

Sheena E Radford

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

285
papers

19,889
citations

74
h-index

131
g-index

302
ext. papers

21,852
ext. citations

8.7
avg, IF

6.93
L-index

#	Paper	IF	Citations
285	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly.. <i>Nature Communications</i> , 2022 , 13, 1040	17.4	2
284	Generating Ensembles of Dynamic Misfolding Proteins.. <i>Frontiers in Neuroscience</i> , 2022 , 16, 881534	5.1	1
283	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. <i>Communications Biology</i> , 2022 , 5,	6.7	2
282	Global Proteotoxicity Caused by Human β Microglobulin Variants Impairs the Unfolded Protein Response in. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
281	Finding the sweet spot for chaperone activity. <i>Nature Chemistry</i> , 2021 , 13, 397-399	17.6	
280	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	6.5	3
279	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. <i>Nature Communications</i> , 2021 , 12, 4174	17.4	4
278	Visualizing and trapping transient oligomers in amyloid assembly pathways. <i>Biophysical Chemistry</i> , 2021 , 268, 106505	3.5	42
277	Structural insights into peptide self-assembly using photo-induced crosslinking experiments and discontinuous molecular dynamics. <i>AIChE Journal</i> , 2021 , 67, e17101	3.6	2
276	Proteostasis of Islet Amyloid Polypeptide: A Molecular Perspective of Risk Factors and Protective Strategies for Type II Diabetes. <i>Chemical Reviews</i> , 2021 , 121, 1845-1893	68.1	38
275	Investigation of D76N β Microglobulin Using Protein Footprinting and Structural Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1583-1592	3.5	0
274	De novo design of transmembrane β barrels. <i>Science</i> , 2021 , 371,	33.3	25
273	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <i>Communications Biology</i> , 2020 , 3, 766	6.7	13
272	The uniqueness of flow in probing the aggregation behavior of clinically relevant antibodies.. <i>Engineering Reports</i> , 2020 , 2, e12147	1.2	4
271	Spot the Difference: Function versus Toxicity in Amyloid Fibrils. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 635-636	10.3	8
270	Structural insight into the formation of lipoprotein- β barrel complexes. <i>Nature Chemical Biology</i> , 2020 , 16, 1019-1025	11.7	20
269	Macromolecular Crowding Enhances the Detection of DNA and Proteins by a Solid-State Nanopore. <i>Nano Letters</i> , 2020 , 20, 5553-5561	11.5	31

268	PyXlinkViewer: A flexible tool for visualization of protein chemical crosslinking data within the PyMOL molecular graphics system. <i>Protein Science</i> , 2020 , 29, 1851-1857	6.3	16
267	A short motif in the N-terminal region of E ₃ synuclein is critical for both aggregation and function. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 249-259	17.6	47
266	Role of the lipid bilayer in outer membrane protein folding in Gram-negative bacteria. <i>Journal of Biological Chemistry</i> , 2020 , 295, 10340-10367	5.4	36
265	Using protein engineering to understand and modulate aggregation. <i>Current Opinion in Structural Biology</i> , 2020 , 60, 157-166	8.1	15
264	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. <i>Nature Communications</i> , 2020 , 11, 2155	17.4	28
263	Determining the Free Energies of Outer Membrane Proteins in Lipid Bilayers. <i>Methods in Molecular Biology</i> , 2020 , 2168, 217-232	1.4	0
262	Dynamics of Membrane Proteins Monitored by Single-Molecule Fluorescence Across Multiple Timescales. <i>Methods in Molecular Biology</i> , 2020 , 2168, 273-297	1.4	
261	Amyloid structures: much more than just a cross- β fold. <i>Current Opinion in Structural Biology</i> , 2020 , 60, 7-16	8.1	72
260	Collagen I Weakly Interacts with the E ₃ sheets of E ₃ microglobulin and Enhances Conformational Exchange To Induce Amyloid Formation. <i>Journal of the American Chemical Society</i> , 2020 , 142, 1321-1331	16.4	8
259	The role of the I-state in D76N E ₃ microglobulin amyloid assembly: A crucial intermediate or an innocuous bystander?. <i>Journal of Biological Chemistry</i> , 2020 , 295, 12474-12484	5.4	5
258	Modulation of E ₃ Amyloid Fibril Formation in Alzheimer's Disease by Microglia and Infection. <i>Frontiers in Molecular Neuroscience</i> , 2020 , 13, 609073	6.1	9
257	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	5.1	12
256	Modulation of Amyloidogenic Protein Self-Assembly Using Tethered Small Molecules. <i>Journal of the American Chemical Society</i> , 2020 , 142, 20845-20854	16.4	7
255	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	17.6	29
254	Potential human transmission of amyloid E ₃ pathology: surveillance and risks. <i>Lancet Neurology</i> , 2020 , 19, 872-878	24.1	23
253	An in vivo platform to select and evolve aggregation-resistant proteins. <i>Nature Communications</i> , 2020 , 11, 1816	17.4	10
252	Thermodynamic phase diagram of amyloid-E ₃ (16-22) peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 2091-2096	11.5	40
251	Molecular insights into the surface-catalyzed secondary nucleation of amyloid-E ₃ (A ₁) by the peptide fragment A ₁ . <i>Science Advances</i> , 2019 , 5, eaav8216	14.3	34

250	Extracellular matrix components modulate different stages in β microglobulin amyloid formation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 9392-9401	5.4	9
249	Design and synthesis of cysteine-specific labels for photo-crosslinking studies.. <i>RSC Advances</i> , 2019 , 9, 7610-7614	3.7	4
248	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	17.6	16
247	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. <i>Analytical Chemistry</i> , 2019 , 91, 15163-15170	7.8	8
246	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. <i>ELife</i> , 2019 , 8,	8.9	27
245	Professor Sir Christopher Martin Dobson (1949-2019). <i>Biochemist</i> , 2019 , 41, 45-45	0.5	
244	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	6.5	11
243	Homage to Chris Dobson. <i>Frontiers in Molecular Biosciences</i> , 2019 , 6, 137	5.6	
242	A peptide-display protein scaffold to facilitate single molecule force studies of aggregation-prone peptides. <i>Protein Science</i> , 2018 , 27, 1205-1217	6.3	3
241	Mass spectrometry-enabled structural biology of membrane proteins. <i>Methods</i> , 2018 , 147, 187-205	4.6	55
240	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	5.4	12
239	Using extensional flow to reveal diverse aggregation landscapes for three IgG1 molecules. <i>Biotechnology and Bioengineering</i> , 2018 , 115, 1216-1225	4.9	11
238	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	1.1	1
237	Dynamic action of the Sec machinery during initiation, protein translocation and termination. <i>ELife</i> , 2018 , 7,	8.9	37
236	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	
235	Comparing Hydrogen Deuterium Exchange and Fast Photochemical Oxidation of Proteins: a Structural Characterisation of Wild-Type and β 6 β Microglobulin. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 2413-2426	3.5	30
234	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 16688-16692	16.4	36
233	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie</i> , 2018 , 130, 16930-16934	3.6	6

232	Orientation of a Diagnostic Ligand Bound to Macroscopically Aligned Amyloid-Fibrils Determined by Solid-State NMR. <i>Journal of Physical Chemistry Letters</i> , 2018 , 9, 6611-6615	6.4	
231	The structure of a β -microglobulin fibril suggests a molecular basis for its amyloid polymorphism. <i>Nature Communications</i> , 2018 , 9, 4517	17.4	85
230	A new era for understanding amyloid structures and disease. <i>Nature Reviews Molecular Cell Biology</i> , 2018 , 19, 755-773	48.7	357
229	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	5.4	12
228	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	11.5	47
227	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. <i>Chemical Science</i> , 2017 , 8, 5030-5040	9.4	31
226	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	3.5	35
225	Outer membrane protein folding from an energy landscape perspective. <i>BMC Biology</i> , 2017 , 15, 123	7.3	43
224	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2017 , 429, 3776-3792	6.5	49
223	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 8844-8852	7.8	13
222	Amyloid plaques beyond A β : a survey of the diverse modulators of amyloid aggregation. <i>Biophysical Reviews</i> , 2017 , 9, 405-419	3.7	55
221	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017 , 39, 90-99	9.7	59
220	Molecular Origins of the Compatibility between Glycosaminoglycans and A β 0 Amyloid Fibrils. <i>Journal of Molecular Biology</i> , 2017 , 429, 2449-2462	6.5	21
219	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	3.5	24
218	Characterization of Amyloid Oligomers by Electrospray Ionization-Ion Mobility Spectrometry-Mass Spectrometry (ESI-IMS-MS). <i>Methods in Molecular Biology</i> , 2016 , 1345, 115-32	1.4	7
217	ESI-IMS-MS: A method for rapid analysis of protein aggregation and its inhibition by small molecules. <i>Methods</i> , 2016 , 95, 62-9	4.6	41
216	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 786-793	17.6	62
215	Lateral opening in the intact β -barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016 , 7, 12865	17.4	117

214	MpUL-multi: Software for Calculation of Amyloid Fibril Mass per Unit Length from TB-TEM Images. <i>Scientific Reports</i> , 2016 , 6, 21078	4.9	10
213	Atomic Details of the Interactions of Glycosaminoglycans with Amyloid- β Fibrils. <i>Journal of the American Chemical Society</i> , 2016 , 138, 8328-31	16.4	38
212	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016 , 12, 94-101	11.7	56
211	Substrate protein folds while it is bound to the ATP-independent chaperone Spy. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 53-58	17.6	55
210	Comparison of the aggregation of homologous α -microglobulin variants reveals protein solubility as a key determinant of amyloid formation. <i>Journal of Molecular Biology</i> , 2016 , 428, 631-643	6.5	12
209	Two-way communication between SecY and SecA suggests a Brownian ratchet mechanism for protein translocation. <i>ELife</i> , 2016 , 5,	8.9	64
208	Engineering the surface properties of a human monoclonal antibody prevents self-association and rapid clearance in vivo. <i>Scientific Reports</i> , 2016 , 6, 38644	4.9	66
207	A Population Shift between Sparsely Populated Folding Intermediates Determines Amyloidogenicity. <i>Journal of the American Chemical Society</i> , 2016 , 138, 6271-80	16.4	21
206	A growing toolbox of techniques for studying β barrel outer membrane protein folding and biogenesis. <i>Biochemical Society Transactions</i> , 2016 , 44, 802-9	5.1	10
205	Mechanisms of amyloid formation revealed by solution NMR. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2015 , 88-89, 86-104	10.4	66
204	Insights into the consequences of co-polymerisation in the early stages of IAPP and A β peptide assembly from mass spectrometry. <i>Analyst, The</i> , 2015 , 140, 6990-9	5	34
203	Force-induced remodelling of proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 2015 , 30, 89-99	8.1	28
202	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, 5691-6	11.5	81
201	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015 , 89, 38-44	4.6	27
200	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015 , 89, 13-21	4.6	49
199	Amyloid Fibres: Inert End-Stage Aggregates or Key Players in Disease?. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 719-727	10.3	86
198	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, 1241-53	7.6	25
197	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometry-mass spectrometry. <i>Nature Chemistry</i> , 2015 , 7, 73-81	17.6	203

196	A comparison of the folding characteristics of free and ribosome-tethered polypeptide chains using limited proteolysis and mass spectrometry. <i>Protein Science</i> , 2015 , 24, 1282-91	6.3	5
195	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	1.9	23
194	Mutational analysis of the ability of resveratrol to inhibit amyloid formation by islet amyloid polypeptide: critical evaluation of the importance of aromatic-inhibitor and histidine-inhibitor interactions. <i>Biochemistry</i> , 2015 , 54, 666-76	3.2	41
193	Amphipols outperform dodecylmaltoside micelles in stabilizing membrane protein structure in the gas phase. <i>Analytical Chemistry</i> , 2015 , 87, 1118-26	7.8	40
192	Extraction of accurate biomolecular parameters from single-molecule force spectroscopy experiments. <i>ACS Nano</i> , 2015 , 9, 1315-24	16.7	14
191	Biophysical Studies of Amyloid Formation and Its Inhibition. <i>FASEB Journal</i> , 2015 , 29, 491.1	0.9	
190	Energy landscapes of functional proteins are inherently risky. <i>Nature Chemical Biology</i> , 2014 , 10, 884-91	11.7	74
189	Insights into the role of the beta-2 microglobulin D-strand in amyloid propensity revealed by mass spectrometry. <i>Molecular BioSystems</i> , 2014 , 10, 412-20		18
188	Visualization of transient protein-protein interactions that promote or inhibit amyloid assembly. <i>Molecular Cell</i> , 2014 , 55, 214-26	17.6	47
187	Ion mobility spectrometry-mass spectrometry defines the oligomeric intermediates in amylin amyloid formation and the mode of action of inhibitors. <i>Journal of the American Chemical Society</i> , 2014 , 136, 660-70	16.4	137
186	Synthesis, characterization and applications of a perdeuterated amphipol. <i>Journal of Membrane Biology</i> , 2014 , 247, 909-24	2.3	36
185	Analysis of amyloid nanostructures using photo-cross-linking: in situ comparison of three widely used photo-cross-linkers. <i>ACS Chemical Biology</i> , 2014 , 9, 761-8	4.9	23
184	Secondary structure in the core of amyloid fibrils formed from human I β and its truncated variant N16. <i>Journal of the American Chemical Society</i> , 2014 , 136, 6313-25	16.4	37
183	The role of high-dimensional diffusive search, stabilization, and frustration in protein folding. <i>Biophysical Journal</i> , 2014 , 106, 1729-40	2.9	5
182	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, 265-80	4.1	38
181	I β -Microglobulin amyloid fibril-induced membrane disruption is enhanced by endosomal lipids and acidic pH. <i>PLoS ONE</i> , 2014 , 9, e104492	3.7	27
180	I 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, 35781-94	5.4	27
179	Distinguishing closely related amyloid precursors using an RNA aptamer. <i>Journal of Biological Chemistry</i> , 2014 , 289, 26859-26871	5.4	7

178	How TriC folds tricky proteins. <i>Cell</i> , 2014 , 159, 1251-2	56.2	4
177	Monitoring oligomer formation from self-aggregating amylin peptides using ESI-IMS-MS. <i>International Journal for Ion Mobility Spectrometry</i> , 2013 , 16, 29-39	1.5	11
176	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	1.9	13
175	Conformational dynamics is more important than helical propensity for the folding of the all β helical protein Im7. <i>Protein Science</i> , 2013 , 22, 1722-38	6.3	4
174	An imaging and systems modeling approach to fibril breakage enables prediction of amyloid behavior. <i>Biophysical Journal</i> , 2013 , 105, 2811-9	2.9	45
173	Aggregation modulators interfere with membrane interactions of β -microglobulin fibrils. <i>Biophysical Journal</i> , 2013 , 105, 745-55	2.9	27
172	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, 3178-91	6.5	42
171	Assessing the causes and consequences of co-polymerization in amyloid formation. <i>Prion</i> , 2013 , 7, 359-68.3	6.3	37
170	A force-activated trip switch triggers rapid dissociation of a colicin from its immunity protein. <i>PLoS Biology</i> , 2013 , 11, e1001489	9.7	22
169	Expanding the repertoire of amyloid polymorphs by co-polymerization of related protein precursors. <i>Journal of Biological Chemistry</i> , 2013 , 288, 7327-37	5.4	32
168	Phosphorylation as a tool to modulate aggregation propensity and to predict fibril architecture. <i>ChemBioChem</i> , 2012 , 13, 271-81	3.8	10
167	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, 20455-60	11.5	140
166	Site-specific identification of an α fibril-heparin interaction site by using solid-state NMR spectroscopy. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 13140-3	16.4	25
165	Site-Specific Identification of an α FibrilHeparin Interaction Site by Using Solid-State NMR Spectroscopy. <i>Angewandte Chemie</i> , 2012 , 124, 13317-13320	3.6	1
164	Covalent cross-linking within supramolecular peptide structures. <i>Analytical Chemistry</i> , 2012 , 84, 6790-7	7.8	19
163	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, 453-64	6.5	24
162	Conformational properties of the unfolded state of Im7 in nondenaturing conditions. <i>Journal of Molecular Biology</i> , 2012 , 416, 300-18	6.5	23
161	Effect of sequence variation on the mechanical response of amyloid fibrils probed by steered molecular dynamics simulation. <i>Biophysical Journal</i> , 2012 , 102, 587-96	2.9	37

160	Amphipathic polymers enable the study of functional membrane proteins in the gas phase. <i>Analytical Chemistry</i> , 2012 , 84, 9841-7	7.8	55
159	N-terminal acetylation of Eynuclein induces increased transient helical propensity and decreased aggregation rates in the intrinsically disordered monomer. <i>Protein Science</i> , 2012 , 21, 911-7	6.3	123
158	The role of conformational flexibility in β -microglobulin amyloid fibril formation at neutral pH. <i>Rapid Communications in Mass Spectrometry</i> , 2012 , 26, 1783-92	2.2	22
157	Linked Landscapes and Conformational Conversions: How Proteins Fold and Misfold 2012 , 1-16		
156	Protein Misfolding and Toxicity in Dialysis-Related Amyloidosis 2012 , 377-405		2
155	Structure and dynamics of oligomeric intermediates in β -microglobulin self-assembly. <i>Biophysical Journal</i> , 2011 , 101, 1238-47	2.9	23
154	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. <i>Nature Chemical Biology</i> , 2011 , 7, 730-9	11.7	85
153	Conformational conversion during amyloid formation at atomic resolution. <i>Molecular Cell</i> , 2011 , 41, 161-176	17.6	142
152	A diversity of assembly mechanisms of a generic amyloid fold. <i>Molecular Cell</i> , 2011 , 43, 8-18	17.6	244
151	Understanding the complex mechanisms of β -microglobulin amyloid assembly. <i>FEBS Journal</i> , 2011 , 278, 3868-83	5.7	84
150	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, 1857-71	3.6	83
149	Dissecting key residues in folding and stability of the bacterial immunity protein 7. <i>Protein Engineering, Design and Selection</i> , 2011 , 24, 517-23	1.9	4
148	The oligomeric state and arrangement of the active bacterial translocon. <i>Journal of Biological Chemistry</i> , 2011 , 286, 4659-69	5.4	52
147	Characterization of the response of primary cells relevant to dialysis-related amyloidosis to β -microglobulin monomer and fibrils. <i>PLoS ONE</i> , 2011 , 6, e27353	3.7	17
146	Stacked sets of parallel, in-register beta-strands of beta2-microglobulin in amyloid fibrils revealed by site-directed spin labeling and chemical labeling. <i>Journal of Biological Chemistry</i> , 2010 , 285, 17137-47	5.4	54
145	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, 4099-104	11.5	115
144	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, 22528-33	11.5	58
143	Elongated oligomers in beta2-microglobulin amyloid assembly revealed by ion mobility spectrometry-mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6794-8	11.5	131

142	Fibril fragmentation in amyloid assembly and cytotoxicity: when size matters. <i>Prion</i> , 2010 , 4, 20-5	2.3	81
141	Intermolecular alignment in β -microglobulin amyloid fibrils. <i>Journal of the American Chemical Society</i> , 2010 , 132, 17077-9	16.4	66
140	Magic angle spinning NMR analysis of beta2-microglobulin amyloid fibrils in two distinct morphologies. <i>Journal of the American Chemical Society</i> , 2010 , 132, 10414-23	16.4	73
139	Desolvation and development of specific hydrophobic core packing during Im7 folding. <i>Journal of Molecular Biology</i> , 2010 , 396, 1329-45	6.5	17
138	Single-molecule studies of the Im7 folding landscape. <i>Journal of Molecular Biology</i> , 2010 , 398, 132-45	6.5	18
137	Hemodialysis-Related Amyloidosis 2010 , 347-379		2
136	Amyloid fibril length distribution quantified by atomic force microscopy single-particle image analysis. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 489-96	1.9	49
135	Glimpses of the molecular mechanisms of beta2-microglobulin fibril formation in vitro: aggregation on a complex energy landscape. <i>FEBS Letters</i> , 2009 , 583, 2623-9	3.8	50
134	Probing dynamics within amyloid fibrils using a novel capping method. <i>Angewandte Chemie - International Edition</i> , 2009 , 48, 5705-7	16.4	12
133	The mechanism of folding of Im7 reveals competition between functional and kinetic evolutionary constraints. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 318-24	17.6	56
132	An expanding arsenal of experimental methods yields an explosion of insights into protein folding mechanisms. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 582-8	17.6	197
131	HDX-ESI-MS reveals enhanced conformational dynamics of the amyloidogenic protein beta(2)-microglobulin upon release from the MHC-1. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 278-86	3.5	33
130	A generic mechanism of beta2-microglobulin amyloid assembly at neutral pH involving a specific proline switch. <i>Journal of Molecular Biology</i> , 2009 , 386, 1312-26	6.5	73
129	Globular tetramers of beta(2)-microglobulin assemble into elaborate amyloid fibrils. <i>Journal of Molecular Biology</i> , 2009 , 389, 48-57	6.5	69
128	Competition between intramolecular and intermolecular interactions in an amyloid-forming protein. <i>Journal of Molecular Biology</i> , 2009 , 389, 776-86	6.5	62
127	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, 1074-86	6.5	9
126	Identification of a mechanical rheostat in the hydrophobic core of protein L. <i>Journal of Molecular Biology</i> , 2009 , 393, 237-48	6.5	48
125	Optimizing protein stability in vivo. <i>Molecular Cell</i> , 2009 , 36, 861-71	17.6	123

124	Thermodynamic description of polymorphism in Q- and N-rich peptide aggregates revealed by atomistic simulation. <i>Biophysical Journal</i> , 2009 , 97, 1-11	2.9	59
123	Tuning the elastic modulus of hydrated collagen fibrils. <i>Biophysical Journal</i> , 2009 , 97, 2985-92	2.9	118
122	Fibril fragmentation enhances amyloid cytotoxicity. <i>Journal of Biological Chemistry</i> , 2009 , 284, 34272-82	5.4	290
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2	Structural insight into the formation of lipoprotein-barrel complexes by the barrel assembly machinery		4
1	Sequence grammar underlying unfolding and phase separation of globular proteins		2