations	15466 65 h-index	30010 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.	1.2	579
2	Histone H2B ubiquitylation disrupts local and higher-order chromatin compaction. Nature Chemical Biology, 2011, 7, 113-119.	3.9	392
3	De Novo Design of Helical Bundles as Models for Understanding Protein Folding and Function. Accounts of Chemical Research, 2000, 33, 745-754.	7.6	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.	3.3	277
5	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometryâ€“mass spectrometry. Nature Chemistry, 2015, 7, 73-81.	6.6	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.	1.2	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.	3.3	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.	3.1	207
9	Rational Modification of Protein Stability by the Mutation of Charged Surface Residuesâ€. Biochemistry, 2000, 39, 872-879.	1.2	197
10	Effects of Sequential Proline Substitutions on Amyloid Formation by Human Amylin20-29â€. Biochemistry, 1999, 38, 1811-1818.	1.2	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.	1.0	177
12	Islet Amyloid Polypeptide: Structure, Function, and Pathophysiology. Journal of Diabetes Research, 2016, 2016, 1-18.	1.0	177
13	A role for helical intermediates in amyloid formation by natively unfolded polypeptides?. Physical Biology, 2009, 6, 015005.	0.8	170
14	Islet amyloid: From fundamental biophysics to mechanisms of cytotoxicity. FEBS Letters, 2013, 587, 1106-1118.	1.3	166
15	De novo protein design: from molten globules to native-like states. Current Opinion in Structural Biology, 1993, 3, 601-610.	2.6	163
16	Toxic oligomers and islet beta cell death: guilty by association or convicted by circumstantial evidence?. Diabetologia, 2010, 53, 1046-1056.	2.9	160
17	Two-dimensional infrared spectroscopy reveals the complex behaviour of an amyloid fibril inhibitor. Nature Chemistry, 2012, 4, 355-360.	6.6	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.	6.6	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.	6.6	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.	3.3	154
21	The Role of His-18 in Amyloid Formation by Human Islet Amyloid Polypeptideâ€. Biochemistry, 2005, 44, 16284-16291.	1.2	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.	1.2	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.	2.0	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.	1.2	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.	3.3	128
26	Time-resolved studies define the nature of toxic IAPP intermediates, providing insight for anti-amyloidosis therapeutics. ELife, 2016, 5, .	2.8	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.	1.2	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.	6.6	122
29	Analysis of the Inhibition and Remodeling of Islet Amyloid Polypeptide Amyloid Fibers by Flavanols. Biochemistry, 2012, 51, 2670-2683.	1.2	122
30	Role of Aromatic Interactions in Amyloid Formation by Peptides Derived from Human Amylinâ€. Biochemistry, 2004, 43, 15901-15908.	1.2	117
31	Residue Specific Resolution of Protein Folding Dynamics Using Isotope-Edited Infrared Temperature Jump Spectroscopyâ€. Biochemistry, 2007, 46, 3279-3285.	1.2	115
32	2DIR Spectroscopy of Human Amylin Fibrils Reflects Stable Î²-Sheet Structure. Journal of the American Chemical Society, 2011, 133, 16062-16071.	6.6	114
33	Morin hydrate inhibits amyloid formation by islet amyloid polypeptide and disaggregates amyloid fibers. Protein Science, 2012, 21, 373-382.	3.1	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.	2.4	111
35	Role of Aromatic Interactions in Amyloid Formation by Islet Amyloid Polypeptide. Biochemistry, 2013, 52, 333-342.	1.2	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.	2.0	110

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37	Islet Amyloid Polypeptide Membrane Interactions: Effects of Membrane Composition. Biochemistry, 2017, 56, 376-390.	1.2	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.	2.0	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.	3.1	104
40	Aggregation of islet amyloid polypeptide: from physical chemistry to cell biology. Current Opinion in Structural Biology, 2013, 23, 82-89.	2.6	104
41	A de Novo Designed Protein Mimics the Native State of Natural Proteins. Journal of the American Chemical Society, 1995, 117, 7558-7559.	6.6	102
42	Rescuing a destabilized protein fold through backbone cyclization. Journal of Molecular Biology, 2001, 308, 1045-1062.	2.0	98
43	The Î²-cell assassin: IAPP cytotoxicity. Journal of Molecular Endocrinology, 2017, 59, R121-R140.	1.1	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.	1.2	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.	3.3	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.	2.0	92
47	Local control of peptide conformation: Stabilization ofcis proline peptide bonds by aromatic proline interactions. , 1998, 45, 381-394.		89
48	Deamidation Accelerates Amyloid Formation and Alters Amylin Fiber Structure. Journal of the American Chemical Society, 2012, 134, 12658-12667.	6.6	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.	1.2	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.	6.6	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.	3.3	82
52	Azidohomoalanine: A Conformationally Sensitive IR Probe of Protein Folding, Protein Structure, and Electrostatics. Angewandte Chemie - International Edition, 2010, 49, 7473-7475.	7.2	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.	3.1	77
54	Submillisecond folding of the peripheral subunit-binding domain 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1999, 293, 763-768.	2.0	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.	2.4	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.	6.6	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.	1.2	75
58	Sensitivity of Amyloid Formation by Human Islet Amyloid Polypeptide to Mutations at Residue 20. Journal of Molecular Biology, 2012, 421, 282-295.	2.0	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.	3.3	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.	1.2	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.	1.2	72
62	Recovery and purification of highly aggregation-prone disulfide-containing peptides: Application to islet amyloid polypeptide. Analytical Biochemistry, 2006, 351, 181-186.	1.1	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.	1.2	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.	1.2	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.	2.0	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.	1.2	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.	6.6	67
68	Temperature-dependent Dynamics of the Villin Headpiece Helical Subdomain, An Unusually Small Thermostable Protein. Journal of Molecular Biology, 2002, 320, 841-854.	2.0	66
69	De novo protein design: what are we learning?. Current Opinion in Structural Biology, 1991, 1, 984-993.	2.6	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.	6.6	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.	2.0	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.	2.0	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.	0.5	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.	6.6	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.	1.2	59
76	RAGE binds preamyloid IAPP intermediates and mediates pancreatic Î² cell proteotoxicity. Journal of Clinical Investigation, 2018, 128, 682-698.	3.9	58
77	Multistate Folding of the Villin Headpiece Domain. Journal of Molecular Biology, 2006, 355, 1066-1077.	2.0	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.	2.0	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.	2.0	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.	2.1	52
81	The Protein Folding Transition State: What Are φ-Values Really Telling Us?. Protein and Peptide Letters, 2005, 12, 117-122.	0.4	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.	2.0	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.	2.0	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.	2.0	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.	1.2	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.	1.2	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.	1.2	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.	3.3	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.	3.3	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.	1.7	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.	2.5	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.	2.0	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.	6.6	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.	2.0	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.	2.4	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.	2.0	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.	6.6	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.	3.3	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.	1.2	43
100	The Fluorescent Amino Acid pâ€Cyanophenylalanine Provides an Intrinsic Probe of Amyloid Formation. ChemBioChem, 2008, 9, 1372-1374.	1.3	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.	6.6	42
102	Raising the Speed Limit for Î²-Hairpin Formation. Journal of the American Chemical Society, 2012, 134, 14476-14482.	6.6	42
103	15NR1ÏMeasurements Allow the Determination of Ultrafast Protein Folding Rates. Journal of the American Chemical Society, 2000, 122, 5387-5388.	6.6	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.	1.4	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.	1.2	40
106	Solution Structure and Folding Characteristics of the C-Terminal SH3 Domain of c-Crk-II,. Biochemistry, 2006, 45, 8874-8884.	1.2	40
107	A peptide model for proline isomerism in the unfolded state of staphylococcal nuclease. Journal of Molecular Biology, 1992, 228, 338-342.	2.0	39
108	Calcium Binding Peptides from Î±-Lactalbumin:Â Implications for Protein Folding and Stabilityâ€. Biochemistry, 1997, 36, 4607-4615.	1.2	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.	1.2	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.	2.0	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.	2.0	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.	2.0	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.	2.0	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.	6.6	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.	2.0	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.	1.2	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.	6.6	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.	1.5	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.	6.6	37
120	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. Chemical Science, 2017, 8, 5030-5040.	3.7	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.	2.0	36
122	Rationally Designed, Nontoxic, Nonamyloidogenic Analogues of Human Islet Amyloid Polypeptide with Improved Solubility. Biochemistry, 2014, 53, 5876-5884.	1.2	36
123	Neprilysin Impedes Islet Amyloid Formation by Inhibition of Fibril Formation Rather Than Peptide Degradation. Journal of Biological Chemistry, 2010, 285, 18177-18183.	1.6	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.	1.6	35
125	Analysis of Core Packing in a Cooperatively Folded Miniature Protein: The Ultrafast Folding Villin Headpiece Helical Subdomain. Biochemistry, 2009, 48, 4607-4616.	1.2	34
126	Changes in glucosylceramide structure affect virulence and membrane biophysical properties of Cryptococcus neoformans. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 2224-2233.	1.4	34

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127	Synthesis and Purification of Amyloidogenic Peptides. Analytical Biochemistry, 2001, 288, 76-82.	1.1	33
128	The Unfolded State of NTL9 Is Compact in the Absence of Denaturantâ€. Biochemistry, 2006, 45, 10110-10116.	1.2	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.	6.6	32
131	Phosphorus-31 magnetic resonance imaging of hydroxyapatite: A model for bone imaging. Magnetic Resonance in Medicine, 1992, 25, 1-11.	1.9	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.	1.2	31
133	Design of a Hyperstable Protein by Rational Consideration of Unfolded State Interactions. Journal of the American Chemical Society, 2006, 128, 3144-3145.	6.6	31
134	Cooperative Cold Denaturation: The Case of the C-Terminal Domain of Ribosomal Protein L9. Biochemistry, 2013, 52, 2402-2409.	1.2	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.	1.2	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.	2.0	30
137	Tuning protein autoinhibition by domain destabilization. Nature Structural and Molecular Biology, 2011, 18, 550-555.	3.6	30
138	Mutational Analysis of Preamyloid Intermediates: The Role of His-Tyr Interactions in Islet Amyloid Formation. Biophysical Journal, 2014, 106, 1520-1527.	0.2	30
139	Domain-Specific Incorporation of Noninvasive Optical Probes into Recombinant Proteins. Journal of the American Chemical Society, 2004, 126, 14004-14012.	6.6	29
140	Rational Design, Structural and Thermodynamic Characterization of a Hyperstable Variant of the Villin Headpiece Helical Subdomain. Biochemistry, 2007, 46, 7497-7505.	1.2	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.	1.2	29
142	Characterizing septum inhibition in Mycobacterium tuberculosis for novel drug discovery. Tuberculosis, 2008, 88, 420-429.	0.8	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.	1.2	28
144	Nucleobindin 1 Is a Calcium-regulated Guanine Nucleotide Dissociation Inhibitor of GÎ±i1. Journal of Biological Chemistry, 2010, 285, 31647-31660.	1.6	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.	1.2	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.	6.6	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.	1.2	27
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