

Daniel P Raleigh

List of Publications by Citations

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243
papers

12,026
citations

63
h-index

97
g-index

248
ext. papers

13,027
ext. citations

6.3
avg, IF

6.39
L-index

#	Paper	IF	Citations
243	Rotational resonance in solid state NMR. <i>Chemical Physics Letters</i> , 1988 , 146, 71-76	2.5	541
242	Histone H2B ubiquitylation disrupts local and higher-order chromatin compaction. <i>Nature Chemical Biology</i> , 2011 , 7, 113-9	11.7	333
241	De novo design of helical bundles as models for understanding protein folding and function. <i>Accounts of Chemical Research</i> , 2000 , 33, 745-54	24.3	274
240	Two-dimensional IR spectroscopy and isotope labeling defines the pathway of amyloid formation with residue-specific resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6614-9	11.5	251
239	The flavanol (-)-epigallocatechin 3-gallate inhibits amyloid formation by islet amyloid polypeptide, disaggregates amyloid fibrils, and protects cultured cells against IAPP-induced toxicity. <i>Biochemistry</i> , 2010 , 49, 8127-33	3.2	214
238	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometry-mass spectrometry. <i>Nature Chemistry</i> , 2015 , 7, 73-81	17.6	203
237	Rational modification of protein stability by the mutation of charged surface residues. <i>Biochemistry</i> , 2000 , 39, 872-9	3.2	188
236	Mechanism of IAPP amyloid fibril formation involves an intermediate with a transient β -sheet. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19285-90	11.5	182
235	Protein folding: defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. <i>Protein Science</i> , 2005 , 14, 602-16	6.3	181
234	Effects of sequential proline substitutions on amyloid formation by human amylin ₂₀₋₂₉ . <i>Biochemistry</i> , 1999 , 38, 1811-8	3.2	178
233	A critical assessment of the role of helical intermediates in amyloid formation by natively unfolded proteins and polypeptides. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 453-9	1.9	161
232	A role for helical intermediates in amyloid formation by natively unfolded polypeptides?. <i>Physical Biology</i> , 2009 , 6, 015005	3	155
231	De novo protein design: from molten globules to native-like states. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 601-610	8.1	155
230	Islet amyloid: from fundamental biophysics to mechanisms of cytotoxicity. <i>FEBS Letters</i> , 2013 , 587, 1106-18	3.8	145
229	Two-dimensional infrared spectroscopy reveals the complex behaviour of an amyloid fibril inhibitor. <i>Nature Chemistry</i> , 2012 , 4, 355-60	17.6	145
228	Toxic oligomers and islet beta cell death: guilty by association or convicted by circumstantial evidence?. <i>Diabetologia</i> , 2010 , 53, 1046-56	10.3	143
227	The role of His-18 in amyloid formation by human islet amyloid polypeptide. <i>Biochemistry</i> , 2005 , 44, 16284-91	3.2	141

226	A single-point mutation converts the highly amyloidogenic human islet amyloid polypeptide into a potent fibrillization inhibitor. <i>Journal of the American Chemical Society</i> , 2007 , 129, 11300-1	16.4	140
225	Islet amyloid deposition limits the viability of human islet grafts but not porcine islet grafts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 4305-10	11.5	139
224	Ion mobility spectrometry-mass spectrometry defines the oligomeric intermediates in amylin amyloid formation and the mode of action of inhibitors. <i>Journal of the American Chemical Society</i> , 2014 , 136, 660-70	16.4	137
223	Islet Amyloid Polypeptide: Structure, Function, and Pathophysiology. <i>Journal of Diabetes Research</i> , 2016 , 2016, 2798269	3.9	127
222	pKa values 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 interactions. <i>Biochemistry</i> , 1999 , 38, 4896-903	3.2	126
221	Analysis of amylin cleavage products provides new insights into the amyloidogenic region of human amylin. <i>Journal of Molecular Biology</i> , 1999 , 294, 1375-85	6.5	125
220	Dynamic NMR line-shape analysis demonstrates that the villin headpiece subdomain folds on the microsecond time scale. <i>Journal of the American Chemical Society</i> , 2003 , 125, 6032-3	16.4	117
219	Aromatic interactions are not required for amyloid fibril formation by islet amyloid polypeptide but do influence the rate of fibril formation and fibril morphology. <i>Biochemistry</i> , 2007 , 46, 3255-61	3.2	111
218	Ionic strength effects on amyloid formation by amylin are a complicated interplay among Debye screening, ion selectivity, and Hofmeister effects. <i>Biochemistry</i> , 2012 , 51, 8478-90	3.2	110
217	Islet amyloid polypeptide toxicity and membrane interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 19279-84	11.5	109
216	Role of aromatic interactions in amyloid formation by peptides derived from human Amylin. <i>Biochemistry</i> , 2004 , 43, 15901-8	3.2	109
215	Global analysis of the effects of temperature and denaturant on the folding and unfolding kinetics of the N-terminal domain of the protein L9. <i>Journal of Molecular Biology</i> , 1998 , 284, 1661-70	6.5	107
214	Analysis of the inhibition and remodeling of islet amyloid polypeptide amyloid fibers by flavanols. <i>Biochemistry</i> , 2012 , 51, 2670-83	3.2	106
213	Residue specific resolution of protein folding dynamics using isotope-edited infrared temperature jump spectroscopy. <i>Biochemistry</i> , 2007 , 46, 3279-85	3.2	105
212	Incorporation of pseudoproline derivatives allows the facile synthesis of human IAPP, a highly amyloidogenic and aggregation-prone polypeptide. <i>Organic Letters</i> , 2005 , 7, 693-6	6.2	102
211	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. <i>Journal of Molecular Biology</i> , 2004 , 338, 827-37	6.5	100
210	2DIR spectroscopy of human amylin fibrils reflects stable β -sheet structure. <i>Journal of the American Chemical Society</i> , 2011 , 133, 16062-71	16.4	99
209	Role of aromatic interactions in amyloid formation by islet amyloid polypeptide. <i>Biochemistry</i> , 2013 , 52, 333-42	3.2	95

208	Low levels of asparagine deamidation can have a dramatic effect on aggregation of amyloidogenic peptides: implications for the study of amyloid formation. <i>Protein Science</i> , 2002 , 11, 342-9	6.3	95
207	Rescuing a destabilized protein fold through backbone cyclization. <i>Journal of Molecular Biology</i> , 2001 , 308, 1045-62	6.5	95
206	A de Novo Designed Protein Mimics the Native State of Natural Proteins. <i>Journal of the American Chemical Society</i> , 1995 , 117, 7558-7559	16.4	95
205	Morin hydrate inhibits amyloid formation by islet amyloid polypeptide and disaggregates amyloid fibers. <i>Protein Science</i> , 2012 , 21, 373-82	6.3	91
204	Aggregation of islet amyloid polypeptide: from physical chemistry to cell biology. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 82-9	8.1	89
203	Local control of peptide conformation: stabilization of cis proline peptide bonds by aromatic proline interactions. <i>Biopolymers</i> , 1998 , 45, 381-94	2.2	85
202	Time-resolved studies define the nature of toxic IAPP intermediates, providing insight for anti-amyloidosis therapeutics. <i>ELife</i> , 2016 , 5,	8.9	85
201	Strategies for extracting structural information from 2D IR spectroscopy of amyloid: application to islet amyloid polypeptide. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 15679-91	3.4	81
200	Destabilization of human IAPP amyloid fibrils by proline mutations outside of the putative amyloidogenic domain: is there a critical amyloidogenic domain in human IAPP?. <i>Journal of Molecular Biology</i> , 2006 , 355, 274-81	6.5	81
199	Deamidation accelerates amyloid formation and alters amylin fiber structure. <i>Journal of the American Chemical Society</i> , 2012 , 134, 12658-67	16.4	79
198	Rational design of potent domain antibody inhibitors of amyloid fibril assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19965-70	11.5	79
197	Rifampicin does not prevent amyloid fibril formation by human islet amyloid polypeptide but does inhibit fibril thioflavin-T interactions: implications for mechanistic studies of beta-cell death. <i>Biochemistry</i> , 2008 , 47, 6016-24	3.2	78
196	Effect of modulating unfolded state structure on the folding kinetics of the villin headpiece subdomain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 16662-7	11.5	78
195	Azidohomoalanine: a conformationally sensitive IR probe of protein folding, protein structure, and electrostatics. <i>Angewandte Chemie - International Edition</i> , 2010 , 49, 7473-5	16.4	75
194	Islet Amyloid Polypeptide Membrane Interactions: Effects of Membrane Composition. <i>Biochemistry</i> , 2017 , 56, 376-390	3.2	72
193	A de novo designed protein shows a thermally induced transition from a native to a molten globule-like state. <i>Journal of the American Chemical Society</i> , 1992 , 114, 10079-10081	16.4	72
192	Submillisecond folding of the peripheral subunit-binding domain. <i>Journal of Molecular Biology</i> , 1999 , 293, 763-8	6.5	71
191	Recovery and purification of highly aggregation-prone disulfide-containing peptides: application to islet amyloid polypeptide. <i>Analytical Biochemistry</i> , 2006 , 351, 181-6	3.1	70

190	Peptide models provide evidence for significant structure in the denatured state of a rapidly folding protein: the villin headpiece subdomain. <i>Biochemistry</i> , 2004 , 43, 3264-72	3.2	70
189	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. <i>Biochemistry</i> , 2009 , 48, 9040-6	3.2	69
188	Global analysis of the thermal and chemical denaturation of the N-terminal domain of the ribosomal protein L9 in H ₂ O and D ₂ O. Determination of the thermodynamic parameters, $\Delta H(o)$, $\Delta S(o)$, and $\Delta C(o)p$ and evaluation of solvent isotope effects. <i>Protein Science</i> , 1998 , 7, 2405-12	6.3	69
187	Exploiting the right side of the Ramachandran plot: substitution of glycines by D-alanine can significantly increase protein stability. <i>Journal of the American Chemical Society</i> , 2004 , 126, 13194-5	16.4	68
186	Structure and stability of the N-terminal domain of the ribosomal protein L9: evidence for rapid two-state folding. <i>Biochemistry</i> , 1998 , 37, 1025-32	3.2	68
185	Experiments and simulations show how long-range contacts can form in expanded unfolded proteins with negligible secondary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 2123-8	11.5	67
184	Mutational analysis demonstrates that specific electrostatic interactions can play a key role in the denatured state ensemble of proteins. <i>Journal of Molecular Biology</i> , 2005 , 353, 174-85	6.5	67
183	Efficient microwave-assisted synthesis of human islet amyloid polypeptide designed to facilitate the specific incorporation of labeled amino acids. <i>Organic Letters</i> , 2010 , 12, 4848-51	6.2	66
182	Sensitivity of amyloid formation by human islet amyloid polypeptide to mutations at residue 20. <i>Journal of Molecular Biology</i> , 2012 , 421, 282-95	6.5	64
181	Surface salt bridges, double-mutant cycles, and protein stability: 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 l9. <i>Biochemistry</i> , 2003 , 42, 7050-60	3.2	64
180	The β -cell assassin: IAPP cytotoxicity. <i>Journal of Molecular Endocrinology</i> , 2017 , 59, R121-R140	4.5	63
179	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. <i>Journal of Molecular Biology</i> , 2006 , 355, 1078-94	6.5	63
178	Temperature-dependent dynamics of the villin headpiece helical subdomain, an unusually small thermostable protein. <i>Journal of Molecular Biology</i> , 2002 , 320, 841-54	6.5	62
177	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. <i>Biochemistry</i> , 2010 , 49, 872-81	3.2	61
176	Two-dimensional infrared spectroscopy provides evidence of an intermediate in the membrane-catalyzed assembly of diabetic amyloid. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 2498-505	3.4	61
175	ϕ -Values beyond the ribosomally encoded amino acids: kinetic and thermodynamic consequences of incorporating trifluoromethyl amino acids in a globular protein. <i>Journal of the American Chemical Society</i> , 2003 , 125, 9286-7	16.4	61
174	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. <i>Journal of Molecular Biology</i> , 2010 , 400, 878-88	6.5	60
173	Defining the molecular basis of amyloid inhibitors: human islet amyloid polypeptide-insulin interactions. <i>Journal of the American Chemical Society</i> , 2014 , 136, 12912-9	16.4	58

172	De novo protein design: what are we learning?. <i>Current Opinion in Structural Biology</i> , 1991 , 1, 984-993	8.1	57
171	Stereological analysis of the human testis after vasectomy indicates impairment of spermatogenic efficiency with increasing obstructive interval. <i>Fertility and Sterility</i> , 2004 , 81, 1595-603	4.8	56
170	Multistate folding of the villin headpiece domain. <i>Journal of Molecular Biology</i> , 2006 , 355, 1066-77	6.5	53
169	Defining the core structure of the alpha-lactalbumin molten globule state. <i>Journal of Molecular Biology</i> , 1999 , 294, 213-21	6.5	51
168	The protein folding transition state: what are Phi-values really telling us?. <i>Protein and Peptide Letters</i> , 2005 , 12, 117-22	1.9	49
167	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. <i>Biochemistry</i> , 2007 , 46, 12308-13	3.2	48
166	Fine structure analysis of a protein folding transition state; distinguishing between hydrophobic stabilization and specific packing. <i>Journal of Molecular Biology</i> , 2005 , 354, 693-705	6.5	48
165	Azido Homocysteine is a Useful Infrared Probe for Monitoring Local Electrostatics and Sidechain Solvation in Proteins. <i>Journal of Physical Chemistry Letters</i> , 2011 , 2, 2158-2162	6.4	47
164	Amyloid formation by pro-islet amyloid polypeptide processing intermediates: examination of the role of protein heparan sulfate interactions and implications for islet amyloid formation in type 2 diabetes. <i>Biochemistry</i> , 2007 , 46, 12091-9	3.2	47
163	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. <i>Journal of Molecular Biology</i> , 2000 , 299, 1091-100	6.5	47
162	Peptide models of local and long-range interactions in the molten globule state of human alpha-lactalbumin. <i>Journal of Molecular Biology</i> , 1998 , 283, 279-91	6.5	47
161	The unfolded state of the villin headpiece helical subdomain: computational studies of the role of locally stabilized structure. <i>Journal of Molecular Biology</i> , 2006 , 360, 1094-107	6.5	46
160	Combination of kinetically selected inhibitors in trans leads to highly effective inhibition of amyloid formation. <i>Journal of the American Chemical Society</i> , 2010 , 132, 14340-2	16.4	42
159	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. <i>Journal of Molecular Biology</i> , 2010 , 400, 555-66	6.5	42
158	A simple and economical method for the production of ¹³ C, ¹⁸ O-labeled Fmoc-amino acids with high levels of enrichment: applications to isotope-edited IR studies of proteins. <i>Organic Letters</i> , 2007 , 9, 4935-7	6.2	42
157	The fluorescent amino acid p-cyanophenylalanine provides an intrinsic probe of amyloid formation. <i>ChemBioChem</i> , 2008 , 9, 1372-4	3.8	42
156	Energetically significant networks of coupled interactions within an unfolded protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 12079-84	11.5	41
155	Mutational analysis of the ability of resveratrol to inhibit amyloid formation by islet amyloid polypeptide: critical evaluation of the importance of aromatic-inhibitor and histidine-inhibitor interactions. <i>Biochemistry</i> , 2015 , 54, 666-76	3.2	41

154	Rapid cooperative two-state folding of a miniature alpha-beta protein and design of a thermostable variant. <i>Journal of Molecular Biology</i> , 2003 , 326, 1261-70	6.5	41
153	A Free Energy Barrier Caused by the Refolding of an Oligomeric Intermediate Controls the Lag Time of Amyloid Formation by hIAPP. <i>Journal of the American Chemical Society</i> , 2017 , 139, 16748-16758	16.4	40
152	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. <i>Biochemistry</i> , 2016 , 55, 510-8	3.2	40
151	An exceptionally stable helix from the ribosomal protein L9: implications for protein folding and stability. <i>Journal of Molecular Biology</i> , 1997 , 270, 640-7	6.5	40
150	NMR characterization of a peptide model provides evidence for significant structure in the unfolded state of the villin headpiece helical subdomain. <i>Biochemistry</i> , 2006 , 45, 6940-6	3.2	40
149	Characterization of the heparin binding site in the N-terminus of human pro-islet amyloid polypeptide: implications for amyloid formation. <i>Biochemistry</i> , 2006 , 45, 9228-37	3.2	40
148	Differential ordering of the protein backbone and side chains during protein folding revealed by site-specific recombinant infrared probes. <i>Journal of the American Chemical Society</i> , 2011 , 133, 20335-40	16.4	38
147	Denatured state effects and the origin of nonclassical phi values in protein folding. <i>Journal of the American Chemical Society</i> , 2006 , 128, 16492-3	16.4	38
146	pH-dependent stability and folding kinetics of a protein with an unusual alpha-beta topology: the C-terminal domain of the ribosomal protein L9. <i>Journal of Molecular Biology</i> , 2002 , 318, 571-82	6.5	38
145	¹⁵ N R1 Measurements Allow the Determination of Ultrafast Protein Folding Rates. <i>Journal of the American Chemical Society</i> , 2000 , 122, 5387-5388	16.4	38
144	Cooperative folding of a protein mini domain: the peripheral subunit-binding domain of the pyruvate dehydrogenase multienzyme complex. <i>Journal of Molecular Biology</i> , 1998 , 276, 479-89	6.5	38
143	Electrostatic interactions in the denatured state ensemble: their effect upon protein folding and protein stability. <i>Archives of Biochemistry and Biophysics</i> , 2008 , 469, 20-8	4.1	37
142	Solution structure and folding characteristics of the C-terminal SH3 domain of c-Crk-II. <i>Biochemistry</i> , 2006 , 45, 8874-84	3.2	37
141	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. <i>Journal of Molecular Biology</i> , 2006 , 359, 1437-46	6.5	37
140	Structure of hexadienoyl-CoA bound to enoyl-CoA hydratase determined by transferred nuclear Overhauser effect measurements: mechanistic predictions based on the X-ray structure of 4-(chlorobenzoyl)-CoA dehalogenase. <i>Biochemistry</i> , 1997 , 36, 2211-20	3.2	36
139	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. <i>Journal of Molecular Biology</i> , 2007 , 368, 256-62	6.5	36
138	Beyond the decoupling approximation in the model free approach for the interpretation of NMR relaxation of macromolecules in solution. <i>Journal of the American Chemical Society</i> , 2003 , 125, 8400-4	16.4	36
137	Rational modification of protein stability by targeting surface sites leads to complicated results. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 11337-42	11.5	35

136	Modulation of p-cyanophenylalanine fluorescence by amino acid side chains and rational design of fluorescence probes of alpha-helix formation. <i>Biochemistry</i> , 2010 , 49, 6290-5	3.2	35
135	Analysis of the pH-dependent folding and stability of histidine point mutants allows characterization of the denatured state and transition state for protein folding. <i>Journal of Molecular Biology</i> , 2005 , 345, 163-73	6.5	35
134	Thermodynamic genetics of the folding of the B1 immunoglobulin-binding domain from streptococcal protein G. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 21, 11-21	4.2	35
133	A peptide model for proline isomerism in the unfolded state of staphylococcal nuclease. <i>Journal of Molecular Biology</i> , 1992 , 228, 338-42	6.5	35
132	Insights into the consequences of co-polymerisation in the early stages of IAPP and A β peptide assembly from mass spectrometry. <i>Analyst, The</i> , 2015 , 140, 6990-9	5	34
131	Raising the speed limit for hairpin formation. <i>Journal of the American Chemical Society</i> , 2012 , 134, 14476-82	6.4	34
130	Molecular Signature for Receptor Engagement in the Metabolic Peptide Hormone Amylin. <i>ACS Pharmacology and Translational Science</i> , 2018 , 1, 32-49	5.9	33
129	The cold denatured state of the C-terminal domain of protein L9 is compact and contains both native and non-native structure. <i>Journal of the American Chemical Society</i> , 2010 , 132, 4669-77	16.4	33
128	Calcium binding peptides from alpha-lactalbumin: implications for protein folding and stability. <i>Biochemistry</i> , 1997 , 36, 4607-15	3.2	33
127	Folding intermediate in the villin headpiece domain arises from disruption of a N-terminal hydrogen-bonded network. <i>Journal of the American Chemical Society</i> , 2007 , 129, 3056-7	16.4	33
126	The unfolded state of NTL9 is compact in the absence of denaturant. <i>Biochemistry</i> , 2006 , 45, 10110-6	3.2	33
125	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. <i>Journal of Molecular Biology</i> , 1999 , 287, 395-407	6.5	32
124	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. <i>Chemical Science</i> , 2017 , 8, 5030-5040	9.4	31
123	Rationally designed, nontoxic, nonamyloidogenic analogues of human islet amyloid polypeptide with improved solubility. <i>Biochemistry</i> , 2014 , 53, 5876-84	3.2	31
122	Synthesis and purification of amyloidogenic peptides. <i>Analytical Biochemistry</i> , 2001 , 288, 76-82	3.1	31
121	Enhancement of the effect of small anisotropies in magic-angle spinning nuclear magnetic resonance. <i>Journal of the Chemical Society Faraday Transactions I</i> , 1988 , 84, 3691		31
120	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. <i>Journal of the American Chemical Society</i> , 2010 , 132, 4052-3	16.4	30
119	Direct characterization of the folded, unfolded and urea-denatured states of the C-terminal domain of the ribosomal protein L9. <i>Journal of Molecular Biology</i> , 2005 , 349, 839-46	6.5	30

118	Design of a hyperstable protein by rational consideration of unfolded state interactions. <i>Journal of the American Chemical Society</i> , 2006 , 128, 3144-5	16.4	30
117	Local interactions drive the formation of nonnative structure in the denatured state of human alpha-lactalbumin: a high resolution structural characterization of a peptide model in aqueous solution. <i>Biochemistry</i> , 1999 , 38, 7380-7	3.2	30
116	RAGE binds preamyloid IAPP intermediates and mediates pancreatic β cell proteotoxicity. <i>Journal of Clinical Investigation</i> , 2018 , 128, 682-698	15.9	30
115	Design and Optimization of Anti-amyloid Domain Antibodies Specific for β Amyloid and Islet Amyloid Polypeptide. <i>Journal of Biological Chemistry</i> , 2016 , 291, 2858-73	5.4	29
114	Neprilysin impedes islet amyloid formation by inhibition of fibril formation rather than peptide degradation. <i>Journal of Biological Chemistry</i> , 2010 , 285, 18177-83	5.4	29
113	Contribution to stability and folding of a buried polar residue at the CARM1 methylation site of the KIX domain of CBP. <i>Biochemistry</i> , 2003 , 42, 7044-9	3.2	29
112	Changes in glucosylceramide structure affect virulence and membrane biophysical properties of <i>Cryptococcus neoformans</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 2224-2233	3.8	29
111	Unfolded states under folding conditions accommodate sequence-specific conformational preferences with random coil-like dimensions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 12301-12310	11.5	28
110	Cooperative cold denaturation: the case of the C-terminal domain of ribosomal protein L9. <i>Biochemistry</i> , 2013 , 52, 2402-9	3.2	28
109	Analysis of core packing in a cooperatively folded miniature protein: the ultrafast folding villin headpiece helical subdomain. <i>Biochemistry</i> , 2009 , 48, 4607-16	3.2	28
108	Rational design, structural and thermodynamic characterization of a hyperstable variant of the villin headpiece helical subdomain. <i>Biochemistry</i> , 2007 , 46, 7497-505	3.2	28
107	Domain-specific incorporation of noninvasive optical probes into recombinant proteins. <i>Journal of the American Chemical Society</i> , 2004 , 126, 14004-12	16.4	28
106	Phosphorus-31 magnetic resonance imaging of hydroxyapatite: a model for bone imaging. <i>Magnetic Resonance in Medicine</i> , 1992 , 25, 1-11	4.4	28
105	Mutational analysis of preamyloid intermediates: the role of his-tyr interactions in islet amyloid formation. <i>Biophysical Journal</i> , 2014 , 106, 1520-7	2.9	27
104	The unfolded state of the C-terminal domain of the ribosomal protein L9 contains both native and non-native structure. <i>Biochemistry</i> , 2009 , 48, 4707-19	3.2	27
103	General strategy for the bioorthogonal incorporation of strongly absorbing, solvation-sensitive infrared probes into proteins. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 7946-53	3.4	26
102	Folding of the multidomain ribosomal protein L9: the two domains fold independently with remarkably different rates. <i>Biochemistry</i> , 1999 , 38, 5643-50	3.2	26
101	Amyloid formation in heterogeneous environments: islet amyloid polypeptide glycosaminoglycan interactions. <i>Journal of Molecular Biology</i> , 2013 , 425, 492-505	6.5	25

100	Tuning protein autoinhibition by domain destabilization. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 550-5	17.6	25
99	Characterizing septum inhibition in <i>Mycobacterium tuberculosis</i> for novel drug discovery. <i>Tuberculosis</i> , 2008 , 88, 420-9	2.6	25
98	Effects of varying the local propensity to form secondary structure on the stability and folding kinetics of a rapid folding mixed alpha/beta protein: characterization of a truncation mutant of the N-terminal domain of the ribosomal protein L9. <i>Journal of Molecular Biology</i> , 1999 , 289, 167-74	6.5	25
97	A structural basis for the regulation of an H-NOX-associated cyclic-di-GMP synthase/phosphodiesterase enzyme by nitric oxide-bound H-NOX. <i>Biochemistry</i> , 2014 , 53, 2126-35	3.2	24
96	Nucleobindin 1 is a calcium-regulated guanine nucleotide dissociation inhibitor of G{alpha}i1. <i>Journal of Biological Chemistry</i> , 2010 , 285, 31647-60	5.4	24
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