

Sheena E Radford

List of Publications by Year in descending order

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282
papers

23,440
citations

6592

79
h-index

10127

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.	13.7	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.	3.3	800
3	The folding of hen lysozyme involves partially structured intermediates and multiple pathways. <i>Nature</i> , 1992, 358, 302-307.	13.7	771
4	A new era for understanding amyloid structures and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 755-773.	16.1	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.	6.6	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.	3.3	414
7	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
8	Understanding how proteins fold: the lysozyme story so far. <i>Trends in Biochemical Sciences</i> , 1994, 19, 31-37.	3.7	353
9	Folding versus aggregation: Polypeptide conformations on competing pathways. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 100-117.	1.4	352
10	Fibril Fragmentation Enhances Amyloid Cytotoxicity. <i>Journal of Biological Chemistry</i> , 2009, 284, 34272-34282.	1.6	326
11	Partially Unfolded States of β 2-Microglobulin and Amyloid Formation in Vitro. <i>Biochemistry</i> , 2000, 39, 8735-8746.	1.2	321
12	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
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.	0.5	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.	3.6	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.	1.2	284
16	A Diversity of Assembly Mechanisms of a Generic Amyloid Fold. <i>Molecular Cell</i> , 2011, 43, 8-18.	4.5	266
17	Demonstration by NMR of folding domains in lysozyme. <i>Nature</i> , 1991, 349, 633-636.	13.7	265
18	The Yin and Yang of protein folding. <i>FEBS Journal</i> , 2005, 272, 5962-5970.	2.2	259

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19	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
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.	2.0	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.	3.6	223
22	Conformation of GroEL-bound β -lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994, 372, 646-651.	13.7	221
23	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
24	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
25	Intermediates: ubiquitous species on folding energy landscapes?. <i>Current Opinion in Structural Biology</i> , 2007, 17, 30-37.	2.6	196
26	β 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
27	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
28	Structural properties of an amyloid precursor of β 2-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 20 ^â 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
30	Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996, 10, 93-101.	0.2	175
31	Engineering of peptide β -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.	3.3	162
33	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
34	Conformational Conversion during Amyloid Formation at Atomic Resolution. <i>Molecular Cell</i> , 2011, 41, 161-172.	4.5	160
35	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Proceeds through a Concerted β Strand Displacement Mechanism. <i>Molecular Cell</i> , 2006, 22, 831-842.	4.5	159
36	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

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37	Lateral opening in the intact β -barrel assembly machinery captured by cryo-EM. Nature Communications, 2016, 7, 12865.	5.8	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.	0.2	154
40	Tertiary Interactions in the Folding Pathway of Hen Lysozyme: Kinetic Studies Using Fluorescent Probes. Biochemistry, 1994, 33, 5212-5220.	1.2	151
41	Amyloid structures: much more than just a cross- β fold. Current Opinion in Structural Biology, 2020, 60, 7-16.	2.6	150
42	Optimizing Protein Stability In Vivo. Molecular Cell, 2009, 36, 861-871.	4.5	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.	3.3	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.	2.0	145
46	Tuning the Elastic Modulus of Hydrated Collagen Fibrils. Biophysical Journal, 2009, 97, 2985-2992.	0.2	143
47	The Refolding of Human Lysozyme: A Comparison with the Structurally Homologous Hen Lysozyme. Biochemistry, 1994, 33, 5867-5876.	1.2	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.	2.0	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.	2.0	137
51	The Effect of Core Destabilization on the Mechanical Resistance of I27. Biophysical Journal, 2002, 83, 458-472.	0.2	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.	3.3	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.	23.0	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.	2.0	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.	5.8	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.	1.2	122
57	Conformational Properties of Four Peptides Spanning the Sequence of Hen Lysozyme. <i>Journal of Molecular Biology</i> , 1995, 252, 483-491.	2.0	121
58	Force mode atomic force microscopy as a tool for protein folding studies. <i>Analytica Chimica Acta</i> , 2003, 479, 87-105.	2.6	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.	1.2	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.	3.6	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.	3.6	112
62	Effects of hydration on the mechanical response of individual collagen fibrils. <i>Applied Physics Letters</i> , 2008, 92, .	1.5	111
63	Mechanical Resistance of Proteins Explained Using Simple Molecular Models. <i>Biophysical Journal</i> , 2006, 90, 287-297.	0.2	106
64	Fibril fragmentation in amyloid assembly and cytotoxicity. <i>Prion</i> , 2010, 4, 20-25.	0.9	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.	1.3	106
66	Amyloid Fibres: Inert End-Stage Aggregates or Key Players in Disease?. <i>Trends in Biochemical Sciences</i> , 2015, 40, 719-727.	3.7	100
67	Visualizing and trapping transient oligomers in amyloid assembly pathways. <i>Biophysical Chemistry</i> , 2021, 268, 106505.	1.5	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.	3.3	95
69	Probing the structure of folding intermediates. <i>Current Opinion in Structural Biology</i> , 1994, 4, 100-106.	2.6	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.	2.0	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.	2.0	93
72	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. <i>Nature Chemical Biology</i> , 2011, 7, 730-739.	3.9	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.	2.0	92
74	Understanding the complex mechanisms of \hat{I}^2 -microglobulin amyloid assembly. <i>FEBS Journal</i> , 2011, 278, 3868-3883.	2.2	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.	3.1	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.	3.3	90
77	Energy landscapes of functional proteins are inherently risky. <i>Nature Chemical Biology</i> , 2014, 10, 884-891.	3.9	90
78	Two-way communication between SecY and SecA suggests a Brownian ratchet mechanism for protein translocation. <i>ELife</i> , 2016, 5, .	2.8	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.	1.6	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.	1.6	88
81	Mechanisms of amyloid formation revealed by solution NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015, 88-89, 86-104.	3.9	85
82	De novo design of transmembrane \hat{I}^2 barrels. <i>Science</i> , 2021, 371, .	6.0	83
83	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	3.6	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.	6.6	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.	2.0	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.	3.3	77
87	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017, 39, 90-99.	2.8	77
88	Mechanically unfolding proteins: The effect of unfolding history and the supramolecular scaffold. <i>Protein Science</i> , 2009, 11, 2759-2765.	3.1	75
89	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	3.9	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.	1.5	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.	3.1	73
92	Globular Tetramers of I ² -Microglobulin Assemble into Elaborate Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2009, 389, 48-57.	2.0	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.	3.3	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.	3.6	71
95	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
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.	3.1	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.	2.0	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.	2.0	69
99	Intermolecular Alignment in I ² -Microglobulin Amyloid Fibrils. <i>Journal of the American Chemical Society</i> , 2010, 132, 17077-17079.	6.6	69
100	Mass spectrometry-enabled structural biology of membrane proteins. <i>Methods</i> , 2018, 147, 187-205.	1.9	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.	1.6	68
102	Competition between Intramolecular and Intermolecular Interactions in an Amyloid-Forming Protein. <i>Journal of Molecular Biology</i> , 2009, 389, 776-786.	2.0	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.	3.6	68
104	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
105	Thermodynamic Description of Polymorphism in Q- and N-Rich Peptide Aggregates Revealed by Atomistic Simulation. <i>Biophysical Journal</i> , 2009, 97, 1-11.	0.2	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.	3.6	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.	2.0	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.	3.3	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.	2.0	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.	2.0	62
111	Outer membrane protein folding from an energy landscape perspective. <i>BMC Biology</i> , 2017, 15, 123.	1.7	62
112	Amphipathic Polymers Enable the Study of Functional Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2012, 84, 9841-9847.	3.2	61
113	Amyloid Under the Atomic Force Microscope. <i>Protein and Peptide Letters</i> , 2006, 13, 261-270.	0.4	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.	1.6	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.	1.2	58
117	Kinetic studies of β -sheet protein folding. <i>Current Opinion in Structural Biology</i> , 1998, 8, 86-92.	2.6	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.	0.7	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.	1.0	58
120	A Common β -Sheet Architecture Underlies in Vitro and in Vivo β 2-Microglobulin Amyloid Fibrils. <i>Journal of Biological Chemistry</i> , 2008, 283, 17279-17286.	1.6	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.	3.1	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.	2.0	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.	1.3	55
124	Identification of a Mechanical Rheostat in the Hydrophobic Core of Protein L. <i>Journal of Molecular Biology</i> , 2009, 393, 237-248.	2.0	55
125	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
126	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

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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.	4.5	55
128	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015, 89, 13-21.	1.9	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.	0.7	54
130	Molecular insights into the surface-catalyzed secondary nucleation of amyloid- β $\times 40$ ($A\beta$) Tj ETQq0 0 0,rgBT /Overlock 10 TF	4.7	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.	2.0	53
132	Dynamic action of the Sec machinery during initiation, protein translocation and termination. <i>ELife</i> , 2018, 7, .	2.8	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.	1.4	52
134	Urea-Induced Unfolding of the Immunity Protein Im9 Monitored by spFRET. <i>Biophysical Journal</i> , 2006, 91, L42-L44.	0.2	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.	1.2	50
136	Amphipols Outperform Dodecylmaltoside Micelles in Stabilizing Membrane Protein Structure in the Gas Phase. <i>Analytical Chemistry</i> , 2015, 87, 1118-1126.	3.2	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.	1.9	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.	1.2	49
139	Viscoelastic Study of the Mechanical Unfolding of a Protein by AFM. <i>Biophysical Journal</i> , 2006, 91, L16-L18.	0.2	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.	1.1	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.	2.0	48
142	Insights into the consequences of co-polymerisation in the early stages of IAPP and $A\beta$ peptide assembly from mass spectrometry. <i>Analyst, The</i> , 2015, 140, 6990-6999.	1.7	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.	6.6	48
144	Rapid Mapping of Protein Interactions Using Tag "Transfer Photocrosslinkers. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 16688-16692.	7.2	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.	5.8	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.	6.6	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.	1.4	46
149	Potential human transmission of amyloid β^2 pathology: surveillance and risks. <i>Lancet Neurology</i> , The, 2020, 19, 872-878.	4.9	46
150	Trapping the On-pathway Folding Intermediate of Im7 at Equilibrium. <i>Journal of Molecular Biology</i> , 2004, 341, 215-226.	2.0	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.	2.0	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.	2.0	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.	1.6	44
154	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. <i>ELife</i> , 2019, 8, .	2.8	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.	0.2	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.	1.2	43
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