Sheena E Radford

List of Publications by Citations

Source: https://exaly.com/author-pdf/3870268/sheena-e-radford-publications-by-citations.pdf
Version: 2024-04-26

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	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. *Nature*, **1997**, 385, 787-93	50.4	980
284	Nucleation of protein fibrillation by nanoparticles. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 8691-6	11.5	722
283	The folding of hen lysozyme involves partially structured intermediates and multiple pathways. *Nature*, **1992**, 358, 302-7	50.4	702
282	pH as a trigger of peptide beta-sheet self-assembly and reversible switching between nematic and isotropic phases. *Journal of the American Chemical Society*, **2003**, 125, 9619-28	16.4	393
281	Systematic analysis of nucleation-dependent polymerization reveals new insights into the mechanism of amyloid self-assembly. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8926-31	11.5	363
280	A new era for understanding amyloid structures and disease. *Nature Reviews Molecular Cell Biology*, **2018**, 19, 755-773	48.7	357
279	Understanding how proteins fold: the lysozyme story so far. *Trends in Biochemical Sciences*, **1994**, 19, 31-7	10.3	325
278	Pulling geometry defines the mechanical resistance of a beta-sheet protein. *Nature Structural and Molecular Biology*, **2003**, 10, 731-7	17.6	315
277	Folding versus aggregation: polypeptide conformations on competing pathways. *Archives of Biochemistry and Biophysics*, **2008**, 469, 100-17	4.1	305
276	Partially unfolded states of beta(2)-microglobulin and amyloid formation in vitro. *Biochemistry*, **2000**, 39, 8735-46	3.2	305
275	Competing pathways determine fibril morphology in the self-assembly of beta2-microglobulin into amyloid. *Journal of Molecular Biology*, **2005**, 351, 850-64	6.5	299
274	Deciphering drift time measurements from travelling wave ion mobility spectrometry-mass spectrometry studies. *European Journal of Mass Spectrometry*, **2009**, 15, 113-30	1.1	293
273	Fibril fragmentation enhances amyloid cytotoxicity. *Journal of Biological Chemistry*, **2009**, 284, 34272-82	5.4	290
272	Amyloid formation under physiological conditions proceeds via a native-like folding intermediate. *Nature Structural and Molecular Biology*, **2006**, 13, 195-201	17.6	281
271	A partially folded state of hen egg white lysozyme in trifluoroethanol: structural characterization and implications for protein folding. *Biochemistry*, **1993**, 32, 669-78	3.2	264
270	A diversity of assembly mechanisms of a generic amyloid fold. *Molecular Cell*, **2011**, 43, 8-18	17.6	244
269	Demonstration by NMR of folding domains in lysozyme. *Nature*, **1991**, 349, 633-6	50.4	241

268	Rapid folding with and without populated intermediates in the homologous four-helix proteins Im7 and Im9. *Journal of Molecular Biology*, **1999**, 286, 1597-608	6.5	230
267	The Yin and Yang of protein folding. *FEBS Journal*, **2005**, 272, 5962-70	5.7	226
266	Hierarchical assembly of beta2-microglobulin amyloid in vitro revealed by atomic force microscopy. *Journal of Molecular Biology*, **2003**, 330, 785-97	6.5	206
265	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometry-mass spectrometry. *Nature Chemistry*, **2015**, 7, 73-81	17.6	203
264	Conformation of GroEL-bound alpha-lactalbumin probed by mass spectrometry. *Nature*, **1994**, 372, 646-51	50.4	202
263	An expanding arsenal of experimental methods yields an explosion of insights into protein folding mechanisms. *Nature Structural and Molecular Biology*, **2009**, 16, 582-8	17.6	197
262	Protein folding: defining a "standard" set of experimental conditions and a preliminary kinetic data set of two-state proteins. *Protein Science*, **2005**, 14, 602-16	6.3	181
261	Beta(2)-microglobulin and its deamidated variant, N17D form amyloid fibrils with a range of morphologies in vitro. *Journal of Molecular Biology*, **2001**, 313, 559-71	6.5	180
260	Intermediates: ubiquitous species on folding energy landscapes?. *Current Opinion in Structural Biology*, **2007**, 17, 30-7	8.1	179
259	Investigation of protein folding by mass spectrometry. *FASEB Journal*, **1996**, 10, 93-101	0.9	169
258	Structural properties of an amyloid precursor of beta(2)-microglobulin. *Nature Structural Biology*, **2002**, 9, 326-31		167
257	Crystal structure of monomeric human beta-2-microglobulin reveals clues to its amyloidogenic properties. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 9771-6	11.5	166
256	Structural insights into the polymorphism of amyloid-like fibrils formed by region 20-29 of amylin revealed by solid-state NMR and X-ray fiber diffraction. *Journal of the American Chemical Society*, **2008**, 130, 14990-5001	16.4	159
255	Engineering of peptide □sheetnanotapes. *Journal of Materials Chemistry*, **1997**, 7, 1135-1145		153
254	Structural and mechanistic basis of immunity toward endonuclease colicins. *Nature Structural Biology*, **1999**, 6, 243-52		148
253	Tertiary interactions in the folding pathway of hen lysozyme: kinetic studies using fluorescent probes. *Biochemistry*, **1994**, 33, 5212-20	3.2	143
252	Conformational conversion during amyloid formation at atomic resolution. *Molecular Cell*, **2011**, 41, 161-72	17.6	142
251	Direct three-dimensional visualization of membrane disruption by amyloid fibrils. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 20455-60	11.5	140

250	Donor-strand exchange in chaperone-assisted pilus assembly proceeds through a concerted beta strand displacement mechanism. *Molecular Cell*, **2006**, 22, 831-842	17.6	140
249	Amyloid-forming peptides from beta2-microglobulin-Insights into the mechanism of fibril formation in vitro. *Journal of Molecular Biology*, **2003**, 325, 249-57	6.5	140
248	Mechanically unfolding the small, topologically simple protein L. *Biophysical Journal*, **2005**, 89, 506-19	2.9	139
247	Ion mobility spectrometry-mass spectrometry defines the oligomeric intermediates in amylin amyloid formation and the mode of action of inhibitors. *Journal of the American Chemical Society*, **2014**, 136, 660-70	16.4	137
246	Im7 folding mechanism: misfolding on a path to the native state. *Nature Structural Biology*, **2002**, 9, 209-16		132
245	Elongated oligomers in beta2-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, 6794-8	11.5	131
244	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	6.5	130
243	A systematic investigation into the effect of protein destabilisation on beta 2-microglobulin amyloid formation. *Journal of Molecular Biology*, **2003**, 330, 943-54	6.5	128
242	Ultrarapid mixing experiments reveal that Im7 folds via an on-pathway intermediate. *Nature Structural Biology*, **2001**, 8, 68-72		128
241	N-terminal acetylation of □synuclein induces increased transient helical propensity and decreased aggregation rates in the intrinsically disordered monomer. *Protein Science*, **2012**, 21, 911-7	6.3	123
240	Optimizing protein stability in vivo. *Molecular Cell*, **2009**, 36, 861-71	17.6	123
239	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	6.5	121
238	The refolding of human lysozyme: a comparison with the structurally homologous hen lysozyme. *Biochemistry*, **1994**, 33, 5867-76	3.2	119
237	Tuning the elastic modulus of hydrated collagen fibrils. *Biophysical Journal*, **2009**, 97, 2985-92	2.9	118
236	The effect of core destabilization on the mechanical resistance of I27. *Biophysical Journal*, **2002**, 83, 458-72	2.9	118
235	Lateral opening in the intact □barrel assembly machinery captured by cryo-EM. *Nature Communications*, **2016**, 7, 12865	17.4	117
234	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, 4099-104	11.5	115
233	Monitoring copopulated conformational states during protein folding events using electrospray ionization-ion mobility spectrometry-mass spectrometry. *Journal of the American Society for Mass Spectrometry*, **2007**, 18, 2180-90	3.5	114

232	Conformational properties of four peptides spanning the sequence of hen lysozyme. *Journal of Molecular Biology*, **1995**, 252, 483-91	6.5	112
231	A systematic study of the effect of physiological factors on beta2-microglobulin amyloid formation at neutral pH. *Biochemistry*, **2006**, 45, 2311-21	3.2	111
230	Force mode atomic force microscopy as a tool for protein folding studies. *Analytica Chimica Acta*, **2003**, 479, 87-105	6.6	106
229	Pseudospecific docking surfaces on electron transfer proteins as illustrated by pseudoazurin, cytochrome c550 and cytochrome cd1 nitrite reductase. *Nature Structural and Molecular Biology*, **1995**, 2, 975-82	17.6	100
228	Mechanical resistance of proteins explained using simple molecular models. *Biophysical Journal*, **2006**, 90, 287-97	2.9	96
227	Effects of hydration on the mechanical response of individual collagen fibrils. *Applied Physics Letters*, **2008**, 92, 233902	3.4	91
226	Fibril growth kinetics reveal a region of beta2-microglobulin important for nucleation and elongation of aggregation. *Journal of Molecular Biology*, **2008**, 378, 251-63	6.5	90
225	Probing the structure of folding intermediates. *Current Opinion in Structural Biology*, **1994**, 4, 100-106	8.1	90
224	Determination of an ensemble of structures representing the intermediate state of the bacterial immunity protein Im7. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 99-104	11.5	89
223	Fast and slow tracks in lysozyme folding: insight into the role of domains in the folding process. *Journal of Molecular Biology*, **1997**, 267, 1068-74	6.5	88
222	Dynamics in the unfolded state of beta2-microglobulin studied by NMR. *Journal of Molecular Biology*, **2005**, 346, 279-94	6.5	88
221	Hydrogen exchange properties of proteins in native and denatured states monitored by mass spectrometry and NMR. *Protein Science*, **1997**, 6, 1316-24	6.3	87
220	Amyloid Fibres: Inert End-Stage Aggregates or Key Players in Disease?. *Trends in Biochemical Sciences*, **2015**, 40, 719-727	10.3	86
219	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. *Nature Chemical Biology*, **2011**, 7, 730-9	11.7	85
218	The structure of a □microglobulin fibril suggests a molecular basis for its amyloid polymorphism. *Nature Communications*, **2018**, 9, 4517	17.4	85
217	Understanding the complex mechanisms of □-microglobulin amyloid assembly. *FEBS Journal*, **2011** , 278, 3868-83	5.7	84
216	Quantifying heterogeneity and conformational dynamics from single molecule FRET of diffusing molecules: recurrence analysis of single particles (RASP). *Physical Chemistry Chemical Physics*, **2011**, 13, 1857-71	3.6	83
215	pH-induced molecular shedding drives the formation of amyloid fibril-derived oligomers. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 5691-6	11.5	81

214	Fibril fragmentation in amyloid assembly and cytotoxicity: when size matters. *Prion*, **2010**, 4, 20-5	2.3	81
213	Energy landscapes of functional proteins are inherently risky. *Nature Chemical Biology*, **2014**, 10, 884-91	11.7	74
212	Magic angle spinning NMR analysis of beta2-microglobulin amyloid fibrils in two distinct morphologies. *Journal of the American Chemical Society*, **2010**, 132, 10414-23	16.4	73
211	A generic mechanism of beta2-microglobulin amyloid assembly at neutral pH involving a specific proline switch. *Journal of Molecular Biology*, **2009**, 386, 1312-26	6.5	73
210	Amyloid structures: much more than just a cross-□fold. *Current Opinion in Structural Biology*, **2020**, 60, 7-16	8.1	72
209	Globular tetramers of beta(2)-microglobulin assemble into elaborate amyloid fibrils. *Journal of Molecular Biology*, **2009**, 389, 48-57	6.5	69
208	Role of the single disulphide bond of beta(2)-microglobulin in amyloidosis in vitro. *Protein Science*, **2001**, 10, 1775-84	6.3	69
207	Role of the N and C-terminal strands of beta 2-microglobulin in amyloid formation at neutral pH. *Journal of Molecular Biology*, **2003**, 330, 935-41	6.5	68
206	Mechanically unfolding proteins: the effect of unfolding history and the supramolecular scaffold. *Protein Science*, **2002**, 11, 2759-65	6.3	67
205	Semisynthesis of a glycosylated Im7 analogue for protein folding studies. *Journal of the American Chemical Society*, **2005**, 127, 12882-9	16.4	67
204	Thermal unfolding of an intermediate is associated with non-Arrhenius kinetics in the folding of hen lysozyme. *Journal of Molecular Biology*, **2000**, 297, 193-210	6.5	67
203	Mechanisms of amyloid formation revealed by solution NMR. *Progress in Nuclear Magnetic Resonance Spectroscopy*, **2015**, 88-89, 86-104	10.4	66
202	Intermolecular alignment in □2-microglobulin amyloid fibrils. *Journal of the American Chemical Society*, **2010**, 132, 17077-9	16.4	66
201	Significant hydrogen exchange protection in GroEL-bound DHFR is maintained during iterative rounds of substrate cycling. *Protein Science*, **1996**, 5, 2506-13	6.3	66
200	Engineering the surface properties of a human monoclonal antibody prevents self-association and rapid clearance in vivo. *Scientific Reports*, **2016**, 6, 38644	4.9	66
199	Two-way communication between SecY and SecA suggests a Brownian ratchet mechanism for protein translocation. *ELife*, **2016**, 5,	8.9	64
198	Co-populated conformational ensembles of beta2-microglobulin uncovered quantitatively by electrospray ionization mass spectrometry. *Journal of Biological Chemistry*, **2004**, 279, 27069-77	5.4	63
197	Skp is a multivalent chaperone of outer-membrane proteins. *Nature Structural and Molecular Biology*, **2016**, 23, 786-793	17.6	62

196	Competition between intramolecular and intermolecular interactions in an amyloid-forming protein. *Journal of Molecular Biology*, **2009**, 389, 776-86	6.5	62
195	Switching two-state to three-state kinetics in the helical protein Im9 via the optimisation of stabilising non-native interactions by design. *Journal of Molecular Biology*, **2004**, 342, 261-73	6.5	61
194	Acidic conditions stabilise intermediates populated during the folding of Im7 and Im9. *Journal of Molecular Biology*, **2001**, 312, 849-63	6.5	60
193	Small molecule probes of protein aggregation. *Current Opinion in Chemical Biology*, **2017**, 39, 90-99	9.7	59
192	Thermodynamic description of polymorphism in Q- and N-rich peptide aggregates revealed by atomistic simulation. *Biophysical Journal*, **2009**, 97, 1-11	2.9	59
191	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, 22528-33	11.5	58
190	An in vivo platform for identifying inhibitors of protein aggregation. *Nature Chemical Biology*, **2016**, 12, 94-101	11.7	56
189	The mechanism of folding of Im7 reveals competition between functional and kinetic evolutionary constraints. *Nature Structural and Molecular Biology*, **2009**, 16, 318-24	17.6	56
188	Kinetic studies of beta-sheet protein folding. *Current Opinion in Structural Biology*, **1998**, 8, 86-92	8.1	56
187	Mass spectrometry-enabled structural biology of membrane proteins. *Methods*, **2018**, 147, 187-205	4.6	55
186	Substrate protein folds while it is bound to the ATP-independent chaperone Spy. *Nature Structural and Molecular Biology*, **2016**, 23, 53-58	17.6	55
185	Amyloid plaques beyond A▯a survey of the diverse modulators of amyloid aggregation. *Biophysical Reviews*, **2017**, 9, 405-419	3.7	55
184	Amphipathic polymers enable the study of functional membrane proteins in the gas phase. *Analytical Chemistry*, **2012**, 84, 9841-7	7.8	55
183	Investigating the structural properties of amyloid-like fibrils formed in vitro from beta2-microglobulin using limited proteolysis and electrospray ionisation mass spectrometry. *Rapid Communications in Mass Spectrometry*, **2006**, 20, 1628-36	2.2	55
182	Stacked sets of parallel, in-register beta-strands of beta2-microglobulin in amyloid fibrils revealed by site-directed spin labeling and chemical labeling. *Journal of Biological Chemistry*, **2010**, 285, 17137-47	5.4	54
181	GroEL accelerates the refolding of hen lysozyme without changing its folding mechanism. *Nature Structural Biology*, **1999**, 6, 683-90		54
180	Amyloid under the atomic force microscope. *Protein and Peptide Letters*, **2006**, 13, 261-70	1.9	53
179	The oligomeric state and arrangement of the active bacterial translocon. *Journal of Biological Chemistry*, **2011**, 286, 4659-69	5.4	52

178	The N-terminal helix is a post-assembly clamp in the bacterial outer membrane protein PagP. *Journal of Molecular Biology*, **2007**, 373, 529-40	6.5	52
177	Far-UV circular dichroism reveals a conformational switch in a peptide fragment from the beta-sheet of hen lysozyme. *Biochemistry*, **1994**, 33, 7345-53	3.2	51
176	Glimpses of the molecular mechanisms of beta2-microglobulin fibril formation in vitro: aggregation on a complex energy landscape. *FEBS Letters*, **2009**, 583, 2623-9	3.8	50
175	Separation of beta2-microglobulin conformers by high-field asymmetric waveform ion mobility spectrometry (FAIMS) coupled to electrospray ionisation mass spectrometry. *Rapid Communications in Mass Spectrometry*, **2004**, 18, 2229-34	2.2	50
174	The origin of the alpha-domain intermediate in the folding of hen lysozyme. *Journal of Molecular Biology*, **1998**, 277, 997-1005	6.5	50
173	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. *Methods*, **2015**, 89, 13-21	4.6	49
172	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. *Journal of Molecular Biology*, **2017**, 429, 3776-3792	6.5	49
171	Amyloid fibril length distribution quantified by atomic force microscopy single-particle image analysis. *Protein Engineering, Design and Selection*, **2009**, 22, 489-96	1.9	49
170	Identification of a mechanical rheostat in the hydrophobic core of protein L. *Journal of Molecular Biology*, **2009**, 393, 237-48	6.5	48
169	A common beta-sheet architecture underlies in vitro and in vivo beta2-microglobulin amyloid fibrils. *Journal of Biological Chemistry*, **2008**, 283, 17279-86	5.4	48
168	Inducing protein aggregation by extensional flow. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 4673-4678	11.5	47
167	A short motif in the N-terminal region of αsynuclein is critical for both aggregation and function. *Nature Structural and Molecular Biology*, **2020**, 27, 249-259	17.6	47
166	Visualization of transient protein-protein interactions that promote or inhibit amyloid assembly. *Molecular Cell*, **2014**, 55, 214-26	17.6	47
165	NMR analysis of the conformational properties of the trapped on-pathway folding intermediate of the bacterial immunity protein Im7. *Journal of Molecular Biology*, **2007**, 366, 1001-15	6.5	47
164	Towards an understanding of the structural molecular mechanism of beta(2)-microglobulin amyloid formation in vitro. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2005**, 1753, 51-63	4	47
163	An imaging and systems modeling approach to fibril breakage enables prediction of amyloid behavior. *Biophysical Journal*, **2013**, 105, 2811-9	2.9	45
162	Viscoelastic study of the mechanical unfolding of a protein by AFM. *Biophysical Journal*, **2006**, 91, L16-8	2.9	45
161	Site-directed mutagenesis and 1H NMR spectroscopy of an interdomain segment in the pyruvate dehydrogenase multienzyme complex of Escherichia coli. *Biochemistry*, **1988**, 27, 289-96	3.2	45

160	Outer membrane protein folding from an energy landscape perspective. *BMC Biology*, **2017**, 15, 123	7.3	43
159	Dissecting the effects of periplasmic chaperones on the in vitro folding of the outer membrane protein PagP. *Journal of Molecular Biology*, **2013**, 425, 3178-91	6.5	42
158	Urea-induced unfolding of the immunity protein Im9 monitored by spFRET. *Biophysical Journal*, **2006**, 91, L42-4	2.9	42
157	Cooperative Elements in Protein Folding Monitored by Electrospray Ionization Mass Spectrometry. *Journal of the American Chemical Society*, **1995**, 117, 7548-7549	16.4	42
156	Visualizing and trapping transient oligomers in amyloid assembly pathways. *Biophysical Chemistry*, **2021**, 268, 106505	3.5	42
155	ESI-IMS-MS: A method for rapid analysis of protein aggregation and its inhibition by small molecules. *Methods*, **2016**, 95, 62-9	4.6	41
154	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. *Biochemistry*, **2015**, 54, 666-76	3.2	41
153	Trapping the on-pathway folding intermediate of Im7 at equilibrium. *Journal of Molecular Biology*, **2004**, 341, 215-26	6.5	41
152	Thermodynamic phase diagram of amyloid-β(16-22) peptide. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 2091-2096	11.5	40
151	Amphipols outperform dodecylmaltoside micelles in stabilizing membrane protein structure in the gas phase. *Analytical Chemistry*, **2015**, 87, 1118-26	7.8	40
150	The Greek key protein apo-pseudoazurin folds through an obligate on-pathway intermediate. *Journal of Molecular Biology*, **1999**, 286, 1621-32	6.5	39
149	Atomic Details of the Interactions of Glycosaminoglycans with Amyloid-β Fibrils. *Journal of the American Chemical Society*, **2016**, 138, 8328-31	16.4	38
148	Mechanistic studies of the biogenesis and folding of outer membrane proteins in vitro and in vivo: what have we learned to date?. *Archives of Biochemistry and Biophysics*, **2014**, 564, 265-80	4.1	38
147	Structural and mechanistic consequences of polypeptide binding by GroEL. *Folding & Design*, **1997**, 2, R93-104		38
146	Characterisation of the conformational properties of urea-unfolded Im7: implications for the early stages of protein folding. *Journal of Molecular Biology*, **2006**, 364, 824-35	6.5	38
145	Comparison of the transition state ensembles for folding of Im7 and Im9 determined using all-atom molecular dynamics simulations with phi value restraints. *Proteins: Structure, Function and Bioinformatics*, **2004**, 54, 513-25	4.2	38
144	Proteostasis of Islet Amyloid Polypeptide: A Molecular Perspective of Risk Factors and Protective Strategies for Type II Diabetes. *Chemical Reviews*, **2021**, 121, 1845-1893	68.1	38
143	Dynamic action of the Sec machinery during initiation, protein translocation and termination. *ELife*, **2018**, 7,	8.9	37

142	Secondary structure in the core of amyloid fibrils formed from human □h and its truncated variant □N6. *Journal of the American Chemical Society*, **2014**, 136, 6313-25	16.4	37
141	Effect of sequence variation on the mechanical response of amyloid fibrils probed by steered molecular dynamics simulation. *Biophysical Journal*, **2012**, 102, 587-96	2.9	37
140	Assessing the causes and consequences of co-polymerization in amyloid formation. *Prion*, **2013**, 7, 359-68	2.3	37
139	Production and characterization of RNA aptamers specific for amyloid fibril epitopes. *Journal of Biological Chemistry*, **2007**, 282, 34500-9	5.4	37
138	Viscoelastic measurements of single molecules on a millisecond time scale by magnetically driven oscillation of an atomic force microscope cantilever. *Langmuir*, **2005**, 21, 4765-72	4	37
137	Role of the lipid bilayer in outer membrane protein folding in Gram-negative bacteria. *Journal of Biological Chemistry*, **2020**, 295, 10340-10367	5.4	36
136	Synthesis, characterization and applications of a perdeuterated amphipol. *Journal of Membrane Biology*, **2014**, 247, 909-24	2.3	36
135	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. *Angewandte Chemie - International Edition*, **2018**, 57, 16688-16692	16.4	36
134	Investigating the Structural Compaction of Biomolecules Upon Transition to the Gas-Phase Using ESI-TWIMS-MS. *Journal of the American Society for Mass Spectrometry*, **2017**, 28, 1855-1862	3.5	35
133	Molecular insights into the surface-catalyzed secondary nucleation of amyloid-□(A□) by the peptide fragment A□*Science Advances*, **2019**, 5, eaav8216	14.3	34
132	Insights into the consequences of co-polymerisation in the early stages of IAPP and A□peptide assembly from mass spectrometry. *Analyst, The*, **2015**, 140, 6990-9	5	34
131	HDX-ESI-MS reveals enhanced conformational dynamics of the amyloidogenic protein beta(2)-microglobulin upon release from the MHC-1. *Journal of the American Society for Mass Spectrometry*, **2009**, 20, 278-86	3.5	33
130	Expanding the repertoire of amyloid polymorphs by co-polymerization of related protein precursors. *Journal of Biological Chemistry*, **2013**, 288, 7327-37	5.4	32
129	Donor-strand exchange in chaperone-assisted pilus assembly revealed in atomic detail by molecular dynamics. *Journal of Molecular Biology*, **2008**, 375, 908-19	6.5	32
128	A near-native state on the slow refolding pathway of hen lysozyme. *Protein Science*, **1999**, 8, 35-44	6.3	32
127	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. *Biochemistry*, **2005**, 44, 3306-15	3.2	32
126	Equilibrium hydrogen exchange reveals extensive hydrogen bonded secondary structure in the on-pathway intermediate of Im7. *Journal of Molecular Biology*, **2004**, 337, 183-93	6.5	32
125	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. *Chemical Science*, **2017**, 8, 5030-5040	9.4	31

124	Macromolecular Crowding Enhances the Detection of DNA and Proteins by a Solid-State Nanopore. *Nano Letters*, **2020**, 20, 5553-5561	11.5	31
123	The effect of protein complexation on the mechanical stability of Im9. *Biophysical Journal*, **2007**, 92, L79-81	2.9	31
122	Accurate Use of Single Molecule Fluorescence Correlation Spectroscopy to Determine Molecular Diffusion Times. *Single Molecules*, **2001**, 2, 177-181		30
121	Using chimeric immunity proteins to explore the energy landscape for alpha-helical protein folding. *Journal of Molecular Biology*, **2001**, 307, 393-405	6.5	30
120	Comparing Hydrogen Deuterium Exchange and Fast Photochemical Oxidation of Proteins: a Structural Characterisation of Wild-Type and □N6 □Microglobulin. *Journal of the American Society for Mass Spectrometry*, **2018**, 29, 2413-2426	3.5	30
119	GroEL: More than Just a folding cage. *Cell*, **2006**, 125, 831-3	56.2	29
118	Fibril structures of diabetes-related amylin variants reveal a basis for surface-templated assembly. *Nature Structural and Molecular Biology*, **2020**, 27, 1048-1056	17.6	29
117	Force-induced remodelling of proteins and their complexes. *Current Opinion in Structural Biology*, **2015**, 30, 89-99	8.1	28
116	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. *Nature Communications*, **2020**, 11, 2155	17.4	28
115	The effect of increasing the stability of non-native interactions on the folding landscape of the bacterial immunity protein Im9. *Journal of Molecular Biology*, **2007**, 371, 554-68	6.5	28
114	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. *Methods*, **2015**, 89, 38-44	4.6	27
113	Aggregation modulators interfere with membrane interactions of □-microglobulin fibrils. *Biophysical Journal*, **2013**, 105, 745-55	2.9	27
112	□-Microglobulin amyloid fibril-induced membrane disruption is enhanced by endosomal lipids and acidic pH. *PLoS ONE*, **2014**, 9, e104492	3.7	27
111	□-microglobulin amyloid fibrils are nanoparticles that disrupt lysosomal membrane protein trafficking and inhibit protein degradation by lysosomes. *Journal of Biological Chemistry*, **2014**, 289, 35781-94	5.4	27
110	Investigation into the role of macrophages in the formation and degradation of beta2-microglobulin amyloid fibrils. *Journal of Biological Chemistry*, **2007**, 282, 29691-700	5.4	27
109	A study of D52S hen lysozyme-GlcNAc oligosaccharide complexes by NMR spectroscopy and electrospray mass spectrometry. *FEBS Letters*, **1992**, 296, 153-7	3.8	27
108	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. *ELife*, **2019**, 8,	8.9	27
107	A partially folded intermediate species of the beta-sheet protein apo-pseudoazurin is trapped during proline-limited folding. *Protein Science*, **2001**, 10, 1216-24	6.3	26

106	Examination of Ataxin-3 (atx-3) Aggregation by Structural Mass Spectrometry Techniques: A Rationale for Expedited Aggregation upon Polyglutamine (polyQ) Expansion. *Molecular and Cellular Proteomics*, **2015**, 14, 1241-53	7.6	25
105	Site-specific identification of an a□fibril-heparin interaction site by using solid-state NMR spectroscopy. *Angewandte Chemie - International Edition*, **2012**, 51, 13140-3	16.4	25
104	Internal friction of single polypeptide chains at high stretch. *Faraday Discussions*, **2008**, 139, 35-51; discussion 105-28, 419-20	3.6	25
103	De novo design of transmembrane □barrels. *Science*, **2021**, 371,	33.3	25
102	FPOP-LC-MS/MS Suggests Differences in Interaction Sites of Amphipols and Detergents with Outer Membrane Proteins. *Journal of the American Society for Mass Spectrometry*, **2017**, 28, 50-55	3.5	24
101	Malleability of the folding mechanism of the outer membrane protein PagP: parallel pathways and the effect of membrane elasticity. *Journal of Molecular Biology*, **2012**, 416, 453-64	6.5	24
100	Unfolding dynamics of proteins under applied force. *Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences*, **2003**, 361, 713-28; discussion 728-30	3	24
99	Analysis of amyloid nanostructures using photo-cross-linking: in situ comparison of three widely used photo-cross-linkers. *ACS Chemical Biology*, **2014**, 9, 761-8	4.9	23
98	Systematic analysis of the use of amphipathic polymers for studies of outer membrane proteins using mass spectrometry. *International Journal of Mass Spectrometry*, **2015**, 391, 54-61	1.9	23
97	Conformational properties of the unfolded state of Im7 in nondenaturing conditions. *Journal of Molecular Biology*, **2012**, 416, 300-18	6.5	23
96	Structure and dynamics of oligomeric intermediates in □-microglobulin self-assembly. *Biophysical Journal*, **2011**, 101, 1238-47	2.9	23
95	The pseudoazurin gene from Thiosphaera pantotropha: analysis of upstream putative regulatory sequences and overexpression in Escherichia coli. *Biochemical Journal*, **1997**, 321 (Pt 3), 699-705	3.8	23
94	Potential human transmission of amyloid □pathology: surveillance and risks. *Lancet Neurology, The*, **2020**, 19, 872-878	24.1	23
93	The role of conformational flexibility in □-microglobulin amyloid fibril formation at neutral pH. *Rapid Communications in Mass Spectrometry*, **2012**, 26, 1783-92	2.2	22
92	A force-activated trip switch triggers rapid dissociation of a colicin from its immunity protein. *PLoS Biology*, **2013**, 11, e1001489	9.7	22
91	Molecular Origins of the Compatibility between Glycosaminoglycans and A□0 Amyloid Fibrils. *Journal of Molecular Biology*, **2017**, 429, 2449-2462	6.5	21
90	A Population Shift between Sparsely Populated Folding Intermediates Determines Amyloidogenicity. *Journal of the American Chemical Society*, **2016**, 138, 6271-80	16.4	21
89	Structural insight into the formation of lipoprotein-□barrel complexes. *Nature Chemical Biology*, **2020**, 16, 1019-1025	11.7	20

88	The structure and dynamics in solution of Cu(I) pseudoazurin from Paracoccus pantotrophus. *Protein Science*, **2000**, 9, 846-58	6.3	20
87	Partially unfolded species populated during equilibrium denaturation of the beta-sheet protein Y74W apo-pseudoazurin. *Biochemistry*, **2000**, 39, 5672-82	3.2	20
86	Covalent cross-linking within supramolecular peptide structures. *Analytical Chemistry*, **2012**, 84, 6790-7	7.8	19
85	Insights into the role of the beta-2 microglobulin D-strand in amyloid propensity revealed by mass spectrometry. *Molecular BioSystems*, **2014**, 10, 412-20		18
84	Single-molecule studies of the Im7 folding landscape. *Journal of Molecular Biology*, **2010**, 398, 132-45	6.5	18
83	Desolvation and development of specific hydrophobic core packing during Im7 folding. *Journal of Molecular Biology*, **2010**, 396, 1329-45	6.5	17
82	Characterization of the response of primary cells relevant to dialysis-related amyloidosis to -microglobulin monomer and fibrils. *PLoS ONE*, **2011**, 6, e27353	3.7	17
81	Dual Role of Ribosome-Binding Domain of NAC as a Potent Suppressor of Protein Aggregation and Aging-Related Proteinopathies. *Molecular Cell*, **2019**, 74, 729-741.e7	17.6	16
80	PyXlinkViewer: A flexible tool for visualization of protein chemical crosslinking data within the PyMOL molecular graphics system. *Protein Science*, **2020**, 29, 1851-1857	6.3	16
79	Trifluoromethyldiazirine: an effective photo-induced cross-linking probe for exploring amyloid formation. *Chemical Communications*, **2008**, 5728-30	5.8	16
78	Using protein engineering to understand and modulate aggregation. *Current Opinion in Structural Biology*, **2020**, 60, 157-166	8.1	15
77	Extraction of accurate biomolecular parameters from single-molecule force spectroscopy experiments. *ACS Nano*, **2015**, 9, 1315-24	16.7	14
76	Helix stability and hydrophobicity in the folding mechanism of the bacterial immunity protein Im9. *Protein Engineering, Design and Selection*, **2005**, 18, 41-50	1.9	14
75	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. *Communications Biology*, **2020**, 3, 766	6.7	13
74	A tale of a tail: Structural insights into the conformational properties of the polyglutamine protein ataxin-3. *International Journal of Mass Spectrometry*, **2013**, 345-347, 63-70	1.9	13
73	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. *Analytical Chemistry*, **2017**, 89, 8844-8852	7.8	13
72	Detailed evaluation of the performance of microfluidic T mixers using fluorescence and ultraviolet resonance Raman spectroscopy. *Review of Scientific Instruments*, **2006**, 77, 055105	1.7	13
71	Conformational flexibility within the nascent polypeptide-associated complex enables its interactions with structurally diverse client proteins. *Journal of Biological Chemistry*, **2018**, 293, 8554-8568	5.4	12

70	Comparison of the aggregation of homologous β2-microglobulin variants reveals protein solubility as a key determinant of amyloid formation. *Journal of Molecular Biology*, **2016**, 428, 631-643	6.5	12
69	Probing dynamics within amyloid fibrils using a novel capping method. *Angewandte Chemie - International Edition*, **2009**, 48, 5705-7	16.4	12
68	Looking Beyond the Core: The Role of Flanking Regions in the Aggregation of Amyloidogenic Peptides and Proteins. *Frontiers in Neuroscience*, **2020**, 14, 611285	5.1	12
67	Epigallocatechin-3-gallate remodels apolipoprotein A-I amyloid fibrils into soluble oligomers in the presence of heparin. *Journal of Biological Chemistry*, **2018**, 293, 12877-12893	5.4	12
66	Using extensional flow to reveal diverse aggregation landscapes for three IgG1 molecules. *Biotechnology and Bioengineering*, **2018**, 115, 1216-1225	4.9	11
65	Monitoring oligomer formation from self-aggregating amylin peptides using ESI-IMS-MS. *International Journal for Ion Mobility Spectrometry*, **2013**, 16, 29-39	1.5	11
64	The Role of SurA PPIase Domains in Preventing Aggregation of the Outer-Membrane Proteins tOmpA and OmpT. *Journal of Molecular Biology*, **2019**, 431, 1267-1283	6.5	11
63	MpUL-multi: Software for Calculation of Amyloid Fibril Mass per Unit Length from TB-TEM Images. *Scientific Reports*, **2016**, 6, 21078	4.9	10
62	Phosphorylation as a tool to modulate aggregation propensity and to predict fibril architecture. *ChemBioChem*, **2012**, 13, 271-81	3.8	10
61	Sulfate-induced effects in the on-pathway intermediate of the bacterial immunity protein Im7. *Biochemistry*, **2006**, 45, 2274-82	3.2	10
60	A growing toolbox of techniques for studying β-barrel outer membrane protein folding and biogenesis. *Biochemical Society Transactions*, **2016**, 44, 802-9	5.1	10
59	An in vivo platform to select and evolve aggregation-resistant proteins. *Nature Communications*, **2020**, 11, 1816	17.4	10
58	Extracellular matrix components modulate different stages in β2-microglobulin amyloid formation. *Journal of Biological Chemistry*, **2019**, 294, 9392-9401	5.4	9
57	Amino acid insertion reveals a necessary three-helical intermediate in the folding pathway of the colicin E7 immunity protein Im7. *Journal of Molecular Biology*, **2009**, 392, 1074-86	6.5	9
56	Modulation of β-Amyloid Fibril Formation in Alzheimer's Disease by Microglia and Infection. *Frontiers in Molecular Neuroscience*, **2020**, 13, 609073	6.1	9
55	Spot the Difference: Function versus Toxicity in Amyloid Fibrils. *Trends in Biochemical Sciences*, **2020**, 45, 635-636	10.3	8
54	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. *Analytical Chemistry*, **2019**, 91, 15163-15170	7.8	8
53	Collagen I Weakly Interacts with the β-Sheets of β2-Microglobulin and Enhances Conformational Exchange To Induce Amyloid Formation. *Journal of the American Chemical Society*, **2020**, 142, 1321-1331	16.4	8

52	Characterization of Amyloid Oligomers by Electrospray Ionization-Ion Mobility Spectrometry-Mass Spectrometry (ESI-IMS-MS). *Methods in Molecular Biology*, **2016**, 1345, 115-32	1.4	7
51	Distinguishing closely related amyloid precursors using an RNA aptamer. *Journal of Biological Chemistry*, **2014**, 289, 26859-26871	5.4	7
50	Modulation of Amyloidogenic Protein Self-Assembly Using Tethered Small Molecules. *Journal of the American Chemical Society*, **2020**, 142, 20845-20854	16.4	7
49	Probing conformations of GroEL-bound substrate proteins by mass spectrometry. *Methods in Enzymology*, **1998**, 290, 296-313	1.7	6
48	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. *Angewandte Chemie*, **2018**, 130, 16930-16934	3.6	6
47	The role of high-dimensional diffusive search, stabilization, and frustration in protein folding. *Biophysical Journal*, **2014**, 106, 1729-40	2.9	5
46	A comparison of the folding characteristics of free and ribosome-tethered polypeptide chains using limited proteolysis and mass spectrometry. *Protein Science*, **2015**, 24, 1282-91	6.3	5
45	□Microglobulin667-695		5
44	Production of15N-labelled hen egg white lysozyme usingAspergillus niger. *Biotechnology Letters*, **1992**, 14, 897-902	3	5
43	The role of the I-state in D76N □microglobulin amyloid assembly: A crucial intermediate or an innocuous bystander?. *Journal of Biological Chemistry*, **2020**, 295, 12474-12484	5.4	5
42	Design and synthesis of cysteine-specific labels for photo-crosslinking studies.. *RSC Advances*, **2019**, 9, 7610-7614	3.7	4
41	The uniqueness of flow in probing the aggregation behavior of clinically relevant antibodies.. *Engineering Reports*, **2020**, 2, e12147	1.2	4
40	Conformational dynamics is more important than helical propensity for the folding of the all □helical protein Im7. *Protein Science*, **2013**, 22, 1722-38	6.3	4
39	How TriC folds tricky proteins. *Cell*, **2014**, 159, 1251-2	56.2	4
38	Dissecting key residues in folding and stability of the bacterial immunity protein 7. *Protein Engineering, Design and Selection*, **2011**, 24, 517-23	1.9	4
37	Avoidance of Epimerization in the Synthesis of Peptide Thioesters Using Fmoc Protection. *Synlett*, **2007**, 2007, 2517-2520	2.2	4
36	Structural insight into the formation of lipoprotein-□barrel complexes by the □barrel assembly machinery		4
35	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. *Nature Communications*, **2021**, 12, 4174	17.4	4

34	A peptide-display protein scaffold to facilitate single molecule force studies of aggregation-prone peptides. *Protein Science*, **2018**, 27, 1205-1217	6.3	3
33	Brazilin Removes Toxic Alpha-Synuclein and Seeding Competent Assemblies from Parkinson Brain by Altering Conformational Equilibrium. *Journal of Molecular Biology*, **2021**, 433, 166878	6.5	3
32	Hemodialysis-Related Amyloidosis **2010**, 347-379		2
31	Global Proteotoxicity Caused by Human Microglobulin Variants Impairs the Unfolded Protein Response in. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
30	Protein Misfolding and Toxicity in Dialysis-Related Amyloidosis **2012**, 377-405		2
29	Structural insights into peptide self-assembly using photo-induced crosslinking experiments and discontinuous molecular dynamics. *AICHE Journal*, **2021**, 67, e17101	3.6	2
28	Sequence grammar underlying unfolding and phase separation of globular proteins		2
27	-Microglobulin and Dialysis-Related Amyloidosis **2007**, 217-239		2
26	Tuning the rate of aggregation of hIAPP into amyloid using small-molecule modulators of assembly.. *Nature Communications*, **2022**, 13, 1040	17.4	2
25	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. *Communications Biology*, **2022**, 5,	6.7	2
24	Identification of a novel site of interaction between ataxin-3 and the amyloid aggregation inhibitor polyglutamine binding peptide 1. *European Journal of Mass Spectrometry*, **2018**, 24, 129-140	1.1	1
23	Site-Specific Identification of an AFibrilHeparin Interaction Site by Using Solid-State NMR Spectroscopy. *Angewandte Chemie*, **2012**, 124, 13317-13320	3.6	1
22	Insights into the molecular mechanisms of protein folding and misfolding **2002**, 352-354		1
21	Energy landscape steering in SecYEG mediates dynamic coupling in ATP driven protein translocation		1
20	PyXlinkViewer: a flexible tool for visualisation of protein chemical crosslinking data within the PyMOL molecular graphics system		1
19	The Dynamical Response of Proteins Under Force **2008**, 205-249		1
18	Generating Ensembles of Dynamic Misfolding Proteins.. *Frontiers in Neuroscience*, **2022**, 16, 881534	5.1	1
17	Determining the Free Energies of Outer Membrane Proteins in Lipid Bilayers. *Methods in Molecular Biology*, **2020**, 2168, 217-232	1.4	0

16	Investigation of D76N Microglobulin Using Protein Footprinting and Structural Mass Spectrometry. *Journal of the American Society for Mass Spectrometry*, **2021**, 32, 1583-1592	3.5	0
15	Linked Landscapes and Conformational Conversions: How Proteins Fold and Misfold **2012**, 1-16		
14	Ribosome-mediated refolding of partially-unfolded ricin A-chain. *Biochemical Society Transactions*, **2000**, 28, A68-A68	5.1	
13	From native state to amyloid; an investigation into partial unfolding of 2-microglobulin. *Biochemical Society Transactions*, **2000**, 28, A68-A68	5.1	
12	Partially folded states in helical protein folding. *Biochemical Society Transactions*, **2000**, 28, A69-A69	5.1	
11	Towards single molecule unfolding of proteins using AFM and its observation using fluorescence. *Biochemical Society Transactions*, **2000**, 28, A69-A69	5.1	
10	Unfolding of the sheet Protein Y74W Apo-pseudoazurin: Evidence of an Equilibrium Intermediate Species. *Biochemical Society Transactions*, **2000**, 28, A69-A69	5.1	
9	Exploring the folding landscape of alpha helical proteins. *Biochemical Society Transactions*, **2000**, 28, A70-A70	5.1	
8	An Investigation into the Properties of a Chaperone Domain and Analysis of the Non-covalently Bound Complexes with Peptide Substrates using Mass Spectrometry. *Biochemical Society Transactions*, **2000**, 28, A70-A70	5.1	
7	Professor Sir Christopher Martin Dobson (1949019). *Biochemist*, **2019**, 41, 45-45	0.5	
6	Dynamics of Membrane Proteins Monitored by Single-Molecule Fluorescence Across Multiple Timescales. *Methods in Molecular Biology*, **2020**, 2168, 273-297	1.4	
5	Biophysical Studies of Amyloid Formation and Its Inhibition. *FASEB Journal*, **2015**, 29, 491.1	0.9	
4	Finding the sweet spot for chaperone activity. *Nature Chemistry*, **2021**, 13, 397-399	17.6	
3	Homage to Chris Dobson. *Frontiers in Molecular Biosciences*, **2019**, 6, 137	5.6	
2	Richard Nelson Perham. 27 April 19374 February 2015. *Biographical Memoirs of Fellows of the Royal Society*, **2018**, 65, 317-339	0.1	
1	Orientation of a Diagnostic Ligand Bound to Macroscopically Aligned Amyloid-Fibrils Determined by Solid-State NMR. *Journal of Physical Chemistry Letters*, **2018**, 9, 6611-6615	6.4	