

Sheena E Radford

List of Publications by Year in descending order

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282
papers

23,440
citations

6613

79
h-index

10158

140
g-index

302
all docs

302
docs citations

302
times ranked

16590
citing authors

#	ARTICLE	IF	CITATIONS
1	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. <i>Nature</i> , 1997, 385, 787-793.	27.8	1,061
2	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.	7.1	800
3	The folding of hen lysozyme involves partially structured intermediates and multiple pathways. <i>Nature</i> , 1992, 358, 302-307.	27.8	771
4	A new era for understanding amyloid structures and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 755-773.	37.0	654
5	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.	13.7	441
6	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.	7.1	414
7	Pulling geometry defines the mechanical resistance of a β -sheet protein. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 731-737.	8.2	356
8	Understanding how proteins fold: the lysozyme story so far. <i>Trends in Biochemical Sciences</i> , 1994, 19, 31-37.	7.5	353
9	Folding versus aggregation: Polypeptide conformations on competing pathways. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 100-117.	3.0	352
10	Fibril Fragmentation Enhances Amyloid Cytotoxicity. <i>Journal of Biological Chemistry</i> , 2009, 284, 34272-34282.	3.4	326
11	Partially Unfolded States of β -Microglobulin and Amyloid Formation in Vitro. <i>Biochemistry</i> , 2000, 39, 8735-8746.	2.5	321
12	Competing Pathways Determine Fibril Morphology in the Self-assembly of β -Microglobulin into Amyloid. <i>Journal of Molecular Biology</i> , 2005, 351, 850-864.	4.2	320
13	Deciphering Drift Time Measurements from Travelling Wave Ion Mobility Spectrometry-Mass Spectrometry Studies. <i>European Journal of Mass Spectrometry</i> , 2009, 15, 113-130.	1.0	312
14	Amyloid formation under physiological conditions proceeds via a native-like folding intermediate. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 195-201.	8.2	308
15	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.	2.5	284
16	A Diversity of Assembly Mechanisms of a Generic Amyloid Fold. <i>Molecular Cell</i> , 2011, 43, 8-18.	9.7	266
17	Demonstration by NMR of folding domains in lysozyme. <i>Nature</i> , 1991, 349, 633-636.	27.8	265
18	The Yin and Yang of protein folding. <i>FEBS Journal</i> , 2005, 272, 5962-5970.	4.7	259

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19	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometryâ€“mass spectrometry. <i>Nature Chemistry</i> , 2015, 7, 73-81.	13.6	255
20	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.	4.2	236
21	An expanding arsenal of experimental methods yields an explosion of insights into protein folding mechanisms. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 582-588.	8.2	223
22	Conformation of GroEL-bound Î±-lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994, 372, 646-651.	27.8	221
23	Hierarchical Assembly of Î²2-Microglobulin Amyloid In Vitro Revealed by Atomic Force Microscopy. <i>Journal of Molecular Biology</i> , 2003, 330, 785-797.	4.2	213
24	Protein folding: Defining a â€œstandardâ€•set of experimental conditions and a preliminary kinetic data set of two-state proteins. <i>Protein Science</i> , 2005, 14, 602-616.	7.6	207
25	Intermediates: ubiquitous species on folding energy landscapes?. <i>Current Opinion in Structural Biology</i> , 2007, 17, 30-37.	5.7	196
26	Î²2-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.	4.2	186
27	Crystal structure of monomeric human Î²2-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.	7.1	178
28	Structural properties of an amyloid precursor of Î²2-microglobulin. <i>Nature Structural Biology</i> , 2002, 9, 326-331.	9.7	177
29	Structural Insights into the Polymorphism of Amyloid-Like Fibrils Formed by Region 20â~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.	13.7	177
30	Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996, 10, 93-101.	0.5	175
31	Engineering of peptide Î²-sheet nanotapes. <i>Journal of Materials Chemistry</i> , 1997, 7, 1135-1145.	6.7	163
32	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.	7.1	162
33	Nâ€terminal acetylation of Î±â€synuclein induces increased transient helical propensity and decreased aggregation rates in the intrinsically disordered monomer. <i>Protein Science</i> , 2012, 21, 911-917.	7.6	161
34	Conformational Conversion during Amyloid Formation at Atomic Resolution. <i>Molecular Cell</i> , 2011, 41, 161-172.	9.7	160
35	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Proceeds through a Concerted Î² Strand Displacement Mechanism. <i>Molecular Cell</i> , 2006, 22, 831-842.	9.7	159
36	Ion Mobility Spectrometryâ€“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.	13.7	158

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37	Lateral opening in the intact β -barrel assembly machinery captured by cryo-EM. Nature Communications, 2016, 7, 12865.	12.8	157
38	Structural and mechanistic basis of immunity toward endonuclease colicins. Nature Structural Biology, 1999, 6, 243-252.	9.7	156
39	Mechanically Unfolding the Small, Topologically Simple Protein L. Biophysical Journal, 2005, 89, 506-519.	0.5	154
40	Tertiary Interactions in the Folding Pathway of Hen Lysozyme: Kinetic Studies Using Fluorescent Probes. Biochemistry, 1994, 33, 5212-5220.	2.5	151
41	Amyloid structures: much more than just a cross- β fold. Current Opinion in Structural Biology, 2020, 60, 7-16.	5.7	150
42	Optimizing Protein Stability In Vivo. Molecular Cell, 2009, 36, 861-871.	9.7	147
43	Elongated oligomers in β -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.	7.1	147
44	Im7 folding mechanism: misfolding on a path to the native state. Nature Structural Biology, 2002, 9, 209-16.	9.7	145
45	Amyloid-forming Peptides from β 2-Microglobulin—Insights into the Mechanism of Fibril Formation in Vitro. Journal of Molecular Biology, 2003, 325, 249-257.	4.2	145
46	Tuning the Elastic Modulus of Hydrated Collagen Fibrils. Biophysical Journal, 2009, 97, 2985-2992.	0.5	143
47	The Refolding of Human Lysozyme: A Comparison with the Structurally Homologous Hen Lysozyme. Biochemistry, 1994, 33, 5867-5876.	2.5	142
48	A Systematic Investigation into the Effect of Protein Destabilisation on Beta 2-Microglobulin Amyloid Formation. Journal of Molecular Biology, 2003, 330, 943-954.	4.2	140
49	Ultrarapid mixing experiments reveal that Im7 folds via an on-pathway intermediate. Nature Structural Biology, 2001, 8, 68-72.	9.7	138
50	Direct Observation of Oligomeric Species formed in the Early Stages of Amyloid Fibril Formation using Electrospray Ionisation Mass Spectrometry. Journal of Molecular Biology, 2006, 364, 9-19.	4.2	137
51	The Effect of Core Destabilization on the Mechanical Resistance of I27. Biophysical Journal, 2002, 83, 458-472.	0.5	132
52	The transition state for folding of an outer membrane protein. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4099-4104.	7.1	129
53	Proteostasis of Islet Amyloid Polypeptide: A Molecular Perspective of Risk Factors and Protective Strategies for Type II Diabetes. Chemical Reviews, 2021, 121, 1845-1893.	47.7	129
54	Structural Analysis of the Rate-limiting Transition States in the Folding of Im7 and Im9: Similarities and Differences in the Folding of Homologous Proteins. Journal of Molecular Biology, 2003, 326, 293-305.	4.2	126

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55	The structure of a β 2-microglobulin fibril suggests a molecular basis for its amyloid polymorphism. <i>Nature Communications</i> , 2018, 9, 4517.	12.8	124
56	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.	2.8	122
57	Conformational Properties of Four Peptides Spanning the Sequence of Hen Lysozyme. <i>Journal of Molecular Biology</i> , 1995, 252, 483-491.	4.2	121
58	Force mode atomic force microscopy as a tool for protein folding studies. <i>Analytica Chimica Acta</i> , 2003, 479, 87-105.	5.4	120
59	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.	2.5	120
60	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.	8.2	116
61	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.	8.2	112
62	Effects of hydration on the mechanical response of individual collagen fibrils. <i>Applied Physics Letters</i> , 2008, 92, .	3.3	111
63	Mechanical Resistance of Proteins Explained Using Simple Molecular Models. <i>Biophysical Journal</i> , 2006, 90, 287-297.	0.5	106
64	Fibril fragmentation in amyloid assembly and cytotoxicity. <i>Prion</i> , 2010, 4, 20-25.	1.8	106
65	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.	2.8	106
66	Amyloid Fibres: Inert End-Stage Aggregates or Key Players in Disease?. <i>Trends in Biochemical Sciences</i> , 2015, 40, 719-727.	7.5	100
67	Visualizing and trapping transient oligomers in amyloid assembly pathways. <i>Biophysical Chemistry</i> , 2021, 268, 106505.	2.8	97
68	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.	7.1	95
69	Probing the structure of folding intermediates. <i>Current Opinion in Structural Biology</i> , 1994, 4, 100-106.	5.7	94
70	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.	4.2	93
71	Fibril Growth Kinetics Reveal a Region of β 2-microglobulin Important for Nucleation and Elongation of Aggregation. <i>Journal of Molecular Biology</i> , 2008, 378, 251-263.	4.2	93
72	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. <i>Nature Chemical Biology</i> , 2011, 7, 730-739.	8.0	93

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73	Dynamics in the Unfolded State of \hat{I}^2 -microglobulin Studied by NMR. <i>Journal of Molecular Biology</i> , 2005, 346, 279-294.	4.2	92
74	Understanding the complex mechanisms of \hat{I}^2 -microglobulin amyloid assembly. <i>FEBS Journal</i> , 2011, 278, 3868-3883.	4.7	92
75	Hydrogen exchange properties of proteins in native and denatured states monitored by mass spectrometry and NMR. <i>Protein Science</i> , 1997, 6, 1316-1324.	7.6	90
76	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.	7.1	90
77	Energy landscapes of functional proteins are inherently risky. <i>Nature Chemical Biology</i> , 2014, 10, 884-891.	8.0	90
78	Two-way communication between SecY and SecA suggests a Brownian ratchet mechanism for protein translocation. <i>ELife</i> , 2016, 5, .	6.0	90
79	Engineering the surface properties of a human monoclonal antibody prevents self-association and rapid clearance in vivo. <i>Scientific Reports</i> , 2016, 6, 38644.	3.3	89
80	Role of the lipid bilayer in outer membrane protein folding in Gram-negative bacteria. <i>Journal of Biological Chemistry</i> , 2020, 295, 10340-10367.	3.4	88
81	Mechanisms of amyloid formation revealed by solution NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015, 88-89, 86-104.	7.5	85
82	De novo design of transmembrane \hat{I}^2 barrels. <i>Science</i> , 2021, 371, .	12.6	83
83	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	8.2	82
84	Magic Angle Spinning NMR Analysis of \hat{I}^2 -Microglobulin Amyloid Fibrils in Two Distinct Morphologies. <i>Journal of the American Chemical Society</i> , 2010, 132, 10414-10423.	13.7	79
85	A Generic Mechanism of \hat{I}^2 -Microglobulin Amyloid Assembly at Neutral pH Involving a Specific Proline Switch. <i>Journal of Molecular Biology</i> , 2009, 386, 1312-1326.	4.2	77
86	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.	7.1	77
87	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017, 39, 90-99.	6.1	77
88	Mechanically unfolding proteins: The effect of unfolding history and the supramolecular scaffold. <i>Protein Science</i> , 2009, 11, 2759-2765.	7.6	75
89	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	8.0	75
90	Amyloid plaques beyond $A\hat{I}^2$: a survey of the diverse modulators of amyloid aggregation. <i>Biophysical Reviews</i> , 2017, 9, 405-419.	3.2	74

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91	Role of the single disulphide bond of I ² -microglobulin in amyloidosis in vitro. <i>Protein Science</i> , 2001, 10, 1775-1784.	7.6	73
92	Globular Tetramers of I ² -Microglobulin Assemble into Elaborate Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2009, 389, 48-57.	4.2	73
93	Perturbing the folding energy landscape of the bacterial immunity protein Im7 by site-specific N-linked glycosylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22528-22533.	7.1	72
94	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.	8.2	71
95	Macromolecular Crowding Enhances the Detection of DNA and Proteins by a Solid-State Nanopore. <i>Nano Letters</i> , 2020, 20, 5553-5561.	9.1	71
96	Significant hydrogen exchange protection in GroEL-bound DHFR is maintained during iterative rounds of substrate cycling. <i>Protein Science</i> , 1996, 5, 2506-2513.	7.6	70
97	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.	4.2	70
98	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.	4.2	69
99	Intermolecular Alignment in I ² -Microglobulin Amyloid Fibrils. <i>Journal of the American Chemical Society</i> , 2010, 132, 17077-17079.	13.7	69
100	Mass spectrometry-enabled structural biology of membrane proteins. <i>Methods</i> , 2018, 147, 187-205.	3.8	69
101	Co-populated Conformational Ensembles of I ² -Microglobulin Uncovered Quantitatively by Electrospray Ionization Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 27069-27077.	3.4	68
102	Competition between Intramolecular and Intermolecular Interactions in an Amyloid-Forming Protein. <i>Journal of Molecular Biology</i> , 2009, 389, 776-786.	4.2	68
103	Substrate protein folds while it is bound to the ATP-independent chaperone Spy. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 53-58.	8.2	68
104	Semisynthesis of a Glycosylated Im7 Analogue for Protein Folding Studies. <i>Journal of the American Chemical Society</i> , 2005, 127, 12882-12889.	13.7	67
105	Thermodynamic Description of Polymorphism in Q- and N-Rich Peptide Aggregates Revealed by Atomistic Simulation. <i>Biophysical Journal</i> , 2009, 97, 1-11.	0.5	65
106	The mechanism of folding of Im7 reveals competition between functional and kinetic evolutionary constraints. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 318-324.	8.2	63
107	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2017, 429, 3776-3792.	4.2	63
108	Thermodynamic phase diagram of amyloid-I ² (16-22) peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2091-2096.	7.1	63

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109	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.	4.2	62
110	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.	4.2	62
111	Outer membrane protein folding from an energy landscape perspective. <i>BMC Biology</i> , 2017, 15, 123.	3.8	62
112	Amphipathic Polymers Enable the Study of Functional Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2012, 84, 9841-9847.	6.5	61
113	Amyloid Under the Atomic Force Microscope. <i>Protein and Peptide Letters</i> , 2006, 13, 261-270.	0.9	60
114	GroEL accelerates the refolding of hen lysozyme without changing its folding mechanism. <i>Nature Structural Biology</i> , 1999, 6, 683-690.	9.7	59
115	The Oligomeric State and Arrangement of the Active Bacterial Translocon. <i>Journal of Biological Chemistry</i> , 2011, 286, 4659-4669.	3.4	59
116	Far-UV Circular Dichroism Reveals a Conformational Switch in a Peptide Fragment from the .beta.-Sheet of Hen Lysozyme. <i>Biochemistry</i> , 1994, 33, 7345-7353.	2.5	58
117	Kinetic studies of β^2 -sheet protein folding. <i>Current Opinion in Structural Biology</i> , 1998, 8, 86-92.	5.7	58
118	Investigating the structural properties of amyloid-like fibrils formed in vitro from β^2 -microglobulin using limited proteolysis and electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1628-1636.	1.5	58
119	Amyloid fibril length distribution quantified by atomic force microscopy single-particle image analysis. <i>Protein Engineering, Design and Selection</i> , 2009, 22, 489-496.	2.1	58
120	A Common β^2 -Sheet Architecture Underlies in Vitro and in Vivo β^2 -Microglobulin Amyloid Fibrils. <i>Journal of Biological Chemistry</i> , 2008, 283, 17279-17286.	3.4	57
121	<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.	7.6	56
122	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.	4.2	55
123	Glimpses of the molecular mechanisms of β^2 -microglobulin fibril formation in vitro: Aggregation on a complex energy landscape. <i>FEBS Letters</i> , 2009, 583, 2623-2629.	2.8	55
124	Identification of a Mechanical Rheostat in the Hydrophobic Core of Protein L. <i>Journal of Molecular Biology</i> , 2009, 393, 237-248.	4.2	55
125	Stacked Sets of Parallel, In-register β^2 -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.	3.4	55
126	An Imaging and Systems Modeling Approach to Fibril Breakage Enables Prediction of Amyloid Behavior. <i>Biophysical Journal</i> , 2013, 105, 2811-2819.	0.5	55

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127	Visualization of Transient Protein-Protein Interactions that Promote or Inhibit Amyloid Assembly. <i>Molecular Cell</i> , 2014, 55, 214-226.	9.7	55
128	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015, 89, 13-21.	3.8	55
129	Separation of α 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.	1.5	54
130	Molecular insights into the surface-catalyzed secondary nucleation of amyloid- β (A β) Tj ETQq0 0 0 rgBT /Overlock 10 TF	10.3	54
131	The origin of the β -domain intermediate in the folding of hen lysozyme. <i>Journal of Molecular Biology</i> , 1998, 277, 997-1005.	4.2	53
132	Dynamic action of the Sec machinery during initiation, protein translocation and termination. <i>ELife</i> , 2018, 7, .	6.0	52
133	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.	2.8	52
134	Urea-Induced Unfolding of the Immunity Protein Im9 Monitored by spFRET. <i>Biophysical Journal</i> , 2006, 91, L42-L44.	0.5	50
135	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, 666-676.	2.5	50
136	Amphipols Outperform Dodecylmaltoside Micelles in Stabilizing Membrane Protein Structure in the Gas Phase. <i>Analytical Chemistry</i> , 2015, 87, 1118-1126.	6.5	50
137	ESI-IMS "MS: A method for rapid analysis of protein aggregation and its inhibition by small molecules. <i>Methods</i> , 2016, 95, 62-69.	3.8	50
138	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.	2.5	49
139	Viscoelastic Study of the Mechanical Unfolding of a Protein by AFM. <i>Biophysical Journal</i> , 2006, 91, L16-L18.	0.5	49
140	Towards an understanding of the structural molecular mechanism of α 2-microglobulin amyloid formation in vitro. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2005, 1753, 51-63.	2.3	48
141	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.	4.2	48
142	Insights into the consequences of co-polymerisation in the early stages of IAPP and A β peptide assembly from mass spectrometry. <i>Analyst</i> , The, 2015, 140, 6990-6999.	3.5	48
143	Atomic Details of the Interactions of Glycosaminoglycans with Amyloid- β Fibrils. <i>Journal of the American Chemical Society</i> , 2016, 138, 8328-8331.	13.7	48
144	Rapid Mapping of Protein Interactions Using Tag "Transfer Photocrosslinkers. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16688-16692.	13.8	48

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145	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. <i>Nature Communications</i> , 2020, 11, 2155.	12.8	48
146	Cooperative Elements in Protein Folding Monitored by Electrospray Ionization Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1995, 117, 7548-7549.	13.7	47
147	Structural and mechanistic consequences of polypeptide binding by GroEL. <i>Folding & Design</i> , 1997, 2, R93-R104.	4.5	47
148	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.	3.0	46
149	Potential human transmission of amyloid β^2 pathology: surveillance and risks. <i>Lancet Neurology</i> , The, 2020, 19, 872-878.	10.2	46
150	Trapping the On-pathway Folding Intermediate of Im7 at Equilibrium. <i>Journal of Molecular Biology</i> , 2004, 341, 215-226.	4.2	45
151	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.	4.2	45
152	The greek key protein apo-pseudoazurin folds through an obligate on-pathway intermediate 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 286, 1621-1632.	4.2	44
153	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.	3.5	44
154	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. <i>ELife</i> , 2019, 8, .	6.0	44
155	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.	0.5	43
156	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.	2.8	43
157	Assessing the causes and consequences of co-polymerization in amyloid formation. <i>Prion</i> , 2013, 7, 359-368.	1.8	42
158	Force-induced remodelling of proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2015, 30, 89-99.	5.7	42
159	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.	2.8	42
160	Comparison of the transition state ensembles for folding of Im7 and Im9 determined using all-atom molecular dynamics simulations with β value restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 513-525.	2.6	41
161	Secondary Structure in the Core of Amyloid Fibrils Formed from Human β^2 and its Truncated Variant β^2 . <i>Journal of the American Chemical Society</i> , 2014, 136, 6313-6325.	13.7	40
162	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.	4.2	39

#	ARTICLE	IF	CITATIONS
163	Production and Characterization of RNA Aptamers Specific for Amyloid Fibril Epitopes. <i>Journal of Biological Chemistry</i> , 2007, 282, 34500-34509.	3.4	37
164	HDX-ESI-MS reveals enhanced conformational dynamics of the amyloidogenic protein α 2-microglobulin upon release from the MHC-1. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 278-286.	2.8	37
165	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. <i>Chemical Science</i> , 2017, 8, 5030-5040.	7.4	37
166	Internal friction of single polypeptide chains at high stretch. <i>Faraday Discussions</i> , 2008, 139, 35.	3.2	36
167	Expanding the Repertoire of Amyloid Polymorphs by Co-polymerization of Related Protein Precursors. <i>Journal of Biological Chemistry</i> , 2013, 288, 7327-7337.	3.4	36
168	Synthesis, Characterization and Applications of a Perdeuterated Amphipol. <i>Journal of Membrane Biology</i> , 2014, 247, 909-924.	2.1	36
169	A near-native state on the slow refolding pathway of hen lysozyme. <i>Protein Science</i> , 1999, 8, 35-44.	7.6	35
170	Modulation of β -Amyloid Fibril Formation in Alzheimer's Disease by Microglia and Infection. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 609073.	2.9	35
171	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.	4.2	34
172	Structural insight into the formation of lipoprotein- β -barrel complexes. <i>Nature Chemical Biology</i> , 2020, 16, 1019-1025.	8.0	34
173	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.	4.2	33
174	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.	2.5	33
175	GroEL: More than Just a Folding Cage. <i>Cell</i> , 2006, 125, 831-833.	28.9	33
176	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.	3.8	33
177	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.	2.8	33
178	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <i>Communications Biology</i> , 2020, 3, 766.	4.4	32
179	A study of D52S hen lysozyme-G1cNAc oligosaccharide complexes by NMR spectroscopy and electrospray mass spectrometry. <i>FEBS Letters</i> , 1992, 296, 153-157.	2.8	31
180	Accurate Use of Single Molecule Fluorescence Correlation Spectroscopy to Determine Molecular Diffusion Times. <i>Single Molecules</i> , 2001, 2, 177-181.	0.9	31

#	ARTICLE	IF	CITATIONS
181	The Effect of Protein Complexation on the Mechanical Stability of Im9. <i>Biophysical Journal</i> , 2007, 92, L79-L81.	0.5	31
182	Î²2-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.	3.4	31
183	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015, 89, 38-44.	3.8	31
184	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.	9.7	31
185	Using chimeric immunity proteins to explore the energy landscape for Î±-helical protein folding. <i>Journal of Molecular Biology</i> , 2001, 307, 393-405.	4.2	30
186	Investigation into the Role of Macrophages in the Formation and Degradation of Î²2-Microglobulin Amyloid Fibrils. <i>Journal of Biological Chemistry</i> , 2007, 282, 29691-29700.	3.4	30
187	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.	4.2	30
188	Î²2-Microglobulin Amyloid Fibril-Induced Membrane Disruption Is Enhanced by Endosomal Lipids and Acidic pH. <i>PLoS ONE</i> , 2014, 9, e104492.	2.5	30
189	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.	1.5	30
190	A Population Shift between Sparsely Populated Folding Intermediates Determines Amyloidogenicity. <i>Journal of the American Chemical Society</i> , 2016, 138, 6271-6280.	13.7	29
191	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 8844-8852.	6.5	28
192	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.	3.7	27
193	Conformational Properties of the Unfolded State of Im7 in Nondenaturing Conditions. <i>Journal of Molecular Biology</i> , 2012, 416, 300-318.	4.2	27
194	Aggregation Modulators Interfere with Membrane Interactions of Î²2-Microglobulin Fibrils. <i>Biophysical Journal</i> , 2013, 105, 745-755.	0.5	27
195	Using protein engineering to understand and modulate aggregation. <i>Current Opinion in Structural Biology</i> , 2020, 60, 157-166.	5.7	27
196	A partially folded intermediate species of the Î²-sheet protein apo-pseudoazurin is trapped during proline-limited folding. <i>Protein Science</i> , 2001, 10, 1216-1224.	7.6	26
197	Site-Specific Identification of an Î² Fibril Heparin Interaction Site by Using Solid-State NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 13140-13143.	13.8	26
198	A Force-Activated Trip Switch Triggers Rapid Dissociation of a Colicin from Its Immunity Protein. <i>PLoS Biology</i> , 2013, 11, e1001489.	5.6	26

#	ARTICLE	IF	CITATIONS
199	Unfolding dynamics of proteins under applied force. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2003, 361, 713-730.	3.4	25
200	Structure and Dynamics of Oligomeric Intermediates in β^2 -Microglobulin Self-Assembly. <i>Biophysical Journal</i> , 2011, 101, 1238-1247.	0.5	25
201	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.	3.4	25
202	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.	4.2	24
203	The role of conformational flexibility in β^2 microglobulin amyloid fibril formation at neutral pH. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1783-1792.	1.5	24
204	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.	2.5	24
205	Molecular Origins of the Compatibility between Glycosaminoglycans and β^2 40 Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2017, 429, 2449-2462.	4.2	23
206	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly. <i>Nature Communications</i> , 2022, 13, 1040.	12.8	23
207	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
208	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.	4.2	22
209	An in vivo platform to select and evolve aggregation-resistant proteins. <i>Nature Communications</i> , 2020, 11, 1816.	12.8	22
210	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. <i>Nature Communications</i> , 2021, 12, 4174.	12.8	22
211	Partially Unfolded Species Populated during Equilibrium Denaturation of the β^2 -Sheet Protein Y74W Apo-Pseudoazurin. <i>Biochemistry</i> , 2000, 39, 5672-5682.	2.5	21
212	Covalent Cross-Linking within Supramolecular Peptide Structures. <i>Analytical Chemistry</i> , 2012, 84, 6790-6797.	6.5	21
213	The structure and dynamics in solution of Cu(I) pseudoazurin from <i>Paracoccus pantotrophus</i> . <i>Protein Science</i> , 2000, 9, 846-858.	7.6	20
214	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.	4.2	20
215	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.	3.4	20
216	Trifluoromethyldiazirine: an effective photo-induced cross-linking probe for exploring amyloid formation. <i>Chemical Communications</i> , 2008, , 5728.	4.1	19

#	ARTICLE	IF	CITATIONS
217	Extracellular matrix components modulate different stages in β 2-microglobulin amyloid formation. <i>Journal of Biological Chemistry</i> , 2019, 294, 9392-9401.	3.4	19
218	Modulation of Amyloidogenic Protein Self-Assembly Using Tethered Small Molecules. <i>Journal of the American Chemical Society</i> , 2020, 142, 20845-20854.	13.7	19
219	Desolvation and Development of Specific Hydrophobic Core Packing during Im7 Folding. <i>Journal of Molecular Biology</i> , 2010, 396, 1329-1345.	4.2	18
220	Single-Molecule Studies of the Im7 Folding Landscape. <i>Journal of Molecular Biology</i> , 2010, 398, 132-145.	4.2	18
221	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.	3.4	18
222	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. <i>Analytical Chemistry</i> , 2019, 91, 15163-15170.	6.5	18
223	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.	1.3	15
224	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.	1.5	15
225	A growing toolbox of techniques for studying β -barrel outer membrane protein folding and biogenesis. <i>Biochemical Society Transactions</i> , 2016, 44, 802-809.	3.4	15
226	Using extensional flow to reveal diverse aggregation landscapes for three IgG1 molecules. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1216-1225.	3.3	15
227	Collagen I Weakly Interacts with the β -Sheets of β 2-Microglobulin and Enhances Conformational Exchange To Induce Amyloid Formation. <i>Journal of the American Chemical Society</i> , 2020, 142, 1321-1331.	13.7	15
228	AlphaFold: A Special Issue and A Special Time for Protein Science. <i>Journal of Molecular Biology</i> , 2021, 433, 167231.	4.2	15
229	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.	2.1	14
230	Extraction of Accurate Biomolecular Parameters from Single-Molecule Force Spectroscopy Experiments. <i>ACS Nano</i> , 2015, 9, 1315-1324.	14.6	14
231	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.	3.4	14
232	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
233	Probing Dynamics within Amyloid Fibrils Using a Novel Capping Method. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 5705-5707.	13.8	12
234	Spot the Difference: Function versus Toxicity in Amyloid Fibrils. <i>Trends in Biochemical Sciences</i> , 2020, 45, 635-636.	7.5	12

#	ARTICLE	IF	CITATIONS
235	High-throughput directed evolution: a golden era for protein science. <i>Trends in Chemistry</i> , 2022, 4, 378-391.	8.5	12
236	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. <i>Communications Biology</i> , 2022, 5, .	4.4	12
237	Phosphorylation as a Tool To Modulate Aggregation Propensity and To Predict Fibril Architecture. <i>ChemBioChem</i> , 2012, 13, 271-281.	2.6	11
238	MpLUL-multi: Software for Calculation of Amyloid Fibril Mass per Unit Length from TB-TEM Images. <i>Scientific Reports</i> , 2016, 6, 21078.	3.3	11
239	Sulfate-Induced Effects in the On-Pathway Intermediate of the Bacterial Immunity Protein Im7*. <i>Biochemistry</i> , 2006, 45, 2274-2282.	2.5	10
240	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.	0.9	10
241	Brazilin Removes Toxic Alpha-Synuclein and Seeding Competent Assemblies from Parkinson Brain by Altering Conformational Equilibrium. <i>Journal of Molecular Biology</i> , 2021, 433, 166878.	4.2	10
242	Amino Acid Insertion Reveals a Necessary Three-Helical Intermediate in the Folding Pathway of the Colicin E7 Immunity Protein Im7. <i>Journal of Molecular Biology</i> , 2009, 392, 1074-1086.	4.2	9
243	Generating Ensembles of Dynamic Misfolding Proteins. <i>Frontiers in Neuroscience</i> , 2022, 16, 881534.	2.8	9
244	Design and synthesis of cysteine-specific labels for photo-crosslinking studies. <i>RSC Advances</i> , 2019, 9, 7610-7614.	3.6	8
245	Trigger factor both holds and folds its client proteins. <i>Nature Communications</i> , 2022, 13, .	12.8	8
246	[24] Probing conformations of GroEL-bound substrate proteins by mass spectrometry. <i>Methods in Enzymology</i> , 1998, 290, 296-313.	1.0	7
247	Distinguishing Closely Related Amyloid Precursors Using an RNA Aptamer. <i>Journal of Biological Chemistry</i> , 2014, 289, 26859-26871.	3.4	7
248	Production of ¹⁵ N-labelled hen egg white lysozyme using <i>Aspergillus niger</i> . <i>Biotechnology Letters</i> , 1992, 14, 897-902.	2.2	6
249	The Role of High-Dimensional Diffusive Search, Stabilization, and Frustration in Protein Folding. <i>Biophysical Journal</i> , 2014, 106, 1729-1740.	0.5	6
250	A comparison of the folding characteristics of free and ribosome-attached polypeptide chains using limited proteolysis and mass spectrometry. <i>Protein Science</i> , 2015, 24, 1282-1291.	7.6	6
251	A peptide-display protein scaffold to facilitate single molecule force studies of aggregation-prone peptides. <i>Protein Science</i> , 2018, 27, 1205-1217.	7.6	6
252	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie</i> , 2018, 130, 16930-16934.	2.0	6

#	ARTICLE	IF	CITATIONS
253	Roll out the barrel! Outer membrane tension resolves an unexpected folding intermediate. <i>Cell</i> , 2022, 185, 1107-1109.	28.9	6
254	Avoidance of Epimerization in the Synthesis of Peptide Thioesters Using Fmoc Protection. <i>Synlett</i> , 2007, 2007, 2517-2520.	1.8	5
255	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.	7.6	5
256	The uniqueness of flow in probing the aggregation behavior of clinically relevant antibodies. <i>Engineering Reports</i> , 2020, 2, e12147.	1.7	5
257	Dissecting key residues in folding and stability of the bacterial immunity protein 7. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 517-523.	2.1	4
258	How TriC Folds Tricky Proteins. <i>Cell</i> , 2014, 159, 1251-1252.	28.9	4
259	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.	1.0	4
260	Structural insights into peptide self-assembly using photo-induced crosslinking experiments and discontinuous molecular dynamics. <i>AIChE Journal</i> , 2021, 67, e17101.	3.6	4
261	Global Proteotoxicity Caused by Human β 2 Microglobulin Variants Impairs the Unfolded Protein Response in <i>C. elegans</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 10752.	4.1	4
262	Investigation of D76N β 2-Microglobulin Using Protein Footprinting and Structural Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1583-1592.	2.8	3
263	β 2-Microglobulin and Dialysis-Related Amyloidosis. , 2007, , 217-239.		2
264	Protein Misfolding and Toxicity in Dialysis-Related Amyloidosis. , 2012, , 377-405.		2
265	The Dynamical Response of Proteins Under Force. , 2008, , 205-249.		1
266	Dynamics of Membrane Proteins Monitored by Single-Molecule Fluorescence Across Multiple Timescales. <i>Methods in Molecular Biology</i> , 2020, 2168, 273-297.	0.9	1
267	Determining the Free Energies of Outer Membrane Proteins in Lipid Bilayers. <i>Methods in Molecular Biology</i> , 2020, 2168, 217-232.	0.9	1
268	Insights into the molecular mechanisms of protein folding and misfolding. , 2002, , 352-354.		1
269	Ribosome-mediated refolding of partially-unfolded ricin A-chain. <i>Biochemical Society Transactions</i> , 2000, 28, A68-A68.	3.4	0
270	From native state to amyloid; an investigation into partial unfolding of β 2-microglobulin. <i>Biochemical Society Transactions</i> , 2000, 28, A68-A68.	3.4	0

#	ARTICLE	IF	CITATIONS
271	Partially folded states in helical protein folding. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	3.4	0
272	Towards single molecule unfolding of proteins using AFM and its observation using fluorescence. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	3.4	0
273	Unfolding of the β -sheet Protein Y74W Apo-pseudoazurin: Evidence of an Equilibrium Intermediate Species. <i>Biochemical Society Transactions</i> , 2000, 28, A69-A69.	3.4	0
274	Exploring the folding landscape of alpha helical proteins. <i>Biochemical Society Transactions</i> , 2000, 28, A70-A70.	3.4	0
275	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.	3.4	0
276	Linked Landscapes and Conformational Conversions: How Proteins Fold and Misfold. <i>Biological and Medical Physics Series</i> , 2012, , 1-16.	0.4	0
277	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
278	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.	4.6	0
279	Homage to Chris Dobson. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 137.	3.5	0
280	Finding the sweet spot for chaperone activity. <i>Nature Chemistry</i> , 2021, 13, 397-399.	13.6	0
281	Biophysical Studies of Amyloid Formation and Its Inhibition. <i>FASEB Journal</i> , 2015, 29, 491.1.	0.5	0
282	Professor Sir Christopher Martin Dobson (1949–2019). <i>Biochemist</i> , 2019, 41, 45-45.	0.5	0