

Sheena E Radford

List of Publications by Year in descending order

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Version: 2024-02-01

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	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly. Nature Communications, 2022, 13, 1040.	12.8	23
2	Roll out the barrel! Outer membrane tension resolves an unexpected folding intermediate. Cell, 2022, 185, 1107-1109.	28.9	6
3	Generating Ensembles of Dynamic Misfolding Proteins. Frontiers in Neuroscience, 2022, 16, 881534.	2.8	9
4	High-throughput directed evolution: a golden era for protein science. Trends in Chemistry, 2022, 4, 378-391.	8.5	12
5	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. Communications Biology, 2022, 5, .	4.4	12
6	Trigger factor both holds and folds its client proteins. Nature Communications, 2022, 13, .	12.8	8
7	Visualizing and trapping transient oligomers in amyloid assembly pathways. Biophysical Chemistry, 2021, 268, 106505.	2.8	97
8	Structural insights into peptide self-assembly using photo-induced crosslinking experiments and discontinuous molecular dynamics. AICHE Journal, 2021, 67, e17101.	3.6	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.	47.7	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.	2.8	3
11	De novo design of transmembrane β barrels. Science, 2021, 371, .	12.6	83
12	Finding the sweet spot for chaperone activity. Nature Chemistry, 2021, 13, 397-399.	13.6	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.	4.2	10
14	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. Nature Communications, 2021, 12, 4174.	12.8	22
15	AlphaFold: A Special Issue and A Special Time for Protein Science. Journal of Molecular Biology, 2021, 433, 167231.	4.2	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.	4.1	4
17	Amyloid structures: much more than just a cross- β fold. Current Opinion in Structural Biology, 2020, 60, 7-16.	5.7	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.	13.7	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.	3.4	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.	2.9	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.	2.8	52
22	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
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.	8.2	71
24	Potential human transmission of amyloid β pathology: surveillance and risks. <i>Lancet Neurology</i> , The, 2020, 19, 872-878.	10.2	46
25	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <i>Communications Biology</i> , 2020, 3, 766.	4.4	32
26	The uniqueness of flow in probing the aggregation behavior of clinically relevant antibodies. <i>Engineering Reports</i> , 2020, 2, e12147.	1.7	5
27	Spot the Difference: Function versus Toxicity in Amyloid Fibrils. <i>Trends in Biochemical Sciences</i> , 2020, 45, 635-636.	7.5	12
28	Structural insight into the formation of lipoprotein- β -barrel complexes. <i>Nature Chemical Biology</i> , 2020, 16, 1019-1025.	8.0	34
29	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
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.	7.6	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.	8.2	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.	3.4	88
33	Using protein engineering to understand and modulate aggregation. <i>Current Opinion in Structural Biology</i> , 2020, 60, 157-166.	5.7	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.	12.8	48
35	An in vivo platform to select and evolve aggregation-resistant proteins. <i>Nature Communications</i> , 2020, 11, 1816.	12.8	22
36	Dynamics of Membrane Proteins Monitored by Single-Molecule Fluorescence Across Multiple Timescales. <i>Methods in Molecular Biology</i> , 2020, 2168, 273-297.	0.9	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.	0.9	1
38	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. <i>Analytical Chemistry</i> , 2019, 91, 15163-15170.	6.5	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.	7.1	63
40	Molecular insights into the surface-catalyzed secondary nucleation of amyloid- β ($A\beta$) Tj ETQq0 0 0 rgBT /Overlock 10 TF	10.3	54
41	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
42	Design and synthesis of cysteine-specific labels for photo-crosslinking studies. <i>RSC Advances</i> , 2019, 9, 7610-7614.	3.6	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.	9.7	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.	4.2	22
45	Homage to Chris Dobson. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 137.	3.5	0
46	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. <i>ELife</i> , 2019, 8, .	6.0	44
47	Professor Sir Christopher Martin Dobson (1949-2019). <i>Biochemist</i> , 2019, 41, 45-45.	0.5	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.	7.6	6
49	Mass spectrometry-enabled structural biology of membrane proteins. <i>Methods</i> , 2018, 147, 187-205.	3.8	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.	3.4	20
51	Using extensional flow to reveal diverse aggregation landscapes for three IgG1 molecules. <i>Biotechnology and Bioengineering</i> , 2018, 115, 1216-1225.	3.3	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.	1.0	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.	2.8	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.	13.8	48
56	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie</i> , 2018, 130, 16930-16934.	2.0	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.	4.6	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.	12.8	124
59	A new era for understanding amyloid structures and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 755-773.	37.0	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.	3.4	18
61	Dynamic action of the Sec machinery during initiation, protein translocation and termination. <i>ELife</i> , 2018, 7, .	6.0	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.	7.1	77
63	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. <i>Chemical Science</i> , 2017, 8, 5030-5040.	7.4	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.	2.8	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.	4.2	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.	6.5	28
67	Amyloid plaques beyond A β : a survey of the diverse modulators of amyloid aggregation. <i>Biophysical Reviews</i> , 2017, 9, 405-419.	3.2	74
68	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017, 39, 90-99.	6.1	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.	4.2	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.	2.8	33
71	Outer membrane protein folding from an energy landscape perspective. <i>BMC Biology</i> , 2017, 15, 123.	3.8	62
72	Two-way communication between SecY and SecA suggests a Brownian ratchet mechanism for protein translocation. <i>ELife</i> , 2016, 5, .	6.0	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.	3.3	89
74	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
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.	3.4	15
76	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	8.2	82
77	Lateral opening in the intact β -barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016, 7, 12865.	12.8	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.	3.3	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.	13.7	48
80	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	8.0	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.	8.2	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.	4.2	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.	0.9	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.	3.8	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.	7.6	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.	1.5	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.	2.5	50
88	Amphipols Outperform Dodecylmaltoside Micelles in Stabilizing Membrane Protein Structure in the Gas Phase. <i>Analytical Chemistry</i> , 2015, 87, 1118-1126.	6.5	50
89	Extraction of Accurate Biomolecular Parameters from Single-Molecule Force Spectroscopy Experiments. <i>ACS Nano</i> , 2015, 9, 1315-1324.	14.6	14
90	Mechanisms of amyloid formation revealed by solution NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015, 88-89, 86-104.	7.5	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.	3.5	48
92	Force-induced remodelling of proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2015, 30, 89-99.	5.7	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.	7.1	95
94	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015, 89, 38-44.	3.8	31
95	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015, 89, 13-21.	3.8	55
96	Amyloid Fibrils: Inert End-Stage Aggregates or Key Players in Disease?. <i>Trends in Biochemical Sciences</i> , 2015, 40, 719-727.	7.5	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.	3.8	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.	13.6	255
99	Biophysical Studies of Amyloid Formation and Its Inhibition. <i>FASEB Journal</i> , 2015, 29, 491.1.	0.5	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.	2.5	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.	3.4	31
102	Distinguishing Closely Related Amyloid Precursors Using an RNA Aptamer. <i>Journal of Biological Chemistry</i> , 2014, 289, 26859-26871.	3.4	7
103	How TriC Folds Tricky Proteins. <i>Cell</i> , 2014, 159, 1251-1252.	28.9	4
104	Energy landscapes of functional proteins are inherently risky. <i>Nature Chemical Biology</i> , 2014, 10, 884-891.	8.0	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.	9.7	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.	13.7	158
108	Synthesis, Characterization and Applications of a Perdeuterated Amphipol. <i>Journal of Membrane Biology</i> , 2014, 247, 909-924.	2.1	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.	3.4	25
110	Secondary Structure in the Core of Amyloid Fibrils Formed from Human β_{2m} and its Truncated Variant I ^N 6. <i>Journal of the American Chemical Society</i> , 2014, 136, 6313-6325.	13.7	40
111	The Role of High-Dimensional Diffusive Search, Stabilization, and Frustration in Protein Folding. <i>Biophysical Journal</i> , 2014, 106, 1729-1740.	0.5	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.	3.0	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.	1.5	15
115	Conformational dynamics is more important than helical propensity for the folding of the all β -helical protein Im7. <i>Protein Science</i> , 2013, 22, 1722-1738.	7.6	5
116	An Imaging and Systems Modeling Approach to Fibril Breakage Enables Prediction of Amyloid Behavior. <i>Biophysical Journal</i> , 2013, 105, 2811-2819.	0.5	55
117	Aggregation Modulators Interfere with Membrane Interactions of β_2 -Microglobulin Fibrils. <i>Biophysical Journal</i> , 2013, 105, 745-755.	0.5	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.	4.2	45
119	Assessing the causes and consequences of co-polymerization in amyloid formation. <i>Prion</i> , 2013, 7, 359-368.	1.8	42
120	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
121	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
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.	7.1	162
123	Site-Specific Identification of an $A\beta$ Fibril-Heparin Interaction Site by Using Solid-State NMR Spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 13140-13143.	13.8	26
124	Covalent Cross-Linking within Supramolecular Peptide Structures. <i>Analytical Chemistry</i> , 2012, 84, 6790-6797.	6.5	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.	4.2	24
126	Conformational Properties of the Unfolded State of Im7 in Nondenaturing Conditions. <i>Journal of Molecular Biology</i> , 2012, 416, 300-318.	4.2	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.	0.5	43
128	Amphipathic Polymers Enable the Study of Functional Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2012, 84, 9841-9847.	6.5	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.	7.6	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.	1.5	24
131	Linked Landscapes and Conformational Conversions: How Proteins Fold and Misfold. <i>Biological and Medical Physics Series</i> , 2012, , 1-16.	0.4	0
132	Phosphorylation as a Tool To Modulate Aggregation Propensity and To Predict Fibril Architecture. <i>ChemBioChem</i> , 2012, 13, 271-281.	2.6	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.	2.8	106
135	Structure and Dynamics of Oligomeric Intermediates in β 2-Microglobulin Self-Assembly. <i>Biophysical Journal</i> , 2011, 101, 1238-1247.	0.5	25
136	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. <i>Nature Chemical Biology</i> , 2011, 7, 730-739.	8.0	93
137	Conformational Conversion during Amyloid Formation at Atomic Resolution. <i>Molecular Cell</i> , 2011, 41, 161-172.	9.7	160
138	A Diversity of Assembly Mechanisms of a Generic Amyloid Fold. <i>Molecular Cell</i> , 2011, 43, 8-18.	9.7	266
139	Understanding the complex mechanisms of β -microglobulin amyloid assembly. <i>FEBS Journal</i> , 2011, 278, 3868-3883.	4.7	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.	2.1	4
141	The Oligomeric State and Arrangement of the Active Bacterial Translocon. <i>Journal of Biological Chemistry</i> , 2011, 286, 4659-4669.	3.4	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.	2.5	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.	3.4	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.	7.1	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.	7.1	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.	7.1	147
147	Fibril fragmentation in amyloid assembly and cytotoxicity. Prion, 2010, 4, 20-25.	1.8	106
148	Intermolecular Alignment in β^2 -Microglobulin Amyloid Fibrils. Journal of the American Chemical Society, 2010, 132, 17077-17079.	13.7	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.	13.7	79
150	Desolvation and Development of Specific Hydrophobic Core Packing during Im7 Folding. Journal of Molecular Biology, 2010, 396, 1329-1345.	4.2	18
151	Single-Molecule Studies of the Im7 Folding Landscape. Journal of Molecular Biology, 2010, 398, 132-145.	4.2	18
152	Amyloid fibril length distribution quantified by atomic force microscopy single-particle image analysis. Protein Engineering, Design and Selection, 2009, 22, 489-496.	2.1	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.	2.8	55
154	Probing Dynamics within Amyloid Fibrils Using a Novel Capping Method. Angewandte Chemie - International Edition, 2009, 48, 5705-5707.	13.8	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.	8.2	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.	8.2	223
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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.	4.2	77
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