

Sheena E Radford

List of Publications by Year in descending order

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Version: 2024-02-01

282
papers

23,440
citations

7672

79
h-index

11608

140
g-index

302
all docs

302
docs citations

302
times ranked

18656
citing authors

#	ARTICLE	IF	CITATIONS
1	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly. Nature Communications, 2022, 13, 1040.	5.8	23
2	Roll out the barrel! Outer membrane tension resolves an unexpected folding intermediate. Cell, 2022, 185, 1107-1109.	13.5	6
3	Generating Ensembles of Dynamic Misfolding Proteins. Frontiers in Neuroscience, 2022, 16, 881534.	1.4	9
4	High-throughput directed evolution: a golden era for protein science. Trends in Chemistry, 2022, 4, 378-391.	4.4	12
5	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. Communications Biology, 2022, 5, .	2.0	12
6	Trigger factor both holds and folds its client proteins. Nature Communications, 2022, 13, .	5.8	8
7	Visualizing and trapping transient oligomers in amyloid assembly pathways. Biophysical Chemistry, 2021, 268, 106505.	1.5	97
8	Structural insights into peptide self-assembly using photo-induced crosslinking experiments and discontinuous molecular dynamics. AICHE Journal, 2021, 67, e17101.	1.8	4
9	Proteostasis of Islet Amyloid Polypeptide: A Molecular Perspective of Risk Factors and Protective Strategies for Type II Diabetes. Chemical Reviews, 2021, 121, 1845-1893.	23.0	129
10	Investigation of D76N β -Microglobulin Using Protein Footprinting and Structural Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2021, 32, 1583-1592.	1.2	3
11	De novo design of transmembrane β barrels. Science, 2021, 371, .	6.0	83
12	Finding the sweet spot for chaperone activity. Nature Chemistry, 2021, 13, 397-399.	6.6	0
13	Brazilin Removes Toxic Alpha-Synuclein and Seeding Competent Assemblies from Parkinson Brain by Altering Conformational Equilibrium. Journal of Molecular Biology, 2021, 433, 166878.	2.0	10
14	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. Nature Communications, 2021, 12, 4174.	5.8	22
15	AlphaFold: A Special Issue and A Special Time for Protein Science. Journal of Molecular Biology, 2021, 433, 167231.	2.0	15
16	Global Proteotoxicity Caused by Human β 2 Microglobulin Variants Impairs the Unfolded Protein Response in C. elegans. International Journal of Molecular Sciences, 2021, 22, 10752.	1.8	4
17	Amyloid structures: much more than just a cross- β fold. Current Opinion in Structural Biology, 2020, 60, 7-16.	2.6	150
18	Collagen I Weakly Interacts with the β -Sheets of β 2-Microglobulin and Enhances Conformational Exchange To Induce Amyloid Formation. Journal of the American Chemical Society, 2020, 142, 1321-1331.	6.6	15

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19	The role of the IT-state in D76N β 2-microglobulin amyloid assembly: A crucial intermediate or an innocuous bystander?. <i>Journal of Biological Chemistry</i> , 2020, 295, 12474-12484.	1.6	14
20	Modulation of β 2-Amyloid Fibril Formation in Alzheimer's Disease by Microglia and Infection. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 609073.	1.4	35
21	Looking Beyond the Core: The Role of Flanking Regions in the Aggregation of Amyloidogenic Peptides and Proteins. <i>Frontiers in Neuroscience</i> , 2020, 14, 611285.	1.4	52
22	Modulation of Amyloidogenic Protein Self-Assembly Using Tethered Small Molecules. <i>Journal of the American Chemical Society</i> , 2020, 142, 20845-20854.	6.6	19
23	Fibril structures of diabetes-related amylin variants reveal a basis for surface-templated assembly. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1048-1056.	3.6	71
24	Potential human transmission of amyloid β pathology: surveillance and risks. <i>Lancet Neurology</i> , The, 2020, 19, 872-878.	4.9	46
25	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <i>Communications Biology</i> , 2020, 3, 766.	2.0	32
26	The uniqueness of flow in probing the aggregation behavior of clinically relevant antibodies. <i>Engineering Reports</i> , 2020, 2, e12147.	0.9	5
27	Spot the Difference: Function versus Toxicity in Amyloid Fibrils. <i>Trends in Biochemical Sciences</i> , 2020, 45, 635-636.	3.7	12
28	Structural insight into the formation of lipoprotein- β -barrel complexes. <i>Nature Chemical Biology</i> , 2020, 16, 1019-1025.	3.9	34
29	Macromolecular Crowding Enhances the Detection of DNA and Proteins by a Solid-State Nanopore. <i>Nano Letters</i> , 2020, 20, 5553-5561.	4.5	71
30	<sc>PyXlinkViewer</sc>: A flexible tool for visualization of protein chemical crosslinking data within the <sc>PyMOL</sc> molecular graphics system. <i>Protein Science</i> , 2020, 29, 1851-1857.	3.1	56
31	A short motif in the N-terminal region of β -synuclein is critical for both aggregation and function. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 249-259.	3.6	116
32	Role of the lipid bilayer in outer membrane protein folding in Gram-negative bacteria. <i>Journal of Biological Chemistry</i> , 2020, 295, 10340-10367.	1.6	88
33	Using protein engineering to understand and modulate aggregation. <i>Current Opinion in Structural Biology</i> , 2020, 60, 157-166.	2.6	27
34	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. <i>Nature Communications</i> , 2020, 11, 2155.	5.8	48
35	An in vivo platform to select and evolve aggregation-resistant proteins. <i>Nature Communications</i> , 2020, 11, 1816.	5.8	22
36	Dynamics of Membrane Proteins Monitored by Single-Molecule Fluorescence Across Multiple Timescales. <i>Methods in Molecular Biology</i> , 2020, 2168, 273-297.	0.4	1

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37	Determining the Free Energies of Outer Membrane Proteins in Lipid Bilayers. <i>Methods in Molecular Biology</i> , 2020, 2168, 217-232.	0.4	1
38	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. <i>Analytical Chemistry</i> , 2019, 91, 15163-15170.	3.2	18
39	Thermodynamic phase diagram of amyloid- β (16-22) peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2091-2096.	3.3	63
40	Molecular insights into the surface-catalyzed secondary nucleation of amyloid- β ($A\beta$) Tj ETQq0 0 0,rgBT /Overlock 10 TF	4.7	54
41	Extracellular matrix components modulate different stages in β 2-microglobulin amyloid formation. <i>Journal of Biological Chemistry</i> , 2019, 294, 9392-9401.	1.6	19
42	Design and synthesis of cysteine-specific labels for photo-crosslinking studies. <i>RSC Advances</i> , 2019, 9, 7610-7614.	1.7	8
43	Dual Role of Ribosome-Binding Domain of NAC as a Potent Suppressor of Protein Aggregation and Aging-Related Proteinopathies. <i>Molecular Cell</i> , 2019, 74, 729-741.e7.	4.5	31
44	The Role of SurA PPlase Domains in Preventing Aggregation of the Outer-Membrane Proteins tOmpA and OmpT. <i>Journal of Molecular Biology</i> , 2019, 431, 1267-1283.	2.0	22
45	Homage to Chris Dobson. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 137.	1.6	0
46	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. <i>ELife</i> , 2019, 8, .	2.8	44
47	Professor Sir Christopher Martin Dobson (1949-2019). <i>Biochemist</i> , 2019, 41, 45-45.	0.2	0
48	A peptide-display protein scaffold to facilitate single molecule force studies of aggregation-prone peptides. <i>Protein Science</i> , 2018, 27, 1205-1217.	3.1	6
49	Mass spectrometry-enabled structural biology of membrane proteins. <i>Methods</i> , 2018, 147, 187-205.	1.9	69
50	Conformational flexibility within the nascent polypeptide-associated complex enables its interactions with structurally diverse client proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 8554-8568.	1.6	20
51	Using extensional flow to reveal diverse aggregation landscapes for three IgG1 molecules. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1216-1225.	1.7	15
52	Identification of a novel site of interaction between ataxin-3 and the amyloid aggregation inhibitor polyglutamine binding peptide 1. <i>European Journal of Mass Spectrometry</i> , 2018, 24, 129-140.	0.5	4
53	Richard Nelson Perham. 27 April 1937-14 February 2015. <i>Biographical Memoirs of Fellows of the Royal Society</i> , 2018, 65, 317-339.	0.1	0
54	Comparing Hydrogen Deuterium Exchange and Fast Photochemical Oxidation of Proteins: a Structural Characterisation of Wild-Type and β 2-Microglobulin. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 2413-2426.	1.2	43

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55	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16688-16692.	7.2	48
56	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie</i> , 2018, 130, 16930-16934.	1.6	6
57	Orientation of a Diagnostic Ligand Bound to Macroscopically Aligned Amyloid- β Fibrils Determined by Solid-State NMR. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 6611-6615.	2.1	0
58	The structure of a β 2-microglobulin fibril suggests a molecular basis for its amyloid polymorphism. <i>Nature Communications</i> , 2018, 9, 4517.	5.8	124
59	A new era for understanding amyloid structures and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 755-773.	16.1	654
60	Epigallocatechin-3-gallate remodels apolipoprotein A-I amyloid fibrils into soluble oligomers in the presence of heparin. <i>Journal of Biological Chemistry</i> , 2018, 293, 12877-12893.	1.6	18
61	Dynamic action of the Sec machinery during initiation, protein translocation and termination. <i>ELife</i> , 2018, 7, .	2.8	52
62	Inducing protein aggregation by extensional flow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4673-4678.	3.3	77
63	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. <i>Chemical Science</i> , 2017, 8, 5030-5040.	3.7	37
64	Investigating the Structural Compaction of Biomolecules Upon Transition to the Gas-Phase Using ESI-TWIMS-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1855-1862.	1.2	42
65	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2017, 429, 3776-3792.	2.0	63
66	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 8844-8852.	3.2	28
67	Amyloid plaques beyond A β : a survey of the diverse modulators of amyloid aggregation. <i>Biophysical Reviews</i> , 2017, 9, 405-419.	1.5	74
68	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017, 39, 90-99.	2.8	77
69	Molecular Origins of the Compatibility between Glycosaminoglycans and A β 40 Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2017, 429, 2449-2462.	2.0	23
70	FPOP-LC-MS/MS Suggests Differences in Interaction Sites of Amphipols and Detergents with Outer Membrane Proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 50-55.	1.2	33
71	Outer membrane protein folding from an energy landscape perspective. <i>BMC Biology</i> , 2017, 15, 123.	1.7	62
72	Two-way communication between SecY and SecA suggests a Brownian ratchet mechanism for protein translocation. <i>ELife</i> , 2016, 5, .	2.8	90

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73	Engineering the surface properties of a human monoclonal antibody prevents self-association and rapid clearance in vivo. <i>Scientific Reports</i> , 2016, 6, 38644.	1.6	89
74	A Population Shift between Sparsely Populated Folding Intermediates Determines Amyloidogenicity. <i>Journal of the American Chemical Society</i> , 2016, 138, 6271-6280.	6.6	29
75	A growing toolbox of techniques for studying β -barrel outer membrane protein folding and biogenesis. <i>Biochemical Society Transactions</i> , 2016, 44, 802-809.	1.6	15
76	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	3.6	82
77	Lateral opening in the intact β -barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016, 7, 12865.	5.8	157
78	MpUL-multi: Software for Calculation of Amyloid Fibril Mass per Unit Length from TB-TEM Images. <i>Scientific Reports</i> , 2016, 6, 21078.	1.6	11
79	Atomic Details of the Interactions of Glycosaminoglycans with Amyloid- β Fibrils. <i>Journal of the American Chemical Society</i> , 2016, 138, 8328-8331.	6.6	48
80	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	3.9	75
81	Substrate protein folds while it is bound to the ATP-independent chaperone Spy. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 53-58.	3.6	68
82	Comparison of the aggregation of homologous β 2-microglobulin variants reveals protein solubility as a key determinant of amyloid formation. <i>Journal of Molecular Biology</i> , 2016, 428, 631-643.	2.0	20
83	Characterization of Amyloid Oligomers by Electrospray Ionization-Ion Mobility Spectrometry-Mass Spectrometry (ESI-IMS-MS). <i>Methods in Molecular Biology</i> , 2016, 1345, 115-132.	0.4	10
84	ESI-IMS-MS: A method for rapid analysis of protein aggregation and its inhibition by small molecules. <i>Methods</i> , 2016, 95, 62-69.	1.9	50
85	A comparison of the folding characteristics of free and ribosome- β -tagged polypeptide chains using limited proteolysis and mass spectrometry. <i>Protein Science</i> , 2015, 24, 1282-1291.	3.1	6
86	Systematic analysis of the use of amphipathic polymers for studies of outer membrane proteins using mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 54-61.	0.7	30
87	Mutational Analysis of the Ability of Resveratrol To Inhibit Amyloid Formation by Islet Amyloid Polypeptide: Critical Evaluation of the Importance of Aromatic- β -Inhibitor and Histidine- β -Inhibitor Interactions. <i>Biochemistry</i> , 2015, 54, 666-676.	1.2	50
88	Amphipols Outperform Dodecylmaltoside Micelles in Stabilizing Membrane Protein Structure in the Gas Phase. <i>Analytical Chemistry</i> , 2015, 87, 1118-1126.	3.2	50
89	Extraction of Accurate Biomolecular Parameters from Single-Molecule Force Spectroscopy Experiments. <i>ACS Nano</i> , 2015, 9, 1315-1324.	7.3	14
90	Mechanisms of amyloid formation revealed by solution NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015, 88-89, 86-104.	3.9	85

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91	Insights into the consequences of co-polymerisation in the early stages of IAPP and A β peptide assembly from mass spectrometry. <i>Analyst</i> , 2015, 140, 6990-6999.	1.7	48
92	Force-induced remodelling of proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2015, 30, 89-99.	2.6	42
93	pH-induced molecular shedding drives the formation of amyloid fibril-derived oligomers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5691-5696.	3.3	95
94	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015, 89, 38-44.	1.9	31
95	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015, 89, 13-21.	1.9	55
96	Amyloid Fibrils: Inert End-Stage Aggregates or Key Players in Disease?. <i>Trends in Biochemical Sciences</i> , 2015, 40, 719-727.	3.7	100
97	Examination of Ataxin-3 (atx-3) Aggregation by Structural Mass Spectrometry Techniques: A Rationale for Expedited Aggregation upon Polyglutamine (polyQ) Expansion*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1241-1253.	2.5	33
98	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometry-mass spectrometry. <i>Nature Chemistry</i> , 2015, 7, 73-81.	6.6	255
99	Biophysical Studies of Amyloid Formation and Its Inhibition. <i>FASEB Journal</i> , 2015, 29, 491.1.	0.2	0
100	A β -Microglobulin Amyloid Fibril-Induced Membrane Disruption Is Enhanced by Endosomal Lipids and Acidic pH. <i>PLoS ONE</i> , 2014, 9, e104492.	1.1	30
101	A β -Microglobulin Amyloid Fibrils Are Nanoparticles That Disrupt Lysosomal Membrane Protein Trafficking and Inhibit Protein Degradation by Lysosomes. <i>Journal of Biological Chemistry</i> , 2014, 289, 35781-35794.	1.6	31
102	Distinguishing Closely Related Amyloid Precursors Using an RNA Aptamer. <i>Journal of Biological Chemistry</i> , 2014, 289, 26859-26871.	1.6	7
103	How TriC Folds Tricky Proteins. <i>Cell</i> , 2014, 159, 1251-1252.	13.5	4
104	Energy landscapes of functional proteins are inherently risky. <i>Nature Chemical Biology</i> , 2014, 10, 884-891.	3.9	90
105	Insights into the role of the beta-2 microglobulin D-strand in amyloid propensity revealed by mass spectrometry. <i>Molecular BioSystems</i> , 2014, 10, 412-420.	2.9	22
106	Visualization of Transient Protein-Protein Interactions that Promote or Inhibit Amyloid Assembly. <i>Molecular Cell</i> , 2014, 55, 214-226.	4.5	55
107	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, 660-670.	6.6	158
108	Synthesis, Characterization and Applications of a Perdeuterated Amphipol. <i>Journal of Membrane Biology</i> , 2014, 247, 909-924.	1.0	36

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109	Analysis of Amyloid Nanostructures Using Photo-cross-linking: <i>In Situ</i> Comparison of Three Widely Used Photo-cross-linkers. <i>ACS Chemical Biology</i> , 2014, 9, 761-768.	1.6	25
110	Secondary Structure in the Core of Amyloid Fibrils Formed from Human I ²⁷ and its Truncated Variant I ^{N6} . <i>Journal of the American Chemical Society</i> , 2014, 136, 6313-6325.	6.6	40
111	The Role of High-Dimensional Diffusive Search, Stabilization, and Frustration in Protein Folding. <i>Biophysical Journal</i> , 2014, 106, 1729-1740.	0.2	6
112	Mechanistic studies of the biogenesis and folding of outer membrane proteins in vitro and in vivo: What have we learned to date?. <i>Archives of Biochemistry and Biophysics</i> , 2014, 564, 265-280.	1.4	46
113	Monitoring oligomer formation from self-aggregating amylin peptides using ESI-IMS-MS. <i>International Journal for Ion Mobility Spectrometry</i> , 2013, 16, 29-39.	1.4	13
114	A tale of a tail: Structural insights into the conformational properties of the polyglutamine protein ataxin-3. <i>International Journal of Mass Spectrometry</i> , 2013, 345-347, 63-70.	0.7	15
115	Conformational dynamics is more important than helical propensity for the folding of the all α -helical protein Im7. <i>Protein Science</i> , 2013, 22, 1722-1738.	3.1	5
116	An Imaging and Systems Modeling Approach to Fibril Breakage Enables Prediction of Amyloid Behavior. <i>Biophysical Journal</i> , 2013, 105, 2811-2819.	0.2	55
117	Aggregation Modulators Interfere with Membrane Interactions of α 2-Microglobulin Fibrils. <i>Biophysical Journal</i> , 2013, 105, 745-755.	0.2	27
118	Dissecting the Effects of Periplasmic Chaperones on the In Vitro Folding of the Outer Membrane Protein PagP. <i>Journal of Molecular Biology</i> , 2013, 425, 3178-3191.	2.0	45
119	Assessing the causes and consequences of co-polymerization in amyloid formation. <i>Prion</i> , 2013, 7, 359-368.	0.9	42
120	A Force-Activated Trip Switch Triggers Rapid Dissociation of a Colicin from Its Immunity Protein. <i>PLoS Biology</i> , 2013, 11, e1001489.	2.6	26
121	Expanding the Repertoire of Amyloid Polymorphs by Co-polymerization of Related Protein Precursors. <i>Journal of Biological Chemistry</i> , 2013, 288, 7327-7337.	1.6	36
122	Direct three-dimensional visualization of membrane disruption by amyloid fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20455-20460.	3.3	162
123	Site-Specific Identification of an α 2 Fibril Heparin Interaction Site by Using Solid-State NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 13140-13143.	7.2	26
124	Covalent Cross-Linking within Supramolecular Peptide Structures. <i>Analytical Chemistry</i> , 2012, 84, 6790-6797.	3.2	21
125	Malleability of the Folding Mechanism of the Outer Membrane Protein PagP: Parallel Pathways and the Effect of Membrane Elasticity. <i>Journal of Molecular Biology</i> , 2012, 416, 453-464.	2.0	24
126	Conformational Properties of the Unfolded State of Im7 in Nondenaturing Conditions. <i>Journal of Molecular Biology</i> , 2012, 416, 300-318.	2.0	27

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127	Effect of Sequence Variation on the Mechanical Response of Amyloid Fibrils Probed by Steered Molecular Dynamics Simulation. <i>Biophysical Journal</i> , 2012, 102, 587-596.	0.2	43
128	Amphipathic Polymers Enable the Study of Functional Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2012, 84, 9841-9847.	3.2	61
129	N-terminal acetylation of β -synuclein induces increased transient helical propensity and decreased aggregation rates in the intrinsically disordered monomer. <i>Protein Science</i> , 2012, 21, 911-917.	3.1	161
130	The role of conformational flexibility in β -microglobulin amyloid fibril formation at neutral pH. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1783-1792.	0.7	24
131	Linked Landscapes and Conformational Conversions: How Proteins Fold and Misfold. <i>Biological and Medical Physics Series</i> , 2012, , 1-16.	0.3	0
132	Phosphorylation as a Tool To Modulate Aggregation Propensity and To Predict Fibril Architecture. <i>ChemBioChem</i> , 2012, 13, 271-281.	1.3	11
133	Protein Misfolding and Toxicity in Dialysis-Related Amyloidosis. , 2012, , 377-405.		2
134	Quantifying heterogeneity and conformational dynamics from single molecule FRET of diffusing molecules: recurrence analysis of single particles (RASP). <i>Physical Chemistry Chemical Physics</i> , 2011, 13, 1857.	1.3	106
135	Structure and Dynamics of Oligomeric Intermediates in β 2-Microglobulin Self-Assembly. <i>Biophysical Journal</i> , 2011, 101, 1238-1247.	0.2	25
136	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. <i>Nature Chemical Biology</i> , 2011, 7, 730-739.	3.9	93
137	Conformational Conversion during Amyloid Formation at Atomic Resolution. <i>Molecular Cell</i> , 2011, 41, 161-172.	4.5	160
138	A Diversity of Assembly Mechanisms of a Generic Amyloid Fold. <i>Molecular Cell</i> , 2011, 43, 8-18.	4.5	266
139	Understanding the complex mechanisms of β -microglobulin amyloid assembly. <i>FEBS Journal</i> , 2011, 278, 3868-3883.	2.2	92
140	Dissecting key residues in folding and stability of the bacterial immunity protein 7. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 517-523.	1.0	4
141	The Oligomeric State and Arrangement of the Active Bacterial Translocon. <i>Journal of Biological Chemistry</i> , 2011, 286, 4659-4669.	1.6	59
142	Characterization of the Response of Primary Cells Relevant to Dialysis-Related Amyloidosis to β 2-Microglobulin Monomer and Fibrils. <i>PLoS ONE</i> , 2011, 6, e27353.	1.1	24
143	Stacked Sets of Parallel, In-register β -Strands of β 2-Microglobulin in Amyloid Fibrils Revealed by Site-directed Spin Labeling and Chemical Labeling. <i>Journal of Biological Chemistry</i> , 2010, 285, 17137-17147.	1.6	55
144	The transition state for folding of an outer membrane protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4099-4104.	3.3	129

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145	Perturbing the folding energy landscape of the bacterial immunity protein Im7 by site-specific N-linked glycosylation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 22528-22533.	3.3	72
146	Elongated oligomers in β^2 -microglobulin amyloid assembly revealed by ion mobility spectrometry-mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6794-6798.	3.3	147
147	Fibril fragmentation in amyloid assembly and cytotoxicity. Prion, 2010, 4, 20-25.	0.9	106
148	Intermolecular Alignment in β^2 -Microglobulin Amyloid Fibrils. Journal of the American Chemical Society, 2010, 132, 17077-17079.	6.6	69
149	Magic Angle Spinning NMR Analysis of β^2 -Microglobulin Amyloid Fibrils in Two Distinct Morphologies. Journal of the American Chemical Society, 2010, 132, 10414-10423.	6.6	79
150	Desolvation and Development of Specific Hydrophobic Core Packing during Im7 Folding. Journal of Molecular Biology, 2010, 396, 1329-1345.	2.0	18
151	Single-Molecule Studies of the Im7 Folding Landscape. Journal of Molecular Biology, 2010, 398, 132-145.	2.0	18
152	Amyloid fibril length distribution quantified by atomic force microscopy single-particle image analysis. Protein Engineering, Design and Selection, 2009, 22, 489-496.	1.0	58
153	Glimpses of the molecular mechanisms of β^2 -microglobulin fibril formation in vitro: Aggregation on a complex energy landscape. FEBS Letters, 2009, 583, 2623-2629.	1.3	55
154	Probing Dynamics within Amyloid Fibrils Using a Novel Capping Method. Angewandte Chemie - International Edition, 2009, 48, 5705-5707.	7.2	12
155	The mechanism of folding of Im7 reveals competition between functional and kinetic evolutionary constraints. Nature Structural and Molecular Biology, 2009, 16, 318-324.	3.6	63
156	An expanding arsenal of experimental methods yields an explosion of insights into protein folding mechanisms. Nature Structural and Molecular Biology, 2009, 16, 582-588.	3.6	223
157	HDX-ESI-MS reveals enhanced conformational dynamics of the amyloidogenic protein β^2 -microglobulin upon release from the MHC-1. Journal of the American Society for Mass Spectrometry, 2009, 20, 278-286.	1.2	37
158	A Generic Mechanism of β^2 -Microglobulin Amyloid Assembly at Neutral pH Involving a Specific Proline Switch. Journal of Molecular Biology, 2009, 386, 1312-1326.	2.0	77
159	Globular Tetramers of β^2 -Microglobulin Assemble into Elaborate Amyloid Fibrils. Journal of Molecular Biology, 2009, 389, 48-57.	2.0	73
160	Competition between Intramolecular and Intermolecular Interactions in an Amyloid-Forming Protein. Journal of Molecular Biology, 2009, 389, 776-786.	2.0	68
161	Amino Acid Insertion Reveals a Necessary Three-Helical Intermediate in the Folding Pathway of the Colicin E7 Immunity Protein Im7. Journal of Molecular Biology, 2009, 392, 1074-1086.	2.0	9
162	Identification of a Mechanical Rheostat in the Hydrophobic Core of Protein L. Journal of Molecular Biology, 2009, 393, 237-248.	2.0	55

#	ARTICLE	IF	CITATIONS
163	Optimizing Protein Stability In Vivo. <i>Molecular Cell</i> , 2009, 36, 861-871.	4.5	147
164	Thermodynamic Description of Polymorphism in Q- and N-Rich Peptide Aggregates Revealed by Atomistic Simulation. <i>Biophysical Journal</i> , 2009, 97, 1-11.	0.2	65
165	Tuning the Elastic Modulus of Hydrated Collagen Fibrils. <i>Biophysical Journal</i> , 2009, 97, 2985-2992.	0.2	143
166	Mechanically unfolding proteins: The effect of unfolding history and the supramolecular scaffold. <i>Protein Science</i> , 2009, 11, 2759-2765.	3.1	75
167	Fibril Fragmentation Enhances Amyloid Cytotoxicity. <i>Journal of Biological Chemistry</i> , 2009, 284, 34272-34282.	1.6	326
168	Deciphering Drift Time Measurements from Travelling Wave Ion Mobility Spectrometry-Mass Spectrometry Studies. <i>European Journal of Mass Spectrometry</i> , 2009, 15, 113-130.	0.5	312
169	Structural Insights into the Polymorphism of Amyloid-Like Fibrils Formed by Region 20 [~] 29 of Amylin Revealed by Solid-State NMR and X-ray Fiber Diffraction. <i>Journal of the American Chemical Society</i> , 2008, 130, 14990-15001.	6.6	177
170	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Revealed in Atomic Detail by Molecular Dynamics. <i>Journal of Molecular Biology</i> , 2008, 375, 908-919.	2.0	34
171	Fibril Growth Kinetics Reveal a Region of I ² -microglobulin Important for Nucleation and Elongation of Aggregation. <i>Journal of Molecular Biology</i> , 2008, 378, 251-263.	2.0	93
172	Folding versus aggregation: Polypeptide conformations on competing pathways. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 100-117.	1.4	352
173	Trifluoromethyldiazirine: an effective photo-induced cross-linking probe for exploring amyloid formation. <i>Chemical Communications</i> , 2008, , 5728.	2.2	19
174	Internal friction of single polypeptide chains at high stretch. <i>Faraday Discussions</i> , 2008, 139, 35.	1.6	36
175	Systematic analysis of nucleation-dependent polymerization reveals new insights into the mechanism of amyloid self-assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8926-8931.	3.3	414
176	A Common I ² -Sheet Architecture Underlies in Vitro and in Vivo I ² -Microglobulin Amyloid Fibrils. <i>Journal of Biological Chemistry</i> , 2008, 283, 17279-17286.	1.6	57
177	Effects of hydration on the mechanical response of individual collagen fibrils. <i>Applied Physics Letters</i> , 2008, 92, .	1.5	111
178	The Dynamical Response of Proteins Under Force. , 2008, , 205-249.		1
179	Investigation into the Role of Macrophages in the Formation and Degradation of I ² -Microglobulin Amyloid Fibrils. <i>Journal of Biological Chemistry</i> , 2007, 282, 29691-29700.	1.6	30
180	Avoidance of Epimerization in the Synthesis of Peptide Thioesters Using Fmoc Protection. <i>Synlett</i> , 2007, 2007, 2517-2520.	1.0	5

#	ARTICLE	IF	CITATIONS
181	NMR Analysis of the Conformational Properties of the Trapped on-pathway Folding Intermediate of the Bacterial Immunity Protein Im7. <i>Journal of Molecular Biology</i> , 2007, 366, 1001-1015.	2.0	48
182	The Effect of Increasing the Stability of Non-native Interactions on the Folding Landscape of the Bacterial Immunity Protein Im9. <i>Journal of Molecular Biology</i> , 2007, 371, 554-568.	2.0	30
183	The N-terminal Helix Is a Post-assembly Clamp in the Bacterial Outer Membrane Protein PagP. <i>Journal of Molecular Biology</i> , 2007, 373, 529-540.	2.0	55
184	Production and Characterization of RNA Aptamers Specific for Amyloid Fibril Epitopes. <i>Journal of Biological Chemistry</i> , 2007, 282, 34500-34509.	1.6	37
185	Nucleation of protein fibrillation by nanoparticles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8691-8696.	3.3	800
186	The Effect of Protein Complexation on the Mechanical Stability of Im9. <i>Biophysical Journal</i> , 2007, 92, L79-L81.	0.2	31
187	Intermediates: ubiquitous species on folding energy landscapes?. <i>Current Opinion in Structural Biology</i> , 2007, 17, 30-37.	2.6	196
188	Monitoring copopulated conformational states during protein folding events using electrospray ionization-ion mobility spectrometry-mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 2180-2190.	1.2	122
189	Î²2-Microglobulin and Dialysis-Related Amyloidosis. , 2007, , 217-239.		2
190	Mechanical Resistance of Proteins Explained Using Simple Molecular Models. <i>Biophysical Journal</i> , 2006, 90, 287-297.	0.2	106
191	Viscoelastic Study of the Mechanical Unfolding of a Protein by AFM. <i>Biophysical Journal</i> , 2006, 91, L16-L18.	0.2	49
192	Urea-Induced Unfolding of the Immunity Protein Im9 Monitored by spFRET. <i>Biophysical Journal</i> , 2006, 91, L42-L44.	0.2	50
193	Sulfate-Induced Effects in the On-Pathway Intermediate of the Bacterial Immunity Protein Im7*. <i>Biochemistry</i> , 2006, 45, 2274-2282.	1.2	10
194	GroEL: More than Just a Folding Cage. <i>Cell</i> , 2006, 125, 831-833.	13.5	33
195	Direct Observation of Oligomeric Species formed in the Early Stages of Amyloid Fibril Formation using Electrospray Ionisation Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2006, 364, 9-19.	2.0	137
196	Characterisation of the Conformational Properties of Urea-unfolded Im7: Implications for the Early Stages of Protein Folding. <i>Journal of Molecular Biology</i> , 2006, 364, 824-835.	2.0	39
197	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Proceeds through a Concerted Î² Strand Displacement Mechanism. <i>Molecular Cell</i> , 2006, 22, 831-842.	4.5	159
198	Investigating the structural properties of amyloid-like fibrils formed in vitro from Î²2-microglobulin using limited proteolysis and electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1628-1636.	0.7	58

#	ARTICLE	IF	CITATIONS
199	Amyloid formation under physiological conditions proceeds via a native-like folding intermediate. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 195-201.	3.6	308
200	A Systematic Study of the Effect of Physiological Factors on β 2-Microglobulin Amyloid Formation at Neutral pH. <i>Biochemistry</i> , 2006, 45, 2311-2321.	1.2	120
201	Determination of an ensemble of structures representing the intermediate state of the bacterial immunity protein Im7. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 99-104.	3.3	90
202	Detailed evaluation of the performance of microfluidic T mixers using fluorescence and ultraviolet resonance Raman spectroscopy. <i>Review of Scientific Instruments</i> , 2006, 77, 055105.	0.6	15
203	Amyloid Under the Atomic Force Microscope. <i>Protein and Peptide Letters</i> , 2006, 13, 261-270.	0.4	60
204	Viscoelastic Measurements of Single Molecules on a Millisecond Time Scale by Magnetically Driven Oscillation of an Atomic Force Microscope Cantilever. <i>Langmuir</i> , 2005, 21, 4765-4772.	1.6	44
205	Towards an understanding of the structural molecular mechanism of β 2-microglobulin amyloid formation in vitro. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1753, 51-63.	1.1	48
206	Semisynthesis of a Glycosylated Im7 Analogue for Protein Folding Studies. <i>Journal of the American Chemical Society</i> , 2005, 127, 12882-12889.	6.6	67
207	The Yin and Yang of protein folding. <i>FEBS Journal</i> , 2005, 272, 5962-5970.	2.2	259
208	Helix stability and hydrophobicity in the folding mechanism of the bacterial immunity protein Im9. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 41-50.	1.0	14
209	Ultraviolet Resonance Raman Studies Reveal the Environment of Tryptophan and Tyrosine Residues in the Native and Partially Folded States of the E Colicin-Binding Immunity Protein Im7. <i>Biochemistry</i> , 2005, 44, 3306-3315.	1.2	33
210	Dynamics in the Unfolded State of β 2-microglobulin Studied by NMR. <i>Journal of Molecular Biology</i> , 2005, 346, 279-294.	2.0	92
211	Competing Pathways Determine Fibril Morphology in the Self-assembly of β 2-Microglobulin into Amyloid. <i>Journal of Molecular Biology</i> , 2005, 351, 850-864.	2.0	320
212	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, 602-616.	3.1	207
213	Mechanically Unfolding the Small, Topologically Simple Protein L. <i>Biophysical Journal</i> , 2005, 89, 506-519.	0.2	154
214	Co-populated Conformational Ensembles of β 2-Microglobulin Uncovered Quantitatively by Electrospray Ionization Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 27069-27077.	1.6	68
215	Separation of β 2-microglobulin conformers by high-field asymmetric waveform ion mobility spectrometry (FAIMS) coupled to electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2229-2234.	0.7	54
216	Equilibrium Hydrogen Exchange Reveals Extensive Hydrogen Bonded Secondary Structure in the On-pathway Intermediate of Im7. <i>Journal of Molecular Biology</i> , 2004, 337, 183-193.	2.0	33

#	ARTICLE	IF	CITATIONS
217	Trapping the On-pathway Folding Intermediate of Im7 at Equilibrium. <i>Journal of Molecular Biology</i> , 2004, 341, 215-226.	2.0	45
218	Switching Two-state to Three-state Kinetics in the Helical Protein Im9 via the Optimisation of Stabilising Non-native Interactions by Design. <i>Journal of Molecular Biology</i> , 2004, 342, 261-273.	2.0	62
219	Force mode atomic force microscopy as a tool for protein folding studies. <i>Analytica Chimica Acta</i> , 2003, 479, 87-105.	2.6	120
220	Comparison of the transition state ensembles for folding of Im7 and Im9 determined using all-atom molecular dynamics simulations with \bar{I} value restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 513-525.	1.5	41
221	Pulling geometry defines the mechanical resistance of a β -sheet protein. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 731-737.	3.6	356
222	Amyloid-forming Peptides from β 2-Microglobulin – Insights into the Mechanism of Fibril Formation in Vitro. <i>Journal of Molecular Biology</i> , 2003, 325, 249-257.	2.0	145
223	Structural Analysis of the Rate-limiting Transition States in the Folding of Im7 and Im9: Similarities and Differences in the Folding of Homologous Proteins. <i>Journal of Molecular Biology</i> , 2003, 326, 293-305.	2.0	126
224	Hierarchical Assembly of β 2-Microglobulin Amyloid In Vitro Revealed by Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2003, 330, 785-797.	2.0	213
225	A Systematic Investigation into the Effect of Protein Destabilisation on Beta 2-Microglobulin Amyloid Formation. <i>Journal of Molecular Biology</i> , 2003, 330, 943-954.	2.0	140
226	Role of the N and C-terminal Strands of Beta 2-Microglobulin in Amyloid Formation at Neutral pH. <i>Journal of Molecular Biology</i> , 2003, 330, 935-941.	2.0	69
227	pH as a Trigger of Peptide β -Sheet Self-Assembly and Reversible Switching between Nematic and Isotropic Phases. <i>Journal of the American Chemical Society</i> , 2003, 125, 9619-9628.	6.6	441
228	Unfolding dynamics of proteins under applied force. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2003, 361, 713-730.	1.6	25
229	Crystal structure of monomeric human β 2-microglobulin reveals clues to its amyloidogenic properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9771-9776.	3.3	178
230	The Effect of Core Destabilization on the Mechanical Resistance of I27. <i>Biophysical Journal</i> , 2002, 83, 458-472.	0.2	132
231	Im7 folding mechanism: misfolding on a path to the native state. <i>Nature Structural Biology</i> , 2002, 9, 209-16.	9.7	145
232	Structural properties of an amyloid precursor of β 2-microglobulin. <i>Nature Structural Biology</i> , 2002, 9, 326-331.	9.7	177
233	Insights into the molecular mechanisms of protein folding and misfolding. , 2002, , 352-354.		1
234	Using chimeric immunity proteins to explore the energy landscape for α -helical protein folding. <i>Journal of Molecular Biology</i> , 2001, 307, 393-405.	2.0	30

#	ARTICLE	IF	CITATIONS
235	Acidic conditions stabilise intermediates populated during the folding of Im7 and Im9 1 Edited by C. R. Matthews. <i>Journal of Molecular Biology</i> , 2001, 312, 849-863.	2.0	62
236	Î ² -microglobulin and its deamidated variant, N17D form amyloid fibrils with a range of morphologies in vitro. <i>Journal of Molecular Biology</i> , 2001, 313, 559-571.	2.0	186
237	Accurate Use of Single Molecule Fluorescence Correlation Spectroscopy to Determine Molecular Diffusion Times. <i>Single Molecules</i> , 2001, 2, 177-181.	1.7	31
238	Role of the single disulphide bond of Î ² -microglobulin in amyloidosis in vitro. <i>Protein Science</i> , 2001, 10, 1775-1784.	3.1	73
239	A partially folded intermediate species of the Î ² -sheet protein apo-pseudoazurin is trapped during proline-limited folding. <i>Protein Science</i> , 2001, 10, 1216-1224.	3.1	26
240	Ultrarapid mixing experiments reveal that Im7 folds via an on-pathway intermediate. <i>Nature Structural Biology</i> , 2001, 8, 68-72.	9.7	138
241	Ribosome-mediated refolding of partially-unfolded ricin A-chain. <i>Biochemical Society Transactions</i> , 2000, 28, A68-A68.	1.6	0
242	From native state to amyloid; an investigation into partial unfolding of Î ² -microglobulin. <i>Biochemical Society Transactions</i> , 2000, 28, A68-A68.	1.6	0
243	Partially folded states in helical protein folding. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	1.6	0
244	Towards single molecule unfolding of proteins using AFM and its observation using fluorescence. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	1.6	0
245	Unfolding of the Î ² -sheet Protein Y74W Apo-pseudoazurin: Evidence of an Equilibrium Intermediate Species. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	1.6	0
246	Exploring the folding landscape of alpha helical proteins. <i>Biochemical Society Transactions</i> , 2000, 28, A70-A70.	1.6	0
247	An Investigation into the Properties of a Chaperone Domain and Analysis of the Non-covalently Bound Complexes with Peptide Substrates using Mass Spectrometry. <i>Biochemical Society Transactions</i> , 2000, 28, A70-A70.	1.6	0
248	The structure and dynamics in solution of Cu(I) pseudoazurin from <i>Paracoccus pantotrophus</i> . <i>Protein Science</i> , 2000, 9, 846-858.	3.1	20
249	Partially Unfolded States of Î ² -Microglobulin and Amyloid Formation in Vitro. <i>Biochemistry</i> , 2000, 39, 8735-8746.	1.2	321
250	Thermal unfolding of an intermediate is associated with non-arrhenius kinetics in the folding of hen lysozyme. <i>Journal of Molecular Biology</i> , 2000, 297, 193-210.	2.0	70
251	Partially Unfolded Species Populated during Equilibrium Denaturation of the Î ² -Sheet Protein Y74W Apo-Pseudoazurin. <i>Biochemistry</i> , 2000, 39, 5672-5682.	1.2	21
252	GroEL accelerates the refolding of hen lysozyme without changing its folding mechanism. <i>Nature Structural Biology</i> , 1999, 6, 683-690.	9.7	59

#	ARTICLE	IF	CITATIONS
253	Structural and mechanistic basis of immunity toward endonuclease colicins. <i>Nature Structural Biology</i> , 1999, 6, 243-252.	9.7	156
254	Rapid folding with and without populated intermediates in the homologous four-helix proteins Im7 and Im9 1 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 286, 1597-1608.	2.0	236
255	The greek key protein apo-pseudoazurin folds through an obligate on-pathway intermediate 1 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 286, 1621-1632.	2.0	44
256	A near-native state on the slow refolding pathway of hen lysozyme. <i>Protein Science</i> , 1999, 8, 35-44.	3.1	35
257	Kinetic studies of β^2 -sheet protein folding. <i>Current Opinion in Structural Biology</i> , 1998, 8, 86-92.	2.6	58
258	The origin of the β^1 -domain intermediate in the folding of hen lysozyme. <i>Journal of Molecular Biology</i> , 1998, 277, 997-1005.	2.0	53
259	[24] Probing conformations of GroEL-bound substrate proteins by mass spectrometry. <i>Methods in Enzymology</i> , 1998, 290, 296-313.	0.4	7
260	The pseudoazurin gene from <i>Thiosphaera pantotropha</i> : analysis of upstream putative regulatory sequences and overexpression in <i>Escherichia coli</i> . <i>Biochemical Journal</i> , 1997, 321, 699-705.	1.7	27
261	Engineering of peptide β^2 -sheet nanotapes. <i>Journal of Materials Chemistry</i> , 1997, 7, 1135-1145.	6.7	163
262	Fast and slow tracks in lysozyme folding: insight into the role of domains in the folding process. <i>Journal of Molecular Biology</i> , 1997, 267, 1068-1074.	2.0	93
263	Hydrogen exchange properties of proteins in native and denatured states monitored by mass spectrometry and NMR. <i>Protein Science</i> , 1997, 6, 1316-1324.	3.1	90
264	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. <i>Nature</i> , 1997, 385, 787-793.	13.7	1,061
265	Structural and mechanistic consequences of polypeptide binding by GroEL. <i>Folding & Design</i> , 1997, 2, R93-R104.	4.5	47
266	Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996, 10, 93-101.	0.2	175
267	Significant hydrogen exchange protection in GroEL-bound DHFR is maintained during iterative rounds of substrate cycling. <i>Protein Science</i> , 1996, 5, 2506-2513.	3.1	70
268	Pseudospecific docking surfaces on electron transfer proteins as illustrated by pseudoazurin, cytochrome c550 and cytochrome cd1 nitrite reductase. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 975-982.	3.6	112
269	Cooperative Elements in Protein Folding Monitored by Electrospray Ionization Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1995, 117, 7548-7549.	6.6	47
270	Conformational Properties of Four Peptides Spanning the Sequence of Hen Lysozyme. <i>Journal of Molecular Biology</i> , 1995, 252, 483-491.	2.0	121

#	ARTICLE	IF	CITATIONS
271	Conformation of GroEL-bound $\hat{\pm}$ -lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994, 372, 646-651.	13.7	221
272	Understanding how proteins fold: the lysozyme story so far. <i>Trends in Biochemical Sciences</i> , 1994, 19, 31-37.	3.7	353
273	Probing the structure of folding intermediates. <i>Current Opinion in Structural Biology</i> , 1994, 4, 100-106.	2.6	94
274	Tertiary Interactions in the Folding Pathway of Hen Lysozyme: Kinetic Studies Using Fluorescent Probes. <i>Biochemistry</i> , 1994, 33, 5212-5220.	1.2	151
275	The Refolding of Human Lysozyme: A Comparison with the Structurally Homologous Hen Lysozyme. <i>Biochemistry</i> , 1994, 33, 5867-5876.	1.2	142
276	Far-UV Circular Dichroism Reveals a Conformational Switch in a Peptide Fragment from the β -Sheet of Hen Lysozyme. <i>Biochemistry</i> , 1994, 33, 7345-7353.	1.2	58
277	A partially folded state of hen egg white lysozyme in trifluoroethanol: structural characterization and implications for protein folding. <i>Biochemistry</i> , 1993, 32, 669-678.	1.2	284
278	A study of D52S hen lysozyme-G1cNAc oligosaccharide complexes by NMR spectroscopy and electrospray mass spectrometry. <i>FEBS Letters</i> , 1992, 296, 153-157.	1.3	31
279	Production of ^{15}N -labelled hen egg white lysozyme using <i>Aspergillus niger</i> . <i>Biotechnology Letters</i> , 1992, 14, 897-902.	1.1	6
280	The folding of hen lysozyme involves partially structured intermediates and multiple pathways. <i>Nature</i> , 1992, 358, 302-307.	13.7	771
281	Demonstration by NMR of folding domains in lysozyme. <i>Nature</i> , 1991, 349, 633-636.	13.7	265
282	Site-directed mutagenesis and proton NMR spectroscopy of an interdomain segment in the pyruvate dehydrogenase multienzyme complex of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1988, 27, 289-296.	1.2	49