Michele Vendruscolo

List of Publications by Year
in descending order

903	109,941	185 151	326 287
papers	citations	h-index	g-index

979	979	979	51134
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Protein Misfolding, Functional Amyloid, and Human Disease. Annual Review of Biochemistry, 2006, 75, 333-366.	5.0	5,737
2	Protein folding and misfolding. Nature, 2003, 426, 884-890.	13.7	4,210
3	Inherent toxicity of aggregates implies a common mechanism for protein misfolding diseases. Nature, 2002, 416, 507-511.	13.7	2,322
4	Protein Misfolding, Amyloid Formation, and Human Disease: A Summary of Progress Over the Last Decade. Annual Review of Biochemistry, 2017, 86, 27-68.	5.0	1,929
5	The amyloid state and its association with protein misfolding diseases. Nature Reviews Molecular Cell Biology, 2014, 15, 384-396.	16.1	1,894
6	Protein misfolding, evolution and disease. Trends in Biochemical Sciences, 1999, 24, 329-332.	3.7	1,858
7	Protein aggregation and aggregate toxicity: new insights into protein folding, misfolding diseases and biological evolution. Journal of Molecular Medicine, 2003, 81, 678-699.	1.7	1,444
8	Proliferation of amyloid-Î²42 aggregates occurs through a secondary nucleation mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9758-9763.	3.3	1,162
9	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. Nature, 1997, 385, 787-793.	13.7	1,061
10	Rationalization of the effects of mutations on peptide andprotein aggregation rates. Nature, 2003, 424, 805-808.	13.7	1,013
11	An Analytical Solution to the Kinetics of Breakable Filament Assembly. Science, 2009, 326, 1533-1537.	6.0	970
12	Hydrodynamic Radii of Native and Denatured Proteins Measured by Pulse Field Gradient NMR Techniquesâ€. Biochemistry, 1999, 38, 16424-16431.	1.2	886
13	Chemical space and biology. Nature, 2004, 432, 824-828.	13.7	862
14	The structural basis of protein folding and its links with human disease. Philosophical Transactions of the Royal Society B: Biological Sciences, 2001, 356, 133-145.	1.8	828
15	Amyloid fibrils from muscle myoglobin. Nature, 2001, 410, 165-166.	13.7	791
16	Parmbsc1: a refined force field for DNA simulations. Nature Methods, 2016, 13, 55-58.	9.0	790
17	Protein Folding: A Perspective from Theory and Experiment. Angewandte Chemie - International Edition, 1998, 37, 868-893.	7.2	778
18	Principles of protein folding, misfolding and aggregation. Seminars in Cell and Developmental Biology, 2004, 15, 3-16.	2.3	772

#	Article	IF	Citations
19	The folding of hen lysozyme involves partially structured intermediates and multiple pathways. Nature, 1992, 358, 302-307.	13.7	771
20	The protofilament structure of insulin amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9196-9201.	3.3	770
21	Direct Observation of the Interconversion of Normal and Toxic Forms of Î±-Synuclein. Cell, 2012, 149, 1048-1059.	13.5	755
22	Amyloid formation by globular proteins under native conditions. Nature Chemical Biology, 2009, 5, 15-22.	3.9	746
23	ALS/FTD Mutation-Induced Phase Transition of FUS Liquid Droplets and Reversible Hydrogels into Irreversible Hydrogels Impairs RNP Granule Function. Neuron, 2015, 88, 678-690.	3.8	716
24	Role of Intermolecular Forces in Defining Material Properties of Protein Nanofibrils. Science, 2007, 318, 1900-1903.	6.0	694
25	FUS Phase Separation Is Modulated by a Molecular Chaperone and Methylation of Arginine Cation-Ï€ Interactions. Cell, 2018, 173, 720-734.e15.	13.5	662
26	Mapping Long-Range Interactions in Î±-Synuclein using Spin-Label NMR and Ensemble Molecular Dynamics Simulations. Journal of the American Chemical Society, 2005, 127, 476-477.	6.6	658
27	Simultaneous determination of protein structure and dynamics. Nature, 2005, 433, 128-132.	13.7	641
28	Amyloid-like Aggregates Sequester Numerous Metastable Proteins with Essential Cellular Functions. Cell, 2011, 144, 67-78.	13.5	604
29	Long-Range Interactions Within a Nonnative Protein. Science, 2002, 295, 1719-1722.	6.0	600
30	Characterization of the nanoscale properties of individual amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15806-15811.	3.3	579
31	Prediction of â€œAggregation-proneâ€•and â€œAggregation-susceptibleâ€•Regions in Proteins Associated with Neurodegenerative Diseases. Journal of Molecular Biology, 2005, 350, 379-392.	2.0	557
32	Solution conditions determine the relative importance of nucleation and growth processes in Î±-synuclein aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7671-7676.	3.3	546
33	Molecular mechanisms of protein aggregation from global fitting of kinetic models. Nature Protocols, 2016, 11, 252-272.	5.5	546
34	Lipid vesicles trigger Î±-synuclein aggregation by stimulating primary nucleation. Nature Chemical Biology, 2015, 11, 229-234.	3.9	532
35	Characterization of a partly folded protein by NMR methods: studies on the molten globule state of guinea pig .alpha.-lactalbumin. Biochemistry, 1989, 28, 7-13.	1.2	504
36	Protein structure determination from NMR chemical shifts. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9615-9620.	3.3	499

#	Article	IF	Citations
37	A causative link between the structure of aberrant protein oligomers and their toxicity. Nature Chemical Biology, 2010, 6, 140-147.	3.9	499
38	High-resolution molecular structure of a peptide in an amyloid fibril determined by magic angle spinning NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 711-716.	3.3	495
39	Structural basis of membrane disruption and cellular toxicity by Î±-synuclein oligomers. Science, 2017, 358, 1440-1443.	6.0	492
40	Cryo-electron microscopy structure of an SH3 amyloid fibril and model of the molecular packing. EMBO Journal, 1999, 18, 815-821.	3.5	487
41	Atomic structure and hierarchical assembly of a cross-Î² amyloid fibril. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5468-5473.	3.3	479
42	Widespread Proteome Remodeling and Aggregation in Aging C.Âelegans. Cell, 2015, 161, 919-932.	13.5	478
43	The Amyloid-Î² Pathway in Alzheimerâ€™s Disease. Molecular Psychiatry, 2021, 26, 5481-5503.	4.1	478
44	The behaviour of polyamino acids reveals an inverse side chain effect in amyloid structure formation. EMBO Journal, 2002, 21, 5682-5690.	3.5	475
45	Understanding protein folding via free-energy surfaces from theory and experiment. Trends in Biochemical Sciences, 2000, 25, 331-339.	3.7	461
46	Formation of insulin amyloid fibrils followed by FTIR simultaneously with CD and electron microscopy. Protein Science, 2000, 9, 1960-1967.	3.1	453
47	Low-populated folding intermediates of Fyn SH3 characterized by relaxation dispersion NMR. Nature, 2004, 430, 586-590.	13.7	445
48	Three key residues form a critical contact network in a protein folding transition state. Nature, 2001, 409, 641-645.	13.7	423
49	Prediction of Aggregation-Prone Regions in Structured Proteins. Journal of Molecular Biology, 2008, 380, 425-436.	2.0	420
50	From Macroscopic Measurements to Microscopic Mechanisms of Protein Aggregation. Journal of Molecular Biology, 2012, 421, 160-171.	2.0	407
51	Differences in nucleation behavior underlie the contrasting aggregation kinetics of the AÎ²40 and AÎ²42 peptides. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9384-9389.	3.3	405
52	Formation and seeding of amyloid fibrils from wild-type hen lysozyme and a peptide fragment from the Î²-domain. Journal of Molecular Biology, 2000, 300, 541-549.	2.0	395
53	Structural characterization of toxic oligomers that are kinetically trapped during Î±-synuclein fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1994-2003.	3.3	384
54	De novo designed peptide-based amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16052-16057.	3.3	381

#	Article	IF	Citations
55	Analysis of Main Chain Torsion Angles in Proteins: Prediction of NMR Coupling Constants for Native and Random Coil Conformations. Journal of Molecular Biology, 1996, 255, 494-506.	2.0	379
56	The fundamentals of protein folding: bringing together theory and experiment. Current Opinion in Structural Biology, 1999, 9, 92-101.	2.6	375
57	Kinetic partitioning of protein folding and aggregation. Nature Structural Biology, 2002, 9, 137-143.	9.7	373
58	A molecular chaperone breaks the catalytic cycle that generates toxic Aî² oligomers. Nature Structural and Molecular Biology, 2015, 22, 207-213.	3.6	373
59	Metastability of Native Proteins and the Phenomenon of Amyloid Formation. Journal of the American Chemical Society, 2011, 133, 14160-14163.	6.6	369
60	Direct observation of the three regions in Î±-synuclein that determine its membrane-bound behaviour. Nature Communications, 2014, 5, 3827.	5.8	357
61	Prefibrillar Amyloid Protein Aggregates Share Common Features of Cytotoxicity. Journal of Biological Chemistry, 2004, 279, 31374-31382.	1.6	346
62	Multiple Tight Phospholipid-Binding Modes of Î±-Synuclein Revealed by Solution NMR Spectroscopy. Journal of Molecular Biology, 2009, 390, 775-790.	2.0	345
63	Half a century of amyloids: past, present and future. Chemical Society Reviews, 2020, 49, 5473-5509.	18.7	345
64	Molecular recycling within amyloid fibrils. Nature, 2005, 436, 554-558.	13.7	342
65	The CamSol Method of Rational Design of Protein Mutants with Enhanced Solubility. Journal of Molecular Biology, 2015, 427, 478-490.	2.0	341
66	Structure of an Intermediate State in Protein Folding and Aggregation. Science, 2012, 336, 362-366.	6.0	339
67	ANS Binding Reveals Common Features of Cytotoxic Amyloid Species. ACS Chemical Biology, 2010, 5, 735-740.	1.6	335
68	Protein-misfolding diseases: Getting out of shape. Nature, 2002, 418, 729-730.	13.7	334
69	RNA Granules Hitchhike on Lysosomes for Long-Distance Transport, Using Annexin A11 as a Molecular Tether. Cell, 2019, 179, 147-164.e20.	13.5	327
70	Determination of Secondary Structure Populations in Disordered States of Proteins Using Nuclear Magnetic Resonance Chemical Shifts. Biochemistry, 2012, 51, 2224-2231.	1.2	316
71	Prediction of the Absolute Aggregation Rates of Amyloidogenic Polypeptide Chains. Journal of Molecular Biology, 2004, 341, 1317-1326.	2.0	307
72	The Zyggregator method for predicting protein aggregation propensities. Chemical Society Reviews, 2008, 37, 1395.	18.7	307

#	Article	IF	Citations
73	Stabilization of neurotoxic Alzheimer amyloid-Î² oligomers by protein engineering. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15595-15600.	3.3	304
74	The concept of a random coil: Residual structure in peptides and denatured proteins. Folding & Design, 1996, 1, R95-R106.	4.5	296
75	Structural and Dynamical Properties of a Denatured Protein. Heteronuclear 3D NMR Experiments and Theoretical Simulations of Lysozyme in 8 M Ureaâ€. Biochemistry, 1997, 36, 8977-8991.	1.2	296
76	The importance of sequence diversity in the aggregation and evolution of proteins. Nature, 2005, 438, 878-881.	13.7	291
77	The extracellular chaperone clusterin influences amyloid formation and toxicity by interacting with prefibrillar structures. FASEB Journal, 2007, 21, 2312-2322.	0.2	285
78	Principles of protein structural ensemble determination. Current Opinion in Structural Biology, 2017, 42, 106-116.	2.6	285
79	Myoglobin forms amyloid fibrils by association of unfolded polypeptide segments. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15463-15468.	3.3	270
80	Nucleated polymerization with secondary pathways. I. Time evolution of the principal moments. Journal of Chemical Physics, 2011, 135, 065105.	1.2	270
81	Studies of the aggregation of mutant proteins in vitro provide insights into the genetics of amyloid diseases. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16419-16426.	3.3	268
82	Location of Aluminum in Substituted Calcium Silicate Hydrate (C-S-H) Gels as Determined by 29Si and 27Al NMR and EELS. Journal of the American Ceramic Society, 1993, 76, 2285-2288.	1.9	266
83	Life on the edge: a link between gene expression levels and aggregation rates of human proteins. Trends in Biochemical Sciences, 2007, 32, 204-206.	3.7	266
84	Alpha-Synuclein Oligomers Interact with Metal Ions to Induce Oxidative Stress and Neuronal Death in Parkinson's Disease. Antioxidants and Redox Signaling, 2016, 24, 376-391.	2.5	266
85	Demonstration by NMR of folding domains in lysozyme. Nature, 1991, 349, 633-636.	13.7	265
86	Characterization of the Oligomeric States of Insulin in Self-Assembly and Amyloid Fibril Formation by Mass Spectrometry. Biophysical Journal, 2000, 79, 1053-1065.	0.2	258
87	Mutational analysis of acylphosphatase suggests the importance of topology and contact order in protein folding. Nature Structural Biology, 1999, 6, 1005-1009.	9.7	257
88	Mutations associated with familial Parkinsonâ€™s disease alter the initiation and amplification steps of Î±-synuclein aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10328-10333.	3.3	252
89	Molecular conformation of a peptide fragment of transthyretin in an amyloid fibril. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16748-16753.	3.3	249
90	A Highly Amyloidogenic Region of Hen Lysozyme. Journal of Molecular Biology, 2004, 340, 1153-1165.	2.0	248

#	Article	IF	Citations
91	Chemical properties of lipids strongly affect the kinetics of the membrane-induced aggregation of Î±-synuclein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7065-7070.	3.3	248
92	Widespread Aggregation and Neurodegenerative Diseases Are Associated with Supersaturated Proteins. Cell Reports, 2013, 5, 781-790.	2.9	245
93	Short amino acid stretches can mediate amyloid formation in globular proteins: The Src homology 3 (SH3) case. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7258-7263.	3.3	241
94	A residue-specific NMR view of the non-cooperative unfolding of a molten globule. Nature Structural Biology, 1997, 4, 630-634.	9.7	236
95	A kinetic study of Î²-lactoglobulin amyloid fibril formation promoted by urea. Protein Science, 2009, 11, 2417-2426.	3.1	233
96	The formation of spherulites by amyloid fibrils of bovine insulin. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14420-14424.	3.3	232
97	The extracellular chaperone clusterin sequesters oligomeric forms of the amyloid-Î²1â˜’40 peptide. Nature Structural and Molecular Biology, 2012, 19, 79-83.	3.6	232
98	A natural product inhibits the initiation of Î±-synuclein aggregation and suppresses its toxicity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1009-E1017.	3.3	231
99	Recovery of protein structure from contact maps. Folding & Design, 1997, 2, 295-306.	4.5	230
100	A camelid antibody fragment inhibits the formation of amyloid fibrils by human lysozyme. Nature, 2003, 424, 783-788.	13.7	227
101	Heat Shock Protein 70 Inhibits Î±-Synuclein Fibril Formation via Preferential Binding to Prefibrillar Species. Journal of Biological Chemistry, 2005, 280, 14733-14740.	1.6	223
102	Fast and Accurate Predictions of Protein NMR Chemical Shifts from Interatomic Distances. Journal of the American Chemical Society, 2009, 131, 13894-13895.	6.6	223
103	Dynamics of oligomer populations formed during the aggregation of Alzheimerâ€™s AÎ²42 peptide. Nature Chemistry, 2020, 12, 445-451.	6.6	223
104	Prefibrillar Amyloid Aggregates Could Be Generic Toxins in Higher Organisms. Journal of Neuroscience, 2006, 26, 8160-8167.	1.7	222
105	Conformation of GroEL-bound Î±-lactalbumin probed by mass spectrometry. Nature, 1994, 372, 646-651.	13.7	221
106	Kinetic analysis reveals the diversity of microscopic mechanisms through which molecular chaperones suppress amyloid formation. Nature Communications, 2016, 7, 10948.	5.8	219
107	The Role of Stable Î±-Synuclein Oligomers in the Molecular Events Underlying Amyloid Formation. Journal of the American Chemical Society, 2014, 136, 3859-3868.	6.6	218
108	Effects of Î±-tubulin acetylation on microtubule structure and stability. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10366-10371.	3.3	216

#	Article	IF	Citations
109	Structural Determinants of Protein Dynamics: Analysis of 15N NMR Relaxation Measurements for Main-Chain and Side-Chain Nuclei of Hen Egg White Lysozyme. Biochemistry, 1995, 34, 4041-4055.	1.2	211
110	Dependence on solution conditions of aggregation and amyloid formation by an SH3 domain. Journal of Molecular Biology, 2001, 311, 325-340.	2.0	208
111	Local cooperativity in the unfolding of an amyloidogenic variant of human lysozyme. Nature Structural Biology, 2002, 9, 308-315.	9.7	208
112	Differential Phospholipid Binding of Î±-Synuclein Variants Implicated in Parkinsonâ€™s Disease Revealed by Solution NMR Spectroscopy. Biochemistry, 2010, 49, 862-871.	1.2	208
113	Following protein folding in real time using NMR spectroscopy. Nature Structural Biology, 1995, 2, 865-870.	9.7	206
114	Characterisation of protein unfolding by NMR diffusion measurements. Journal of Biomolecular NMR, 1997, 10, 199-203.	1.6	206
115	Structural basis of synaptic vesicle assembly promoted by Î±-synuclein. Nature Communications, 2016, 7, 12563.	5.8	203
116	Different Subdomains are Most Protected From Hydrogen Exchange in the Molten Globule and Native States of Human Î±-Lactalbumin. Journal of Molecular Biology, 1995, 253, 651-657.	2.0	200
117	Ostwaldâ€™s rule of stages governs structural transitions and morphology of dipeptide supramolecular polymers. Nature Communications, 2014, 5, 5219.	5.8	197
118	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	6.5	195
119	Structural Reorganisation and Potential Toxicity of Oligomeric Species Formed during the Assembly of Amyloid Fibrils. PLoS Computational Biology, 2007, 3, e173.	1.5	194
120	Quenched disorder, memory, and self-organization. Physical Review E, 1996, 53, R13-R16.	0.8	193
121	Amyloid Fibril Formation by Bovine Milk Î²-Casein and Its Inhibition by the Molecular Chaperones Î±S- and Î²-Casein. Biochemistry, 2005, 44, 17027-17036.	1.2	193
122	Progressive Changes in the Structure of Hardened C3S Cement Pastes due to Carbonation. Journal of the American Ceramic Society, 1991, 74, 2891-2896.	1.9	191
123	Chemical kinetics for drug discovery to combat protein aggregation diseases. Trends in Pharmacological Sciences, 2014, 35, 127-135.	4.0	191
124	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	6.5	190
125	Determination of the Free Energy Landscape of Î±-Synuclein Using Spin Label Nuclear Magnetic Resonance Measurements. Journal of the American Chemical Society, 2009, 131, 18314-18326.	6.6	187
126	Kinetics and thermodynamics of amyloid formation from direct measurements of fluctuations in fibril mass. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10016-10021.	3.3	186

#	Article	IF	Citations
127	Cholesterol catalyses AÎ²42 aggregation through a heterogeneous nucleation pathway in the presence of lipid membranes. Nature Chemistry, 2018, 10, 673-683.	6.6	186
128	Ultrastructural Organization of Amyloid Fibrils byAtomic Force Microscopy. Biophysical Journal, 2000, 79, 3282-3293.	0.2	185
129	Î±-Synuclein Senses Lipid Packing Defects and Induces Lateral Expansion of Lipids Leading to Membrane Remodeling. Journal of Biological Chemistry, 2013, 288, 20883-20895.	1.6	183
130	Protein amyloids develop an intrinsic fluorescence signature during aggregation. Analyst, The, 2013, 138, 2156.	1.7	182
131	Kinetic model of the aggregation of alpha-synuclein provides insights into prion-like spreading. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1206-15.	3.3	181
132	Proline isomerism in staphylococcal nuclease characterized by NMR and site-directed mutagenesis. Nature, 1987, 329, 266-268.	13.7	180
133	Functionalised amyloid fibrils for roles in cell adhesion. Biomaterials, 2008, 29, 1553-1562.	5.7	180
134	Direct characterization of amyloidogenic oligomers by single-molecule fluorescence. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14424-14429.	3.3	180
135	Metainference: A Bayesian inference method for heterogeneous systems. Science Advances, 2016, 2, e1501177.	4.7	180
136	An anticancer drug suppresses the primary nucleation reaction that initiates the production of the toxic AÎ²42 aggregates linked with Alzheimerâ€™s disease. Science Advances, 2016, 2, e1501244.	4.7	180
137	Systematic development of small molecules to inhibit specific microscopic steps of AÎ²42 aggregation in Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E200-E208.	3.3	180
138	Widespread occurrence of the droplet state of proteins in the human proteome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 33254-33262.	3.3	178
139	Investigation of protein folding by mass spectrometry. FASEB Journal, 1996, 10, 93-101.	0.2	175
140	Cucurbit[8]uril and Blue-Box: High-Energy Water Release Overwhelms Electrostatic Interactions. Journal of the American Chemical Society, 2013, 135, 14879-14888.	6.6	174
141	Systematic In Vivo Analysis of the Intrinsic Determinants of Amyloid Î² Pathogenicity. PLoS Biology, 2007, 5, e290.	2.6	171
142	Folding of a four-helix bundle: studies of acyl-coenzyme A binding protein. Biochemistry, 1995, 34, 7217-7224.	1.2	169
143	Molecular dynamics simulations with replica-averaged structural restraints generate structural ensembles according to the maximum entropy principle. Journal of Chemical Physics, 2013, 138, 094112.	1.2	169
144	Amyloid Fibril Formation by Lens Crystallin Proteins and Its Implications for Cataract Formation. Journal of Biological Chemistry, 2004, 279, 3413-3419.	1.6	166

#	Article	IF	Citations
145	Exploring amyloid formation by a de novo design. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4435-4440.	3.3	166
146	Nucleated polymerization with secondary pathways. II. Determination of self-consistent solutions to growth processes described by non-linear master equations. Journal of Chemical Physics, 2011, 135, 065106.	1.2	166
147	Toxicity of Protein Oligomers Is Rationalized by a Function Combining Size and Surface Hydrophobicity. ACS Chemical Biology, 2014, 9, 2309-2317.	1.6	166
148	Structure and Properties of a Complex of Î±-Synuclein and a Single-Domain Camelid Antibody. Journal of Molecular Biology, 2010, 402, 326-343.	2.0	164
149	Chemical Kinetics for Bridging Molecular Mechanisms and Macroscopic Measurements of Amyloid Fibril Formation. Annual Review of Physical Chemistry, 2018, 69, 273-298.	4.8	161
150	Toward a Description of the Conformations of Denatured States of Proteins. Comparison of a Random Coil Model with NMR Measurements. The Journal of Physical Chemistry, 1996, 100, 2661-2666.	2.9	160
151	Protein misfolding and disease: from the test tube to the organism. Current Opinion in Chemical Biology, 2008, 12, 25-31.	2.8	160
152	Intermolecular Structure Determination of Amyloid Fibrils with Magic-Angle Spinning and Dynamic Nuclear Polarization NMR. Journal of the American Chemical Society, 2011, 133, 13967-13974.	6.6	160
153	A refined solution structure of hen lysozyme determined using residual dipolar coupling data. Protein Science, 2001, 10, 677-688.	3.1	159
154	Direct Observation of Heterogeneous Amyloid Fibril Growth Kinetics via Two-Color Super-Resolution Microscopy. Nano Letters, 2014, 14, 339-345.	4.5	159
155	Interaction of the Molecular Chaperone DNAJB6 with Growing Amyloid-beta 42 (Aî²42) Aggregates Leads to Sub-stoichiometric Inhibition of Amyloid Formation. Journal of Biological Chemistry, 2014, 289, 31066-31076.	1.6	158
156	Formation of Mixed Fibrils Demonstrates the Generic Nature and Potential Utility of Amyloid Nanostructures. Journal of the American Chemical Society, 2000, 122, 12707-12713.	6.6	155
157	Determination of an Ensemble of Structures Representing the Denatured State of the Bovine Acyl-Coenzyme A Binding Protein. Journal of the American Chemical Society, 2004, 126, 3291-3299.	6.6	155
158	Protein Aggregation and Its Consequences for Human Disease. Protein and Peptide Letters, 2006, 13, 219-227.	0.4	154
159	A tau homeostasis signature is linked with the cellular and regional vulnerability of excitatory neurons to tau pathology. Nature Neuroscience, 2019, 22, 47-56.	7.1	154
160	The Folding Kinetics and Thermodynamics of the Fyn-SH3 Domainâ€. Biochemistry, 1998, 37, 2529-2537.	1.2	152
161	Multi-dimensional super-resolution imaging enables surface hydrophobicity mapping. Nature Communications, 2016, 7, 13544.	5.8	152
162	Rapid collapse and slow structural reorganisation during the refolding of bovine Î±-lactalbumin. Journal of Molecular Biology, 1999, 288, 673-688.	2.0	151

#	Article	IF	Citations
163	In Situ Measurements of the Formation and Morphology of Intracellular Î²-Amyloid Fibrils by Super-Resolution Fluorescence Imaging. Journal of the American Chemical Society, 2011, 133, 12902-12905.	6.6	151
164	Physicochemical principles that regulate the competition between functional and dysfunctional association of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10159-10164.	3.3	148
165	ALS mutations in FUS cause neuronal dysfunction and death in Caenorhabditis elegans by a dominant gain-of-function mechanism. Human Molecular Genetics, 2012, 21, 1-9.	1.4	148
166	Altered aggregation properties of mutant Î³-crystallins cause inherited cataract. EMBO Journal, 2002, 21, 6005-6014.	3.5	147
167	Supersaturation is a major driving force for protein aggregation in neurodegenerative diseases. Trends in Pharmacological Sciences, 2015, 36, 72-77.	4.0	147
168	A Labelâ€Free, Quantitative Assay of Amyloid Fibril Growth Based on Intrinsic Fluorescence. ChemBioChem, 2013, 14, 846-850.	1.3	145
169	Structural characterization of a highlyâ€“ordered â€˜molten globuleâ€™ at low pH. Nature Structural and Molecular Biology, 1994, 1, 23-29.	3.6	144
170	Binding of the Molecular Chaperone Î±B-Crystallin to AÎ² Amyloid Fibrils Inhibits Fibril Elongation. Biophysical Journal, 2011, 101, 1681-1689.	0.2	143
171	Protein Aggregation in Crowded Environments. Journal of the American Chemical Society, 2010, 132, 5170-5175.	6.6	142
172	Amyloid Fibril Formation Can Proceed from Different Conformations of a Partially Unfolded Protein. Biophysical Journal, 2005, 89, 4201-4210.	0.2	141
173	Using NMR Chemical Shifts as Structural Restraints in Molecular Dynamics Simulations of Proteins. Structure, 2010, 18, 923-933.	1.6	141
174	The S/T-Rich Motif in the DNAJB6 Chaperone Delays Polyglutamine Aggregation and the Onset of Disease in a Mouse Model. Molecular Cell, 2016, 62, 272-283.	4.5	140
175	Different soluble aggregates of AÎ²42 can give rise to cellular toxicity through different mechanisms. Nature Communications, 2019, 10, 1541.	5.8	140
176	Temperature dependent molecular motion of a tyrosine residue of ferrocytochromeC. FEBS Letters, 1976, 70, 96-100.	1.3	138
177	Molecular mechanisms used by chaperones to reduce the toxicity of aberrant protein oligomers. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12479-12484.	3.3	137
178	Pairwise contact potentials are unsuitable for protein folding. Journal of Chemical Physics, 1998, 109, 11101-11108.	1.2	136
179	Relation between native ensembles and experimental structures of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10901-10906.	3.3	136
180	The Interaction of Î±B-Crystallin with Mature Î±-Synuclein Amyloid Fibrils Inhibits Their Elongation. Biophysical Journal, 2010, 98, 843-851.	0.2	136

#	Article	IF	Citations
181	Calcium is a key factor in Î±-synuclein induced neurotoxicity. Journal of Cell Science, 2016, 129, 1792-801.	1.2	136
182	Chromatin Unfolding by Epigenetic Modifications Explained by Dramatic Impairment of Internucleosome Interactions: A Multiscale Computational Study. Journal of the American Chemical Society, 2015, 137, 10205-10215.	6.6	135
183	A structural ensemble of a ribosomeâ€“nascent chain complex during cotranslational protein folding. Nature Structural and Molecular Biology, 2016, 23, 278-285.	3.6	135
184	Hydrophobic clustering in nonnative states of a protein: Interpretation of chemical shifts in NMR spectra of denatured states of lysozyme. Proteins: Structure, Function and Bioinformatics, 1991, 9, 248-266.	1.5	134
185	Observation of spatial propagation of amyloid assembly from single nuclei. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14746-14751.	3.3	134
186	Identification of the Core Structure of Lysozyme Amyloid Fibrils by Proteolysis. Journal of Molecular Biology, 2006, 361, 551-561.	2.0	133
187	Determination of conformationally heterogeneous states of proteins. Current Opinion in Structural Biology, 2007, 17, 15-20.	2.6	132
188	Reduced proteasome activity in the aging brain results in ribosome stoichiometry loss and aggregation. Molecular Systems Biology, 2020, 16, e9596.	3.2	131
189	Analysis of .vphi. and .chi.1 torsion angles for hen lysozyme in solution from proton NMR spin-spin coupling constants. Biochemistry, 1991, 30, 986-996.	1.2	130
190	Evidence for a Mechanism of Amyloid Formation Involving Molecular Reorganisation within Native-like Precursor Aggregates. Journal of Molecular Biology, 2005, 351, 910-922.	2.0	129
191	Dynamic binding mode of a Synaptotagmin-1â€“SNARE complex in solution. Nature Structural and Molecular Biology, 2015, 22, 555-564.	3.6	129
192	Distinct thermodynamic signatures of oligomer generation in the aggregation of the amyloid-Î² peptide. Nature Chemistry, 2018, 10, 523-531.	6.6	129
193	Preparation and Characterization of Purified Amyloid Fibrils. Journal of the American Chemical Society, 2001, 123, 8141-8142.	6.6	128
194	Nature and Significance of the Interactions between Amyloid Fibrils and Biological Polyelectrolytesâ€. Biochemistry, 2006, 45, 12806-12815.	1.2	128
195	Secondary nucleation and elongation occur at different sites on Alzheimerâ€™s amyloid-Î² aggregates. Science Advances, 2019, 5, eaau3112.	4.7	127
196	Collapse and cooperativity in protein folding. Current Opinion in Structural Biology, 1996, 6, 31-42.	2.6	126
197	Determination of Protein Structures Consistent with NMR Order Parameters. Journal of the American Chemical Society, 2004, 126, 8090-8091.	6.6	126
198	The MUMO (minimal under-restraining minimal over-restraining) method for the determination of native state ensembles of proteins. Journal of Biomolecular NMR, 2007, 37, 117-135.	1.6	126

#	Article	IF	Citations
199	Targeting the Intrinsically Disordered Structural Ensemble of Î±-Synuclein by Small Molecules as a Potential Therapeutic Strategy for Parkinsonâ€™s Disease. PLoS ONE, 2014, 9, e87133.	1.1	126
200	Comparison of MD Simulations and NMR Experiments for Hen Lysozyme. Analysis of Local Fluctuations, Cooperative Motions, and Global Changes. Biochemistry, 1995, 34, 10918-10931.	1.2	124
201	Parapred: antibody paratope prediction using convolutional and recurrent neural networks. Bioinformatics, 2018, 34, 2944-2950.	1.8	124
202	Hydration of Tricalcium Silicate Followed by 29Si NMR with Cross-Polarization. Journal of the American Ceramic Society, 1988, 71, 91-96.	1.9	123
203	Characterization of the nucleation barriers for protein aggregation and amyloid formation. HFSP Journal, 2007, 1, 137-146.	2.5	123
204	Kinetic fingerprints differentiate the mechanisms of action of anti-AÎ² antibodies. Nature Structural and Molecular Biology, 2020, 27, 1125-1133.	3.6	123
205	The release of toxic oligomers from Î±-synuclein fibrils induces dysfunction in neuronal cells. Nature Communications, 2021, 12, 1814.	5.8	123
206	Molecular dynamics simulations of native and substrate-bound lysozyme. Journal of Molecular Biology, 1986, 190, 455-479.	2.0	122
207	Rare Fluctuations of Native Proteins Sampled by Equilibrium Hydrogen Exchange. Journal of the American Chemical Society, 2003, 125, 15686-15687.	6.6	122
208	Experimental investigation of protein folding and misfolding. Methods, 2004, 34, 4-14.	1.9	122
209	Characterization of the free-energy landscapes of proteins by NMR-guided metadynamics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6817-6822.	3.3	122
210	Alpha-lactalbumin forms a compact molten globule in the absence of disulfide bonds. Nature Structural Biology, 1999, 6, 948-952.	9.7	121
211	A Coupled Equilibrium Shift Mechanism in Calmodulin-Mediated Signal Transduction. Structure, 2008, 16, 736-746.	1.6	121
212	Perturbation of the Stability of Amyloid Fibrils through Alteration of Electrostatic Interactions. Biophysical Journal, 2011, 100, 2783-2791.	0.2	121
213	Protein Microgels from Amyloid Fibril Networks. ACS Nano, 2015, 9, 43-51.	7.3	121
214	The inverted free energy landscape of an intrinsically disordered peptide by simulations and experiments. Scientific Reports, 2015, 5, 15449.	1.6	118
215	Amyloid fibril formation by a helical cytochrome. FEBS Letters, 2001, 495, 184-186.	1.3	117
216	Structure and dynamics of a ribosome-bound nascent chain by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16516-16521.	3.3	116

#	Article	IF	Citations
217	Protein folding on the ribosome. Current Opinion in Structural Biology, 2010, 20, 33-45.	2.6	116
218	Selective targeting of primary and secondary nucleation pathways in Aî²42 aggregation using a rational antibody scanning method. Science Advances, 2017, 3, e1700488.	4.7	116
219	Structural Interpretation of Hydrogen Exchange Protection Factors in Proteins: Characterization of the Native State Fluctuations of CI2. Structure, 2006, 14, 97-106.	1.6	115
220	Proteome-wide observation of the phenomenon of life on the edge of solubility. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1015-1020.	3.3	115
221	Multiple conformations of a protein demonstrated by magnetization transfer NMR spectroscopy. Nature, 1986, 320, 192-194.	13.7	114
222	Rational design of antibodies targeting specific epitopes within intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9902-9907.	3.3	113
223	Simultaneous quantification of protein order and disorder. Nature Chemical Biology, 2017, 13, 339-342.	3.9	113
224	Detailed Analysis of the Energy Barriers for Amyloid Fibril Growth. Angewandte Chemie - International Edition, 2012, 51, 5247-5251.	7.2	112
225	Protein folding and misfolding: a paradigm of selfâ€“assembly and regulation in complex biological systems. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2003, 361, 1205-1222.	1.6	111
226	Clusterin facilitates in vivo clearance of extracellular misfolded proteins. Cellular and Molecular Life Sciences, 2011, 68, 3919-3931.	2.4	111
227	Direct Observations of Amyloid Î² Self-Assembly in Live Cells Provide Insights into Differences in the Kinetics of Aî²(1â€“40) and Aî²(1â€“42) Aggregation. Chemistry and Biology, 2014, 21, 732-742.	6.2	111
228	Trodusquemine enhances Aî²42 aggregation but suppresses its toxicity by displacing oligomers from cell membranes. Nature Communications, 2019, 10, 225.	5.8	111
229	The Amyloid Phenomenon and Its Significance in Biology and Medicine. Cold Spring Harbor Perspectives in Biology, 2020, 12, a033878.	2.3	111
230	Structural basis of the stability of a lysozyme molten globule. Nature Structural Biology, 1995, 2, 871-875.	9.7	110
231	Chaperone proteostasis in Parkinson's disease: stabilization of the Hsp70/Î±-synuclein complex by Hip. EMBO Journal, 2009, 28, 3758-3770.	3.5	110
232	Protein engineering as a strategy to avoid formation of amyloid fibrils. Protein Science, 2000, 9, 1700-1708.	3.1	109
233	How to guarantee optimal stability for most representative structures in the protein data bank. Proteins: Structure, Function and Bioinformatics, 2001, 44, 79-96.	1.5	109
234	Experimental characterization of disordered and ordered aggregates populated during the process of amyloid fibril formation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7828-7833.	3.3	109

#	Article	IF	Citations
235	Atomic force microscopy for single molecule characterisation of protein aggregation. Archives of Biochemistry and Biophysics, 2019, 664, 134-148.	1.4	109
236	The Amyloid Phenomenon and Its Links with Human Disease. Cold Spring Harbor Perspectives in Biology, 2017, 9, a023648.	2.3	108
237	Determination of a Transition State at Atomic Resolution from Protein Engineering Data. Journal of Molecular Biology, 2002, 324, 151-163.	2.0	107
238	Binding affinity of amyloid oligomers to cellular membranes is a generic indicator of cellular dysfunction in protein misfolding diseases. Scientific Reports, 2016, 6, 32721.	1.6	107
239	Slow folding of muscle acylphosphatase in the absence of intermediates 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 283, 883-891.	2.0	106
240	A Generic Mechanism of Emergence of Amyloid Protofilaments from Disordered Oligomeric Aggregates. PLoS Computational Biology, 2008, 4, e1000222.	1.5	106
241	Inhibition of Î±-Synuclein Fibrillization by Dopamine Is Mediated by Interactions with Five C-Terminal Residues and with E83 in the NAC Region. PLoS ONE, 2008, 3, e3394.	1.1	106
242	Microfluidic Diffusion Analysis of the Sizes and Interactions of Proteins under Native Solution Conditions. ACS Nano, 2016, 10, 333-341.	7.3	105
243	Three-Dimensional Structures of Translating Ribosomes by Cryo-EM. Molecular Cell, 2004, 14, 57-66.	4.5	104
244	Rational design of aggregation-resistant bioactive peptides: Reengineering human calcitonin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10105-10110.	3.3	104
245	Kinetic diversity of amyloid oligomers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12087-12094.	3.3	103
246	Can a pairwise contact potential stabilize native protein folds against decoys obtained by threading?. , 2000, 38, 134-148.		102
247	Protein folding and the organization of the protein topology universe. Trends in Biochemical Sciences, 2005, 30, 13-19.	3.7	101
248	Reduced Global Cooperativity is a Common Feature Underlying the Amyloidogenicity of Pathogenic Lysozyme Mutations. Journal of Molecular Biology, 2005, 346, 773-788.	2.0	100
249	Single-Molecule Imaging of Individual Amyloid Protein Aggregates in Human Biofluids. ACS Chemical Neuroscience, 2016, 7, 399-406.	1.7	99
250	A FRET Sensor for Nonâ€Invasive Imaging of Amyloid Formation in Vivo. ChemPhysChem, 2011, 12, 673-680.	1.0	98
251	Rapid and accurate in silico solubility screening of a monoclonal antibody library. Scientific Reports, 2017, 7, 8200.	1.6	97
252	The small heat shock protein Hsp27 binds Î±-synuclein fibrils, preventing elongation and cytotoxicity. Journal of Biological Chemistry, 2018, 293, 4486-4497.	1.6	97

#	Article	IF	Citations
253	Nature and Regulation of Protein Folding on the Ribosome. Trends in Biochemical Sciences, 2019, 44, 914-926.	3.7	97
254	The effects of guanidine hydrochloride on the 'random coil' conformations and NMR chemical shifts of the peptide series GGXGG. Journal of Biomolecular NMR, 1997, 10, 221-230.	1.6	96
255	Silk micrococoons for protein stabilisation and molecular encapsulation. Nature Communications, 2017, 8, 15902.	5.8	96
256	Hsp70 Inhibits the Nucleation and Elongation of Tau and Sequesters Tau Aggregates with High Affinity. ACS Chemical Biology, 2018, 13, 636-646.	1.6	96
257	Defining Î±-synuclein species responsible for Parkinsonâ€™s disease phenotypes in mice. Journal of Biological Chemistry, 2019, 294, 10392-10406.	1.6	96
258	High Hydrostatic Pressure Dissociates Early Aggregates of TTR105â€“115, but not the Mature Amyloid Fibrils. Journal of Molecular Biology, 2005, 347, 903-909.	2.0	95
259	The Non-Core Regions of Human Lysozyme Amyloid Fibrils Influence Cytotoxicity. Journal of Molecular Biology, 2010, 402, 783-796.	2.0	95
260	Intrinsic disorder modulates protein self-assembly and aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6951-6956.	3.3	95
261	Small-molecule sequestration of amyloid-Î² as a drug discovery strategy for Alzheimerâ€™s disease. Science Advances, 2020, 6, .	4.7	95
262	Amyloid Formation by the Pro-Inflammatory S100A8/A9 Proteins in the Ageing Prostate. PLoS ONE, 2009, 4, e5562.	1.1	95
263	STRUCTURAL BIOLOGY: Dynamic Visions of Enzymatic Reactions. Science, 2006, 313, 1586-1587.	6.0	94
264	Third generation antibody discovery methods:in silicorational design. Chemical Society Reviews, 2018, 47, 9137-9157.	18.7	94
265	Generic nature of the condensed states of proteins. Nature Cell Biology, 2021, 23, 587-594.	4.6	94
266	Characterisation of Amyloid Fibril Formation by Small Heat-shock Chaperone Proteins Human Î±A-, Î±B- and R120G Î±B-Crystallins. Journal of Molecular Biology, 2007, 372, 470-484.	2.0	93
267	ADP ribosylation adapts an ER chaperone response to short-term fluctuations in unfolded protein load. Journal of Cell Biology, 2012, 198, 371-385.	2.3	93
268	Slow Cooperative Folding of a Small Globular Protein HPrâ€. Biochemistry, 1998, 37, 622-637.	1.2	92
269	Normal and Aberrant Biological Self-Assembly:â€‰ Insights from Studies of Human Lysozyme and Its Amyloidogenic Variants. Accounts of Chemical Research, 2006, 39, 603-610.	7.6	92
270	Probing the Mechanism of Amyloidogenesis through a Tandem Repeat of the PI3-SH3 Domain Suggests a Generic Model for Protein Aggregation and Fibril Formation. Journal of Molecular Biology, 2006, 356, 189-208.	2.0	92

#	Article	IF	Citations
271	Conserved C-Terminal Charge Exerts a Profound Influence on the Aggregation Rate of Î±-Synuclein. Journal of Molecular Biology, 2011, 411, 329-333.	2.0	92
272	Nucleated polymerization with secondary pathways. III. Equilibrium behavior and oligomer populations. Journal of Chemical Physics, 2011, 135, 065107.	1.2	92
273	Single-molecule FRET studies on alpha-synuclein oligomerization of Parkinsonâ€™s disease genetically related mutants. Scientific Reports, 2015, 5, 16696.	1.6	92
274	Single molecule secondary structure determination of proteins through infrared absorption nanospectroscopy. Nature Communications, 2020, 11, 2945.	5.8	92
275	Preconditioning of Microglia by Î±-Synuclein Strongly Affects the Response Induced by Toll-like Receptor (TLR) Stimulation. PLoS ONE, 2013, 8, e79160.	1.1	92
276	Molecular determinants of the aggregation behavior of Î±â€•and Î²â€‹synuclein. Protein Science, 2008, 17, 887-898.	3.1	91
277	Towards a structural biology of the hydrophobic effect in protein folding. Scientific Reports, 2016, 6, 28285.	1.6	91
278	Spinal motor neuron protein supersaturation patterns are associated with inclusion body formation in ALS. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3935-E3943.	3.3	91
279	Hydrogen exchange properties of proteins in native and denatured states monitored by mass spectrometry and NMR. Protein Science, 1997, 6, 1316-1324.	3.1	90
280	Formation of Native and Non-native Interactions in Ensembles of Denatured ACBP Molecules from Paramagnetic Relaxation Enhancement Studies. Journal of Molecular Biology, 2005, 347, 1053-1062.	2.0	90
281	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.	3.3	90
282	Theoretical Approaches to Protein Aggregation. Protein and Peptide Letters, 2006, 13, 287-293.	0.4	90
283	Bridging the gap: From protein misfolding to protein misfolding diseases. FEBS Letters, 2009, 583, 2581-2586.	1.3	90
284	A Condensation-Ordering Mechanism in Nanoparticle-Catalyzed Peptide Aggregation. PLoS Computational Biology, 2009, 5, e1000458.	1.5	90
285	Nanobodies Raised against Monomeric Î±-Synuclein Distinguish between Fibrils at Different Maturation Stages. Journal of Molecular Biology, 2013, 425, 2397-2411.	2.0	90
286	Physical determinants of the self-replication of protein fibrils. Nature Physics, 2016, 12, 874-880.	6.5	90
287	Self-Templated Nucleation in Peptide and Protein Aggregation. Physical Review Letters, 2008, 101, 258101.	2.9	89
288	Glial Innate Immunity Generated by Non-Aggregated Alpha-Synuclein in Mouse: Differences between Wild-type and Parkinson's Disease-Linked Mutants. PLoS ONE, 2010, 5, e13481.	1.1	89

#	Article	IF	Citations
289	In-Cell NMR Characterization of the Secondary Structure Populations of a Disordered Conformation of Î±-Synuclein within E. coli Cells. PLoS ONE, 2013, 8, e72286.	1.1	89
290	Hen Egg White Lysozyme Expressed in and Secreted from, Aspergillus niger is Correctly Processed and Folded. Nature Biotechnology, 1990, 8, 741-745.	9.4	88
291	Stimulation and inhibition of fibril formation by a peptide in the presence of different concentrations of SDS. FEBS Letters, 2002, 529, 193-197.	1.3	88
292	Transition states for protein folding have native topologies despite high structural variability. Nature Structural and Molecular Biology, 2004, 11, 443-449.	3.6	88
293	On the Mechanism of Nonspecific Inhibitors of Protein Aggregation: Dissecting the Interactions of Î±-Synuclein with Congo Red and Lacmoid. Biochemistry, 2009, 48, 8322-8334.	1.2	88
294	In vivo translation rates can substantially delay the cotranslational folding of the Escherichia coli cytosolic proteome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E132-40.	3.3	88
295	Electrostatic Effects in Filamentous Protein Aggregation. Biophysical Journal, 2013, 104, 1116-1126.	0.2	88
296	Simultaneous Determination of Protein Structure and Dynamics Using Cryo-Electron Microscopy. Biophysical Journal, 2018, 114, 1604-1613.	0.2	88
297	Optimal Protein Design Procedure. Physical Review Letters, 1996, 77, 1901-1904.	2.9	87
298	Acceleration of the folding of acylphosphatase by stabilization of local secondary structure. Nature Structural Biology, 1999, 6, 380-387.	9.7	87
299	Heteronuclear NMR investigations of dynamic regions of intact Escherichia coli ribosomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10949-10954.	3.3	87
300	New Scenarios of Protein Folding Can Occur on the Ribosome. Journal of the American Chemical Society, 2011, 133, 513-526.	6.6	87
301	Prediction of variable translation rate effects on cotranslational protein folding. Nature Communications, 2012, 3, 868.	5.8	87
302	Targeting disordered proteins with small molecules using entropy. Trends in Biochemical Sciences, 2015, 40, 491-496.	3.7	87
303	Molecular Recognition by Templated Folding of an Intrinsically Disordered Protein. Scientific Reports, 2016, 6, 21994.	1.6	87
304	Stopped-Flow Photo-CIDNP Observation of Protein Folding. Journal of the American Chemical Society, 1997, 119, 5049-5050.	6.6	86
305	Reversal of Protein Aggregation Provides Evidence for Multiple Aggregated States. Journal of Molecular Biology, 2005, 346, 603-616.	2.0	86
306	Inversion of the Balance between Hydrophobic and Hydrogen Bonding Interactions in Protein Folding and Aggregation. PLoS Computational Biology, 2011, 7, e1002169.	1.5	86

#	Article	IF	Citations
307	Multistep Inhibition of Î±-Synuclein Aggregation and Toxicity in Vitro and in Vivo by Trodusquemine. ACS Chemical Biology, 2018, 13, 2308-2319.	1.6	86
308	Mapping of Two Networks of Residues That Exhibit Structural and Dynamical Changes upon Binding in a PDZ Domain Protein. Journal of the American Chemical Society, 2008, 130, 8931-8939.	6.6	85
309	Î±2-Macroglobulin and Haptoglobin Suppress Amyloid Formation by Interacting with Prefibrillar Protein Species. Journal of Biological Chemistry, 2009, 284, 4246-4254.	1.6	85
310	Accurate Random Coil Chemical Shifts from an Analysis of Loop Regions in Native States of Proteins. Journal of the American Chemical Society, 2009, 131, 16332-16333.	6.6	85
311	Sequence-Based Prediction of Protein Solubility. Journal of Molecular Biology, 2012, 421, 237-241.	2.0	85
312	Understanding the Influence of Codon Translation Rates on Cotranslational Protein Folding. Accounts of Chemical Research, 2014, 47, 1536-1544.	7.6	85
313	The Extracellular Chaperone Clusterin Potently Inhibits Human Lysozyme Amyloid Formation by Interacting with Prefibrillar Species. Journal of Molecular Biology, 2007, 369, 157-167.	2.0	84
314	Immunological features of Î±â€synuclein in Parkinson's disease. Journal of Cellular and Molecular Medicine, 2008, 12, 1820-1829.	1.6	84
315	Characterization of Oligomeric Species on the Aggregation Pathway of Human Lysozyme. Journal of Molecular Biology, 2009, 387, 17-27.	2.0	84
316	Characterization of the Conformational Equilibrium between the Two Major Substates of RNase A Using NMR Chemical Shifts. Journal of the American Chemical Society, 2012, 134, 3968-3971.	6.6	84
317	A protein homeostasis signature in healthy brains recapitulates tissue vulnerability to Alzheimerâ€™s disease. Science Advances, 2016, 2, e1600947.	4.7	84
318	Protein Solubility and Protein Homeostasis: A Generic View of Protein Misfolding Disorders. Cold Spring Harbor Perspectives in Biology, 2011, 3, a010454-a010454.	2.3	83
319	A Clear View of Polymorphism, Twist, and Chirality in Amyloid Fibril Formation. ACS Nano, 2013, 7, 10443-10448.	7.3	83
320	Rare Individual Amyloid-Î² Oligomers Act on Astrocytes to Initiate Neuronal Damage. Biochemistry, 2014, 53, 2442-2453.	1.2	83
321	Structural Ensembles of Membrane-bound Î±-Synuclein Reveal the Molecular Determinants of Synaptic Vesicle Affinity. Scientific Reports, 2016, 6, 27125.	1.6	83
322	Mapping Surface Hydrophobicity of Î±-Synuclein Oligomers at the Nanoscale. Nano Letters, 2018, 18, 7494-7501.	4.5	83
323	Higher Order Amyloid Fibril Structure by MAS NMR and DNP Spectroscopy. Journal of the American Chemical Society, 2013, 135, 19237-19247.	6.6	82
324	Neutral Evolution of Model Proteins: Diffusion in Sequence Space and Overdispersion. Journal of Theoretical Biology, 1999, 200, 49-64.	0.8	81

#	Article	IF	Citations
325	Effective interactions between chaotropic agents and proteins. Proteins: Structure, Function and Bioinformatics, 2005, 61, 492-499.	1.5	81
326	Probing ribosome-nascent chain complexes produced in vivo by NMR spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22239-22244.	3.3	81
327	Fast Flow Microfluidics and Single-Molecule Fluorescence for the Rapid Characterization of Î±-Synuclein Oligomers. Analytical Chemistry, 2015, 87, 8818-8826.	3.2	81
328	Inhibition of protein crystallization by evolutionary negative design. Physical Biology, 2004, 1, P9-P13.	0.8	77
329	Competition between Folding, Native-State Dimerisation and Amyloid Aggregation in Î²-Lactoglobulin. Journal of Molecular Biology, 2009, 386, 878-890.	2.0	77
330	The s2D Method: Simultaneous Sequence-Based Prediction of the Statistical Populations of Ordered and Disordered Regions in Proteins. Journal of Molecular Biology, 2015, 427, 982-996.	2.0	77
331	Protein homeostasis of a metastable subproteome associated with Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5703-E5711.	3.3	77
332	Common Regulatory Pathways Mediate Activity of MicroRNAs Inducing Cardiomyocyte Proliferation. Cell Reports, 2019, 27, 2759-2771.e5.	2.9	77
333	Sequence-Based Prediction of Fuzzy Protein Interactions. Journal of Molecular Biology, 2020, 432, 2289-2303.	2.0	77
334	An Equilibrium Partially Folded State of Human Lysozyme at Low pH. Journal of Molecular Biology, 1995, 246, 382-387.	2.0	76
335	X-ray Scattering Study of the Effect of Hydration on the Cross-Î² Structure of Amyloid Fibrils. Journal of the American Chemical Society, 2006, 128, 11738-11739.	6.6	76
336	Protein Dynamics: Moore's Law in Molecular Biology. Current Biology, 2011, 21, R68-R70.	1.8	76
337	Metadynamic metainference: Enhanced sampling of the metainference ensemble using metadynamics. Scientific Reports, 2016, 6, 31232.	1.6	76
338	Investigating the Effects of Mutations on Protein Aggregation in the Cell. Journal of Biological Chemistry, 2005, 280, 10607-10613.	1.6	75
339	Membrane lipid composition and its physicochemical properties define cell vulnerability to aberrant protein oligomers. Journal of Cell Science, 2012, 125, 2416-27.	1.2	75
340	Amyloid-Î² Oligomers are Sequestered by both Intracellular and Extracellular Chaperones. Biochemistry, 2012, 51, 9270-9276.	1.2	75
341	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
342	Single Molecule Characterization of the Interactions between Amyloid-Î² Peptides and the Membranes of Hippocampal Cells. Journal of the American Chemical Society, 2013, 135, 1491-1498.	6.6	75

#	Article	IF	Citations
343	Quantification of the Relative Contributions of Loss-of-function and Gain-of-function Mechanisms in TAR DNA-binding Protein 43 (TDP-43) Proteinopathies. Journal of Biological Chemistry, 2016, 291, 19437-19448.	1.6	75
344	Amyloid Formation from HypF-N under Conditions in which the Protein is Initially in its Native State. Journal of Molecular Biology, 2005, 347, 323-335.	2.0	74
345	A transcriptional signature of Alzheimerâ€™s disease is associated with a metastable subproteome at risk for aggregation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4753-4758.	3.3	74
346	Towards complete descriptions of the freeâ€“energy landscapes of proteins. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2005, 363, 433-452.	1.6	73
347	Trigger Factor Slows Co-translational Folding through Kinetic Trapping while Sterically Protecting the Nascent Chain from Aberrant Cytosolic Interactions. Journal of the American Chemical Society, 2012, 134, 10920-10932.	6.6	73
348	Towards Multiparametric Fluorescent Imaging of Amyloid Formation: Studies of a YFP Model of Î±-Synuclein Aggregation. Journal of Molecular Biology, 2010, 395, 627-642.	2.0	72
349	Population of Nonnative States of Lysozyme Variants Drives Amyloid Fibril Formation. Journal of the American Chemical Society, 2011, 133, 7737-7743.	6.6	72
350	Identification of small-molecule binding pockets in the soluble monomeric form of the AÎ²42 peptide. Journal of Chemical Physics, 2013, 139, 035101.	1.2	72
351	The chaperone HSPB8 reduces the accumulation of truncated TDP-43 species in cells and protects against TDP-43-mediated toxicity. Human Molecular Genetics, 2016, 25, 3908-3924.	1.4	72
352	Ultrasensitive Measurement of Ca²⁺ Influx into Lipid Vesicles Induced by Protein Aggregates. Angewandte Chemie - International Edition, 2017, 56, 7750-7754.	7.2	72
353	In vitro and in silico assessment of the developability of a designed monoclonal antibody library. MAbs, 2019, 11, 388-400.	2.6	72
354	Structures and relative free energies of partially folded states of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14817-14821.	3.3	71
355	Principal eigenvector of contact matrices and hydrophobicity profiles in proteins. Proteins: Structure, Function and Bioinformatics, 2004, 58, 22-30.	1.5	71
356	Spatial Persistence of Angular Correlations in Amyloid Fibrils. Physical Review Letters, 2006, 96, 238301.	2.9	71
357	Kinetic studies of protein folding using NMR spectroscopy. Nature Structural Biology, 1998, 5, 504-507.	9.7	70
358	Sequestration of the AÎ² Peptide Prevents Toxicity and Promotes Degradation In Vivo. PLoS Biology, 2010, 8, e1000334.	2.6	70
359	PROTEIN CHEMISTRY: In the Footsteps of Alchemists. Science, 2004, 304, 1259-1262.	6.0	69
360	A PDZ domain recapitulates a unifying mechanism for protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 128-133.	3.3	69

#	Article	IF	Citations
361	Use of Protonless NMR Spectroscopy To Alleviate the Loss of Information Resulting from Exchange-Broadening. Journal of the American Chemical Society, 2009, 131, 7222-7223.	6.6	69
362	Transient Tertiary Structure Formation within the Ribosome Exit Port. Journal of the American Chemical Society, 2010, 132, 16928-16937.	6.6	69
363	Kinetic modelling indicates that fast-translating codons can coordinate cotranslational protein folding by avoiding misfolded intermediates. Nature Communications, 2014, 5, 2988.	5.8	69
364	Statistical Mechanics of the Denatured State of a Protein Using Replica-Averaged Metadynamics. Journal of the American Chemical Society, 2014, 136, 8982-8991.	6.6	69
365	Amyloid-Î² and Î±-Synuclein Decrease the Level of Metal-Catalyzed Reactive Oxygen Species by Radical Scavenging and Redox Silencing. Journal of the American Chemical Society, 2016, 138, 3966-3969.	6.6	69
366	Competition between Intramolecular and Intermolecular Interactions in an Amyloid-Forming Protein. Journal of Molecular Biology, 2009, 389, 776-786.	2.0	68
367	Toward an Accurate Determination of Free Energy Landscapes in Solution States of Proteins. Journal of the American Chemical Society, 2009, 131, 3810-3811.	6.6	68
368	Functional interactions as a survival strategy against abnormal aggregation. FASEB Journal, 2011, 25, 45-54.	0.2	68
369	Cyclophilin A catalyzes proline isomerization by an electrostatic handle mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10203-10208.	3.3	68
370	SOD1 protein aggregates stimulate macropinocytosis in neurons to facilitate their propagation. Molecular Neurodegeneration, 2015, 10, 57.	4.4	68
371	The molecular chaperones DNAJB6 and Hsp70 cooperate to suppress Î±-synuclein aggregation. Scientific Reports, 2017, 7, 9039.	1.6	67
372	Determination of protein structural ensembles using cryo-electron microscopy. Current Opinion in Structural Biology, 2019, 56, 37-45.	2.6	67
373	Multiple subsets of side-chain packing in partially folded states of Â-lactalbumins. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8899-8904.	3.3	66
374	Engineering a Camelid Antibody Fragment That Binds to the Active Site of Human Lysozyme and Inhibits Its Conversion into Amyloid Fibrils. Biochemistry, 2008, 47, 11041-11054.	1.2	66
375	Detergent-like Interaction of Congo Red with the Amyloid Î² Peptide. Biochemistry, 2010, 49, 1358-1360.	1.2	66
376	Structure and Intermolecular Dynamics of Aggregates Populated during Amyloid Fibril Formation Studied by Hydrogen/Deuterium Exchange. Accounts of Chemical Research, 2010, 43, 1072-1079.	7.6	66
377	Physical Determinants of Amyloid Assembly in Biofilm Formation. MBio, 2019, 10, .	1.8	66
378	Hsp70 Oligomerization Is Mediated by an Interaction between the Interdomain Linker and the Substrate-Binding Domain. PLoS ONE, 2013, 8, e67961.	1.1	66

#	Article	IF	Citations
379	A Simple Lattice Model That Captures Protein Folding, Aggregation and Amyloid Formation. PLoS ONE, 2014, 9, e85185.	1.1	66
380	Vicinal coupling constants and protein dynamics. Biochemistry, 1985, 24, 3831-3841.	1.2	65
381	Application of Selective 29Si Isotopic Enrichment to Studies of the Structure of Calcium Silicate Hydrate (C-S-H) Gels. Journal of the American Ceramic Society, 1994, 77, 593-596.	1.9	65
382	Connectivity of Neutral Networks, Overdispersion, and Structural Conservation in Protein Evolution. Journal of Molecular Evolution, 2003, 56, 243-254.	0.8	65
383	Molecular Dynamics Studies of the Process of Amyloid Aggregation of Peptide Fragments of Transthyretin. Journal of Molecular Biology, 2004, 340, 555-569.	2.0	65
384	Time Averaging of NMR Chemical Shifts in the MLF Peptide in the Solid State. Journal of the American Chemical Society, 2010, 132, 5993-6000.	6.6	65
385	Structure-based prediction of methyl chemical shifts in proteins. Journal of Biomolecular NMR, 2011, 50, 331-346.	1.6	65
386	Experimental free energy surfaces reveal the mechanisms of maintenance of protein solubility. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21057-21062.	3.3	65
387	The H50Q Mutation Induces a 10-fold Decrease in the Solubility of Î±-Synuclein. Journal of Biological Chemistry, 2015, 290, 2395-2404.	1.6	65
388	Î²-Synuclein suppresses both the initiation and amplification steps of Î±-synuclein aggregation via competitive binding to surfaces. Scientific Reports, 2016, 6, 36010.	1.6	65
389	Scaling behaviour and rate-determining steps in filamentous self-assembly. Chemical Science, 2017, 8, 7087-7097.	3.7	65
390	Observation of an Î±-synuclein liquid droplet state and its maturation into Lewy body-like assemblies. Journal of Molecular Cell Biology, 2021, 13, 282-294.	1.5	65
391	Dynamics of the multidomain fibrinolytic protein urokinase from two-dimensional NMR. Nature, 1989, 337, 579-582.	13.7	64
392	Comparison of the structural and dynamical properties of holo and apo bovine Î±-lactalbumin by NMR spectroscopy11Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 307, 885-898.	2.0	64
393	Transition State Contact Orders Correlate with Protein Folding Rates. Journal of Molecular Biology, 2005, 352, 495-500.	2.0	64
394	Replica-Averaged Metadynamics. Journal of Chemical Theory and Computation, 2013, 9, 5610-5617.	2.3	64
395	C-terminal truncation of Î±-synuclein promotes amyloid fibril amplification at physiological pH. Chemical Science, 2018, 9, 5506-5516.	3.7	64
396	Soluble aggregates present in cerebrospinal fluid change in size and mechanism of toxicity during Alzheimerâ€™s disease progression. Acta Neuropathologica Communications, 2019, 7, 120.	2.4	64

#	Article	IF	Citations
397	A single ultrasensitive assay for detection and discrimination of tau aggregates of Alzheimer and Pick diseases. Acta Neuropathologica Communications, 2020, 8, 22.	2.4	64
398	Real-Time NMR Studies of Protein Folding. Accounts of Chemical Research, 1998, 31, 773-780.	7.6	63
399	Formation of amyloid fibrils by peptides derived from the bacterial cold shock protein CspB. Protein Science, 1999, 8, 1350-1357.	3.1	63
400	The mechanism of folding of Im7 reveals competition between functional and kinetic evolutionary constraints. Nature Structural and Molecular Biology, 2009, 16, 318-324.	3.6	63
401	Frequency Factors in a Landscape Model of Filamentous Protein Aggregation. Physical Review Letters, 2010, 104, 228101.	2.9	63
402	Interactions between Amyloidophilic Dyes and Their Relevance to Studies of Amyloid Inhibitors. Biophysical Journal, 2010, 99, 3492-3497.	0.2	63
403	Nanoscopic insights into seeding mechanisms and toxicity of Î±-synuclein species in neurons. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3815-3819.	3.3	63
404	Networks of Dynamic Allostery Regulate Enzyme Function. Structure, 2017, 25, 276-286.	1.6	63
405	The docking of synaptic vesicles on the presynaptic membrane induced by Î±-synuclein is modulated by lipid composition. Nature Communications, 2021, 12, 927.	5.8	63
406	Reduction of the amyloidogenicity of a protein by specific binding of ligands to the native conformation. Protein Science, 2001, 10, 879-886.	3.1	62
407	The Circularization of Amyloid Fibrils Formed by Apolipoprotein C-II. Biophysical Journal, 2003, 85, 3979-3990.	0.2	62
408	Sequence Specificity in the Entropy-Driven Binding of a Small Molecule and a Disordered Peptide. Journal of Molecular Biology, 2017, 429, 2772-2779.	2.0	62
409	The contribution of biophysical and structural studies of protein self-assembly to the design of therapeutic strategies for amyloid diseases. Neurobiology of Disease, 2018, 109, 178-190.	2.1	62
410	Sequence Determinants of the Aggregation of Proteins Within Condensates Generated by Liquid-liquid Phase Separation. Journal of Molecular Biology, 2022, 434, 167201.	2.0	62
411	Exploration of partially unfolded states of human Î±-lactalbumin by molecular dynamics simulation11Edited by B. Honig. Journal of Molecular Biology, 2001, 306, 329-347.	2.0	61
412	Native and non-native interactions along protein folding and unfolding pathways. Proteins: Structure, Function and Bioinformatics, 2002, 47, 379-392.	1.5	61
413	Determination of the folding transition states of barnase by using Â-value-restrained simulations validated by double mutant ÂIJ-values. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12389-12394.	3.3	61
414	Hypochlorite-induced structural modifications enhance the chaperone activity of human Î±₂-macroglobulin. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2081-90.	3.3	61

#	Article	IF	Citations
415	Nanobodies raised against monomeric É‘-synuclein inhibit fibril formation and destabilize toxic oligomeric species. BMC Biology, 2017, 15, 57.	1.7	61
416	Proteasome-targeted nanobodies alleviate pathology and functional decline in an Î±-synuclein-based Parkinsonâ€™s disease model. Npj Parkinson's Disease, 2018, 4, 25.	2.5	61
417	Rational design of a conformation-specific antibody for the quantification of AÎ² oligomers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13509-13518.	3.3	61
418	The physical chemistry of the amyloid phenomenon: thermodynamics and kinetics of filamentous protein aggregation. Essays in Biochemistry, 2014, 56, 11-39.	2.1	60
419	Modulation of electrostatic interactions to reveal a reaction network unifying the aggregation behaviour of the AÎ²42 peptide and its variants. Chemical Science, 2017, 8, 4352-4362.	3.7	60
420	Phage display and kinetic selection of antibodies that specifically inhibit amyloid self-replication. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6444-6449.	3.3	60
421	Comparison of successive transition states for folding reveals alternative early folding pathways of two homologous proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19241-19246.	3.3	59
422	Factors That Affect the Degree of Twist in Î²-Sheet Structures: A Molecular Dynamics Simulation Study of a Cross-Î² Filament of the GNNQQNY Peptide. Journal of Physical Chemistry B, 2009, 113, 1728-1737.	1.2	59
423	Transthyretin Inhibits Primary and Secondary Nucleations of Amyloid-Î² Peptide Aggregation and Reduces the Toxicity of Its Oligomers. Biomacromolecules, 2020, 21, 1112-1125.	2.6	59
424	Single-Molecule Characterization of the Interactions between Extracellular Chaperones and Toxic Î±-Synuclein Oligomers. Cell Reports, 2018, 23, 3492-3500.	2.9	59
425	29Si MAS NMR study of the hydration of tricalcium silicate in the presence of finely divided silica. Journal of Materials Science, 1988, 23, 4108-4114.	1.7	58
426	The Influence of Pathogenic Mutations in Î±-Synuclein on Biophysical and Structural Characteristics of Amyloid Fibrils. ACS Nano, 2020, 14, 5213-5222.	7.3	58
427	Conformational Stability of Muscle Acylphosphatase:Â The Role of Temperature, Denaturant Concentration, and pHâ€. Biochemistry, 1998, 37, 1447-1455.	1.2	57
428	Protein Folding in Contact Map Space. Physical Review Letters, 1999, 82, 656-659.	2.9	57
429	Response of native and denatured hen lysozyme to high pressure studied by 15 N/1 H NMR spectroscopy. FEBS Journal, 2001, 268, 1782-1793.	0.2	57
430	The Component Polypeptide Chains of Bovine Insulin Nucleate or Inhibit Aggregation of the Parent Protein in a Conformation-dependent Manner. Journal of Molecular Biology, 2006, 360, 497-509.	2.0	56
431	Prediction of Local Structural Stabilities of Proteins from Their Amino Acid Sequences. Structure, 2007, 15, 139-143.	1.6	56
432	Correlation between mRNA expression levels and protein aggregation propensities in subcellular localisations. Molecular BioSystems, 2009, 5, 1873.	2.9	56

#	Article	IF	Citations
433	Antibodies and protein misfolding: From structural research tools to therapeutic strategies. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 1907-1919.	1.1	56
434	Latent analysis of unmodified biomolecules and their complexes in solution with attomole detection sensitivity. Nature Chemistry, 2015, 7, 802-809.	6.6	56
435	Methods of probing the interactions between small molecules and disordered proteins. Cellular and Molecular Life Sciences, 2017, 74, 3225-3243.	2.4	56
436	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6447-E6456.	3.3	56
437	Million-fold sensitivity enhancement in proteopathic seed amplification assays for biospecimens by Hofmeister ion comparisons. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23029-23039.	3.3	56
438	Quantifying misfolded protein oligomers as drug targets and biomarkers in Alzheimer and Parkinson diseases. Nature Reviews Chemistry, 2021, 5, 277-294.	13.8	56
439	Dissection of multi-protein complexes using mass spectrometry: Subunit interactions in transthyretin and retinol-binding protein complexes. , 1998, 33, 3-11.		55
440	Self-consistent determination of the transition state for protein folding: Application to a fibronectin type III domain. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 394-399.	3.3	55
441	BPPred: A Web-based computational tool for predicting biophysical parameters of proteins. Protein Science, 2006, 16, 125-134.	3.1	55
442	The Distribution of Residues in a Polypeptide Sequence Is a Determinant of Aggregation Optimized by Evolution. Biophysical Journal, 2007, 93, 4382-4391.	0.2	55
443	Similarities in the thermodynamics and kinetics of aggregation of disease-related AÎ²(1-40) peptides. Protein Science, 2007, 16, 1214-1222.	3.1	55
444	Structure Determination of Proteinâ^'Protein Complexes Using NMR Chemical Shifts: Case of an Endonuclease Colicinâ^'Immunity Protein Complex. Journal of the American Chemical Society, 2008, 130, 15990-15996.	6.6	55
445	Local Cooperativity in an Amyloidogenic State of Human Lysozyme Observed at Atomic Resolution. Journal of the American Chemical Society, 2010, 132, 15580-15588.	6.6	55
446	Human pregnancy zone protein stabilizes misfolded proteins including preeclampsia- and Alzheimerâ€™s-associated amyloid beta peptide. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6101-6110.	3.3	55
447	Structural characterization of the interaction of Î±-synuclein nascent chains with the ribosomal surface and trigger factor. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5012-5017.	3.3	54
448	Structure of a low-population binding intermediate in protein-RNA recognition. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7171-7176.	3.3	54
449	Determination of Structural Ensembles of Proteins: Restraining vs Reweighting. Journal of Chemical Theory and Computation, 2018, 14, 6632-6641.	2.3	54
450	SAR by kinetics for drug discovery in protein misfolding diseases. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10245-10250.	3.3	54

#	Article	IF	Citations
451	Stabilisation of Î±-helices by site-directed mutagenesis reveals the importance of secondary structure in the transition state for acylphosphatase folding. Journal of Molecular Biology, 2000, 300, 633-647.	2.0	53
452	Prediction by Graph Theoretic Measures of Structural Effects in Proteins Arising from Non-Synonymous Single Nucleotide Polymorphisms. PLoS Computational Biology, 2008, 4, e1000135.	1.5	53
453	A Relationship between mRNA Expression Levels and Protein Solubility in E. coli. Journal of Molecular Biology, 2009, 388, 381-389.	2.0	53
454	Structural characterization of a misfolded intermediate populated during the folding process of a PDZ domain. Nature Structural and Molecular Biology, 2010, 17, 1431-1437.	3.6	53
455	Disulfide Bonds Reduce the Toxicity of the Amyloid Fibrils Formed by an Extracellular Protein. Angewandte Chemie - International Edition, 2011, 50, 7048-7051.	7.2	53
456	Identification of Small Molecule Inhibitors of Tau Aggregation by Targeting Monomeric Tau As a Potential Therapeutic Approach for Tauopathies. Current Alzheimer Research, 2015, 12, 814-828.	0.7	53
457	Structural Ensemble Modulation upon Small-Molecule Binding to Disordered Proteins. Journal of Molecular Biology, 2018, 430, 2288-2292.	2.0	53
458	The Aggregation and Neurotoxicity of TDP-43 and Its ALS-Associated 25 kDa Fragment Are Differentially Affected by Molecular Chaperones in Drosophila. PLoS ONE, 2012, 7, e31899.	1.1	53
459	High-Resolution MAS NMR Analysis of PI3-SH3 Amyloid Fibrils: Backbone Conformation and Implications for Protofilament Assembly and Structure,. Biochemistry, 2010, 49, 7474-7484.	1.2	52
460	Physicochemical Determinants of Chaperone Requirements. Journal of Molecular Biology, 2010, 400, 579-588.	2.0	52
461	Proteome-Level Interplay between Folding and Aggregation Propensities of Proteins. Journal of Molecular Biology, 2010, 402, 919-928.	2.0	52
462	Druggability of Intrinsically Disordered Proteins. Advances in Experimental Medicine and Biology, 2015, 870, 383-400.	0.8	52
463	Massively parallel C. elegans tracking provides multi-dimensional fingerprints for phenotypic discovery. Journal of Neuroscience Methods, 2018, 306, 57-67.	1.3	52
464	Nanoscopic Characterisation of Individual Endogenous Protein Aggregates in Human Neuronal Cells. ChemBioChem, 2018, 19, 2033-2038.	1.3	52
465	Conserved S/T Residues of the Human Chaperone DNAJB6 Are Required for Effective Inhibition of Aî²42 Amyloid Fibril Formation. Biochemistry, 2018, 57, 4891-4902.	1.2	52
466	Infrared nanospectroscopy reveals the molecular interaction fingerprint of an aggregation inhibitor with single Aî²42 oligomers. Nature Communications, 2021, 12, 688.	5.8	52
467	1H-NMR assignments and local environments of aromatic residues in bovine, human and guinea pig variants of alpha-lactalbumin. FEBS Journal, 1992, 210, 699-709.	0.2	51
468	A statistical mechanical method to optimize energy functions for protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 3977-3981.	3.3	51

#	Article	IF	Citations
469	A Tensor-Free Method for the Structural and Dynamical Refinement of Proteins using Residual Dipolar Couplings. Journal of Physical Chemistry B, 2015, 119, 653-661.	1.2	51
470	Bifunctional Anti-Non-Amyloid Component Î±-Synuclein Nanobodies Are Protective In Situ. PLoS ONE, 2016, 11, e0165964.	1.1	51
471	Intrinsically aggregation-prone proteins form amyloid-like aggregates and contribute to tissue aging in Caenorhabditis elegans. ELife, 2019, 8, .	2.8	51
472	Fluctuations and averaging of proton chemical shifts in the bovine pancreatic trypsin inhibitor. Biochemistry, 1982, 21, 1118-1125.	1.2	50
473	The domain organization of streptokinase: Nuclear magnetic resonance, circular dichroism, and functional characterization of proteolytic fragments. Protein Science, 1996, 5, 693-704.	3.1	50
474	Validity of GÅ•Models: Comparison with a Solvent-Shielded Empirical Energy Decomposition. Biophysical Journal, 2002, 83, 3032-3038.	0.2	50
475	Protein folding: bringing theory and experiment closer together. Current Opinion in Structural Biology, 2003, 13, 82-87.	2.6	50
476	Nucleated Polymerisation in the Presence of Pre-Formed Seed Filaments. International Journal of Molecular Sciences, 2011, 12, 5844-5852.	1.8	50
477	A Relationship between the Transient Structure in the Monomeric State and the Aggregation Propensities of Î±-Synuclein and Î²-Synuclein. Biochemistry, 2014, 53, 7170-7183.	1.2	50
478	Bayesian Weighing of Electron Cryo-Microscopy Data for Integrative Structural Modeling. Structure, 2019, 27, 175-188.e6.	1.6	50
479	Study of the Tryptophan Residues of Lysozyme Using 1H Nuclear Magnetic Resonance. FEBS Journal, 1978, 92, 81-97.	0.2	49
480	Thermodynamic and kinetic design principles for amyloid-aggregation inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24251-24257.	3.3	49
481	Interactions of Î±-synuclein oligomers with lipid membranes. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183536.	1.4	49
482	Cytosolic aggregation of mitochondrial proteins disrupts cellular homeostasis by stimulating the aggregation of other proteins. ELife, 2021, 10, .	2.8	49
483	An engineered monomer binding-protein for Î±-synuclein efficiently inhibits the proliferation of amyloid fibrils. ELife, 2019, 8, .	2.8	49
484	Effects of the Known Pathogenic Mutations on the Aggregation Pathway of the Amyloidogenic Peptide of Apolipoprotein A-I. Journal of Molecular Biology, 2011, 407, 465-476.	2.0	48
485	Twisting Transition between Crystalline and Fibrillar Phases of Aggregated Peptides. Physical Review Letters, 2012, 109, 158101.	2.9	48
486	Quantitative thermophoretic study of disease-related protein aggregates. Scientific Reports, 2016, 6, 22829.	1.6	48

#	Article	IF	Citations
487	A molecular dynamics analysis of protein structural elements. Proteins: Structure, Function and Bioinformatics, 1989, 5, 337-354.	1.5	47
488	Analysis of the distributed computing approach applied to the folding of a small Î² peptide. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8217-8222.	3.3	47
489	Probing the origins, diagnosis and treatment of amyloid diseases using antibodies. Biochimie, 2004, 86, 589-600.	1.3	47
490	A Toy Model for Predicting the Rate of Amyloid Formation from Unfolded Protein. Journal of Molecular Biology, 2005, 351, 195-205.	2.0	47
491	Measurement of Amyloid Fibril Length Distributions by Inclusion of Rotational Motion in Solution NMR Diffusion Measurements. Angewandte Chemie - International Edition, 2008, 47, 3385-3387.	7.2	47
492	Solution conditions can promote formation of either amyloid protofilaments or mature fibrils from the HypF Nâ€terminal domain. Protein Science, 2001, 10, 2541-2547.	3.1	47
493	Positionâ€Dependent Electrostatic Protection against Protein Aggregation. ChemBioChem, 2009, 10, 1309-1312.	1.3	47
494	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. Scientific Reports, 2016, 6, 25559.	1.6	47
495	Inhibition of Î±-Synuclein Fibril Elongation by Hsp70 Is Governed by a Kinetic Binding Competition between Î±-Synuclein Species. Biochemistry, 2017, 56, 1177-1180.	1.2	47
496	Clusterin protects neurons against intracellular proteotoxicity. Acta Neuropathologica Communications, 2017, 5, 81.	2.4	47
497	The N-terminal Acetylation of Î±-Synuclein Changes the Affinity for Lipid Membranes but not the Structural Properties of the Bound State. Scientific Reports, 2020, 10, 204.	1.6	47
498	Interpreting Dynamically-Averaged Scalar Couplings in Proteins. Journal of Biomolecular NMR, 2005, 32, 273-280.	1.6	46
499	A protein evolution model with independent sites that reproduces site-specific amino acid distributions from the Protein Data Bank. BMC Evolutionary Biology, 2006, 6, 43.	3.2	46
500	Determination of structural fluctuations of proteins from structure-based calculations of residual dipolar couplings. Journal of Biomolecular NMR, 2012, 53, 281-292.	1.6	46
501	Hydrophobicity and Conformational Change as Mechanistic Determinants for Nonspecific Modulators of Amyloid Î² Self-Assembly. Biochemistry, 2012, 51, 126-137.	1.2	46
502	Modified configurational bias Monte Carlo method for simulation of polymer systems. Journal of Chemical Physics, 1997, 106, 2970-2976.	1.2	45
503	Folding and Aggregation Are Selectively Influenced by the Conformational Preferences of the Î±-Helices of Muscle Acylphosphatase. Journal of Biological Chemistry, 2001, 276, 37149-37154.	1.6	45
504	Reconstruction of Protein Structures from a Vectorial Representation. Physical Review Letters, 2004, 92, 218101.	2.9	45

#	Article	IF	Citations
505	Biosensorâ€based labelâ€free assays of amyloid growth. FEBS Letters, 2009, 583, 2587-2592.	1.3	45
506	Intrinsic Determinants of Neurotoxic Aggregate Formation by the Amyloid Î² Peptide. Biophysical Journal, 2010, 98, 1677-1684.	0.2	45
507	The A53T Mutation is Key in Defining the Differences in the Aggregation Kinetics of Human and Mouse Î±-Synuclein. Journal of the American Chemical Society, 2011, 133, 13465-13470.	6.6	45
508	Quantitative analysis of co-oligomer formation by amyloid-beta peptide isoforms. Scientific Reports, 2016, 6, 28658.	1.6	45
509	Monomeric and fibrillar Î±-synuclein exert opposite effects on the catalytic cycle that promotes the proliferation of AÎ²42 aggregates. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8005-8010.	3.3	45
510	Comparison of the Transition States for Folding of Two Ig-like Proteins from Different Superfamilies. Journal of Molecular Biology, 2004, 343, 1111-1123.	2.0	44
511	Investigating the Mechanisms of Amylolysis of Starch Granules by Solution-State NMR. Biomacromolecules, 2015, 16, 1614-1621.	2.6	44
512	Direct Observation of Oligomerization by Single Molecule Fluorescence Reveals a Multistep Aggregation Mechanism for the Yeast Prion Protein Ure2. Journal of the American Chemical Society, 2018, 140, 2493-2503.	6.6	44
513	Trodusquemine displaces protein misfolded oligomers from cell membranes and abrogates their cytotoxicity through a generic mechanism. Communications Biology, 2020, 3, 435.	2.0	44
514	Widespread remodeling of proteome solubility in response to different protein homeostasis stresses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2422-2431.	3.3	44
515	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. ELife, 2017, 6, .	2.8	44
516	FuzDrop on AlphaFold: visualizing the sequence-dependent propensity of liquidâ€“liquid phase separation and aggregation of proteins. Nucleic Acids Research, 2022, 50, W337-W344.	6.5	44
517	Rationalising Lysozyme Amyloidosis: Insights from the Structure and Solution Dynamics of T70N Lysozyme. Journal of Molecular Biology, 2005, 352, 823-836.	2.0	43
518	Understanding the frustration arising from the competition between function, misfolding, and aggregation in a globular protein. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14141-14146.	3.3	43
519	Enzymatically Active Microgels from Self-Assembling Protein Nanofibrils for Microflow Chemistry. ACS Nano, 2015, 9, 5772-5781.	7.3	43
520	Lipid Dynamics and Phase Transition within Î±-Synuclein Amyloid Fibrils. Journal of Physical Chemistry Letters, 2019, 10, 7872-7877.	2.1	43
521	ThX â€“ a next-generation probe for the early detection of amyloid aggregates. Chemical Science, 2020, 11, 4578-4583.	3.7	43
522	Comparison of four independently determined structures of human recombinant interleukinâ€“4. Nature Structural and Molecular Biology, 1994, 1, 301-310.	3.6	42

#	Article	IF	Citations
523	Toward an energy function for the contact map representation of proteins. Proteins: Structure, Function and Bioinformatics, 2000, 40, 237-248.	1.5	42
524	Statistical Properties of Neutral Evolution. Journal of Molecular Evolution, 2003, 57, S103-S119.	0.8	42
525	Determination of Protein Structures in the Solid State from NMR Chemical Shifts. Structure, 2008, 16, 1764-1769.	1.6	42
526	Surface Attachment of Protein Fibrils via Covalent Modification Strategies. Journal of Physical Chemistry B, 2010, 114, 10925-10938.	1.2	42
527	Cavity hydration as a gateway to unfolding: An NMR study of hen lysozyme at high pressure and low temperature. Biophysical Chemistry, 2011, 156, 24-30.	1.5	42
528	A Nanobody Binding to Non-Amyloidogenic Regions of the Protein Human Lysozyme Enhances Partial Unfolding but Inhibits Amyloid Fibril Formation. Journal of Physical Chemistry B, 2013, 117, 13245-13258.	1.2	42
529	Emergence and evolution of an interaction between intrinsically disordered proteins. ELife, 2017, 6, .	2.8	42
530	Stabilization and Characterization of Cytotoxic AÎ²₄₀ Oligomers Isolated from an Aggregation Reaction in the Presence of Zinc Ions. ACS Chemical Neuroscience, 2018, 9, 2959-2971.	1.7	42
531	Protein Solubility Predictions Using the CamSol Method in the Study of Protein Homeostasis. Cold Spring Harbor Perspectives in Biology, 2019, 11, a033845.	2.3	42
532	A kinetic ensemble of the Alzheimerâ€™s AÎ² peptide. Nature Computational Science, 2021, 1, 71-78.	3.8	42
533	Analysis of the interactions between streptokinase domains and human plasminogen. Protein Science, 1998, 7, 2190-2199.	3.1	41
534	Two-Dimensional 15Nâ^'1H Photo-CIDNP as a Surface Probe of Native and Partially Structured Proteins. Journal of the American Chemical Society, 1999, 121, 6505-6506.	6.6	41
535	Comparison of the transition state ensembles for folding of Im7 and Im9 determined using all-atom molecular dynamics simulations with Ï• value restraints. Proteins: Structure, Function and Bioinformatics, 2003, 54, 513-525.	1.5	41
536	Assessment of the Use of NMR Chemical Shifts as Replica-Averaged Structural Restraints in Molecular Dynamics Simulations to Characterize the Dynamics of Proteins. Journal of Physical Chemistry B, 2013, 117, 1838-1843.	1.2	41
537	Sequence-based prediction of protein binding mode landscapes. PLoS Computational Biology, 2020, 16, e1007864.	1.5	41
538	Proton NMR studies of denatured lysozyme. FEBS Letters, 1984, 168, 331-334.	1.3	40
539	Automated assignment of SCOP and CATH protein structure classifications from FSSP scores. Proteins: Structure, Function and Bioinformatics, 2002, 46, 405-415.	1.5	40
540	More charges against aggregation. Nature, 2007, 449, 555-555.	13.7	40

#	Article	IF	Citations
541	Translationally optimal codons associate with aggregationâ€prone sites in proteins. Proteomics, 2010, 10, 4163-4171.	1.3	40
542	Detection of early locomotor abnormalities in a Drosophila model of Alzheimer's disease. Journal of Neuroscience Methods, 2011, 197, 186-189.	1.3	40
543	Expression in Drosophila of Tandem Amyloid Î² Peptides Provides Insights into Links between Aggregation and Neurotoxicity. Journal of Biological Chemistry, 2012, 287, 20748-20754.	1.6	40
544	MOAG-4 promotes the aggregation of Î±-synuclein by competing with self-protective electrostatic interactions. Journal of Biological Chemistry, 2017, 292, 8269-8278.	1.6	40
545	Optical Structural Analysis of Individual Î±â€Synuclein Oligomers. Angewandte Chemie - International Edition, 2018, 57, 4886-4890.	7.2	40
546	Microfluidic deposition for resolving single-molecule protein architecture and heterogeneity. Nature Communications, 2018, 9, 3890.	5.8	40
547	Energetics of enzyme stability. Trends in Biotechnology, 2002, 20, 1-2.	4.9	39
548	Importance of Metastable States in the Free Energy Landscapes of Polypeptide Chains. Physical Review Letters, 2007, 99, 178104.	2.9	39
549	Proteome folding and aggregation. Current Opinion in Structural Biology, 2012, 22, 138-143.	2.6	39
550	Nucleation-conversion-polymerization reactions of biological macromolecules with prenucleation clusters. Physical Review E, 2014, 89, 032712.	0.8	39
551	Oxetane Grafts Installed Siteâ€Selectively on Native Disulfides to Enhance Protein Stability and Activity Inâ€...Vivo. Angewandte Chemie - International Edition, 2017, 56, 14963-14967.	7.2	39
552	Systematic mapping of free energy landscapes of a growing filamin domain during biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9744-9749.	3.3	39
553	Characterization of the residual structure in the unfolded state of the Î”131Î” fragment of staphylococcal nuclease. Proteins: Structure, Function and Bioinformatics, 2006, 65, 145-152.	1.5	38
554	Structure and Dynamics of a Partially Folded Protein Are Decoupled from Its Mechanism of Aggregation. Journal of the American Chemical Society, 2008, 130, 13040-13050.	6.6	38
555	Quantifying Co-Oligomer Formation by Î±-Synuclein. ACS Nano, 2018, 12, 10855-10866.	7.3	38
556	Direct measurement of lipid membrane disruption connects kinetics and toxicity of AÎ²42 aggregation. Nature Structural and Molecular Biology, 2020, 27, 886-891.	3.6	38
557	Recombinant amyloid beta-peptide production by coexpression with an affibody ligand. BMC Biotechnology, 2008, 8, 82.	1.7	37
558	Probing Side-Chain Dynamics of a Ribosome-Bound Nascent Chain Using Methyl NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 8366-8367.	6.6	37

#	Article	IF	Citations
559	The Hsp70 Chaperone System Stabilizes a Thermo-sensitive Subproteome in E.Âcoli. Cell Reports, 2019, 28, 1335-1345.e6.	2.9	37
560	The Hsc70 disaggregation machinery removes monomer units directly from Î±-synuclein fibril ends. Nature Communications, 2021, 12, 5999.	5.8	37
561	Proton NMR studies of the association and folding of glucagon in solution. FEBS Letters, 1980, 119, 265-270.	1.3	36
562	Statistical properties of contact maps. Physical Review E, 1999, 59, 977-984.	0.8	36
563	Prediction of Site-Specific Amino Acid Distributions and Limits of Divergent Evolutionary Changes in Protein Sequences. Molecular Biology and Evolution, 2005, 22, 630-638.	3.5	36
564	Probing small molecule binding to amyloid fibrils. Physical Chemistry Chemical Physics, 2011, 13, 20044.	1.3	36
565	Role of Elongation and Secondary Pathways in S6 Amyloid Fibril Growth. Biophysical Journal, 2012, 102, 2167-2175.	0.2	36
566	Biophysical studies of the development of amyloid fibrils from a peptide fragment of cold shock protein B. FEBS Journal, 2000, 267, 2609-2616.	0.2	35
567	Longâ€Range Correlations between Aliphatic ¹³C Nuclei in Protein MAS NMR Spectroscopy. Angewandte Chemie - International Edition, 2009, 48, 5708-5710.	7.2	35
568	Determination of Conformational Equilibria in Proteins Using Residual Dipolar Couplings. Journal of Chemical Theory and Computation, 2011, 7, 4189-4195.	2.3	35
569	Rapid Distinction of Intracellular and Extracellular Proteins Using NMR Diffusion Measurements. Journal of the American Chemical Society, 2012, 134, 11312-11315.	6.6	35
570	Characterization of the Interdomain Motions in Hen Lysozyme Using Residual Dipolar Couplings as Replica-Averaged Structural Restraints in Molecular Dynamics Simulations. Biochemistry, 2013, 52, 6480-6486.	1.2	35
571	A Fragment-Based Method of Creating Small-Molecule Libraries to Target the Aggregation of Intrinsically Disordered Proteins. ACS Combinatorial Science, 2016, 18, 144-153.	3.8	35
572	AÎ² Oligomers Dysregulate Calcium Homeostasis by Mechanosensitive Activation of AMPA and NMDA Receptors. ACS Chemical Neuroscience, 2021, 12, 766-781.	1.7	35
573	Efficient dynamics in the space of contact maps. Folding & Design, 1998, 3, 329-336.	4.5	34
574	Comparison of two optimization methods to derive energy parameters for protein folding: Perceptron andZ score. Proteins: Structure, Function and Bioinformatics, 2000, 41, 192-201.	1.5	34
575	Determination of the structures of distinct transition state ensembles for a Î²-sheet peptide with parallel folding pathways. Journal of Chemical Physics, 2002, 117, 9510-9517.	1.2	34
576	The Toxicity of Misfolded Protein Oligomers Is Independent of Their Secondary Structure. ACS Chemical Biology, 2019, 14, 1593-1600.	1.6	34

#	Article	IF	Citations
577	Biophysical Techniques in Structural Biology. Annual Review of Biochemistry, 2019, 88, 25-33.	5.0	34
578	Squalamine and Its Derivatives Modulate the Aggregation of Amyloid-Î² and Î±-Synuclein and Suppress the Toxicity of Their Oligomers. Frontiers in Neuroscience, 2021, 15, 680026.	1.4	34
579	Lack of Self-Averaging in Neutral Evolution of Proteins. Physical Review Letters, 2002, 89, 208101.	2.9	33
580	Analysis of the Contributions of Ring Current and Electric Field Effects to the Chemical Shifts of RNA Bases. Journal of Physical Chemistry B, 2013, 117, 1989-1998.	1.2	33
581	Influence of specific HSP70 domains on fibril formation of the yeast prion protein Ure2. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20110410.	1.8	33
582	Equilibrium simulations of proteins using molecular fragment replacement and NMR chemical shifts. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13852-13857.	3.3	33
583	Probing the Origin of the Toxicity of Oligomeric Aggregates of Î±-Synuclein with Antibodies. ACS Chemical Biology, 2019, 14, 1352-1362.	1.6	33
584	Structure of a low-population intermediate state in the release of an enzyme product. ELife, 2015, 4, .	2.8	33
585	Finding the right fold. Nature Structural Biology, 1995, 2, 513-517.	9.7	32
586	Stability Threshold as a Selection Principle for Protein Design. Physical Review Letters, 1997, 78, 3967-3970.	2.9	32
587	Geometry, Energetics, and Dynamics of Hydrogen Bonds in Proteins:Â Structural Information Derived from NMR Scalar Couplings. Journal of the American Chemical Society, 2006, 128, 15127-15135.	6.6	32
588	Biological function in a non-native partially folded state of a protein. EMBO Journal, 2008, 27, 1525-35.	3.5	32
589	Structure, Dynamics and Folding of an Immunoglobulin Domain of the Gelation Factor (ABP-120) from Dictyostelium discoideum. Journal of Molecular Biology, 2009, 388, 865-879.	2.0	32
590	Hamiltonian Dynamics of Protein Filament Formation. Physical Review Letters, 2016, 116, 038101.	2.9	32
591	Soluble amyloid beta-containing aggregates are present throughout the brain at early stages of Alzheimerâ€™s disease. Brain Communications, 2021, 3, fcab147.	1.5	32
592	A study of D52S hen lysozyme-G1cNAc oligosaccharide complexes by NMR spectroscopy and electrospray mass spectrometry. FEBS Letters, 1992, 296, 153-157.	1.3	31
593	High-Dimensional Bak-Sneppen Model. Physical Review Letters, 1998, 80, 5746-5749.	2.9	31
594	Calculation of Mutational Free Energy Changes in Transition States for Protein Folding. Biophysical Journal, 2003, 85, 1207-1214.	0.2	31

#	Article	IF	Citations
595	ALMOST: An all atom molecular simulation toolkit for protein structure determination. Journal of Computational Chemistry, 2014, 35, 1101-1105.	1.5	31
596	Biophotonics of Native Silk Fibrils. Macromolecular Bioscience, 2018, 18, e1700295.	2.1	31
597	Kinetic barriers to Î±-synuclein protofilament formation and conversion into mature fibrils. Chemical Communications, 2018, 54, 7854-7857.	2.2	31
598	Hinge-bending and folding. Nature, 1990, 348, 198-199.	13.7	30
599	The iFly tracking system for an automated locomotor and behavioural analysis of Drosophila melanogaster. Integrative Biology (United Kingdom), 2011, 3, 755.	0.6	30
600	Integration and characterization of solid wall electrodes in microfluidic devices fabricated in a single photolithography step. Applied Physics Letters, 2013, 102, .	1.5	30
601	Molecular determinants of the interaction of EGCG with ordered and disordered proteins. Biopolymers, 2018, 109, e23117.	1.2	30
602	Fast Fluorescence Lifetime Imaging Reveals the Aggregation Processes of Î±-Synuclein and Polyglutamine in Aging Caenorhabditis elegans. ACS Chemical Biology, 2019, 14, 1628-1636.	1.6	30
603	The extent of protein hydration dictates the preference for heterogeneous or homogeneous nucleation generating either parallel or antiparallel Î²-sheet Î±-synuclein aggregates. Chemical Science, 2020, 11, 11902-11914.	3.7	30
604	A Role of Cholesterol in Modulating the Binding of Î±-Synuclein to Synaptic-Like Vesicles. Frontiers in Neuroscience, 2020, 14, 18.	1.4	30
605	Complete Assignment of the ¹H NMR Spectrum of the Aromatic Residues of Lysozyme. FEBS Journal, 1982, 128, 527-531.	0.2	29
606	1H, 13C and 15N assignments of a camelid nanobody directed against human Î±-synuclein. Biomolecular NMR Assignments, 2009, 3, 231-233.	0.4	29
607	The relevance of contact-independent cell-to-cell transfer of TDP-43 and SOD1 in amyotrophic lateral sclerosis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 2762-2771.	1.8	29
608	Fabrication and Characterization of Reconstituted Silk Microgels for the Storage and Release of Small Molecules. Macromolecular Rapid Communications, 2019, 40, e1800898.	2.0	29
609	A Structural Ensemble of a Tau-Microtubule Complex Reveals Regulatory Tau Phosphorylation and Acetylation Mechanisms. ACS Central Science, 2021, 7, 1986-1995.	5.3	29
610	Nuclear-Magnetic-Resonance Studies of 5'-Ribonucleotide and 5'-Deoxyribonucleotide Conformations in Solution Using the Lanthanide Probe Method. FEBS Journal, 1978, 88, 259-266.	0.2	28
611	Identification of glycine spin systems in 1 H NMR spectra of proteins using multiple quantum coherences. FEBS Letters, 1985, 186, 35-40.	1.3	28
612	Molecular dynamics simulations of human ?-lactalbumin: Changes to the structural and dynamical properties of the protein at low pH. , 1999, 36, 77-86.		28

#	Article	IF	Citations
613	Folding of Small Proteins by Monte Carlo Simulations with Chemical Shift Restraints without the Use of Molecular Fragment Replacement or Structural Homology. Journal of Physical Chemistry B, 2009, 113, 7890-7896.	1.2	28
614	Thermodynamics of Polypeptide Supramolecular Assembly in the Short-Chain Limit. Journal of the American Chemical Society, 2017, 139, 16134-16142.	6.6	28
615	Thermal stability of the three domains of streptokinase studied by circular dichroism and nuclear magnetic resonance. Protein Science, 1996, 5, 2583-2591.	3.1	27
616	Relationship between Prion Propensity and the Rates of Individual Molecular Steps of Fibril Assembly. Journal of Biological Chemistry, 2011, 286, 12101-12107.	1.6	27
617	Synthesis of Nonequilibrium Supramolecular Peptide Polymers on a Microfluidic Platform. Journal of the American Chemical Society, 2016, 138, 9589-9596.	6.6	27
618	Particle-Based Monte-Carlo Simulations of Steady-State Mass Transport at Intermediate PÃ©clet Numbers. International Journal of Nonlinear Sciences and Numerical Simulation, 2016, 17, 175-183.	0.4	27
619	Microfluidic approaches for probing amyloid assembly and behaviour. Lab on A Chip, 2018, 18, 999-1016.	3.1	27
620	Screening of small molecules using the inhibition of oligomer formation in Î±-synuclein aggregation as a selection parameter. Communications Chemistry, 2020, 3, .	2.0	27
621	Squalamine and trodusquemine: two natural products for neurodegenerative diseases, from physical chemistry to the clinic. Natural Product Reports, 2022, 39, 742-753.	5.2	27
622	Development of Enzymatic Activity during Protein Folding. Journal of Biological Chemistry, 1999, 274, 20151-20158.	1.6	26
623	A partially folded intermediate species of the Î²-sheet protein apo-pseudoazurin is trapped during proline-limited folding. Protein Science, 2001, 10, 1216-1224.	3.1	26
624	Influence of the fluctuations of the alignment tensor on the analysis of the structure and dynamics of proteins using residual dipolar couplings. Journal of Biomolecular NMR, 2008, 40, 71-81.	1.6	26
625	Characterizing Intermolecular Interactions That Initiate Native-Like Protein Aggregation. Biophysical Journal, 2012, 102, 2595-2604.	0.2	26
626	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. Journal of Molecular Biology, 2020, 432, 845-860.	2.0	26
627	Assessment of Therapeutic Antibody Developability by Combinations of In Vitro and In Silico Methods. Methods in Molecular Biology, 2022, 2313, 57-113.	0.4	26
628	A method of incorporating rate constants as kinetic constraints in molecular dynamics simulations. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	26
629	Neuronal Cx3cr1 Deficiency Protects against Amyloid Î²-Induced Neurotoxicity. PLoS ONE, 2015, 10, e0127730.	1.1	26
630	Protein folding using contact maps. Vitamins and Hormones, 2000, 58, 171-212.	0.7	25

#	Article	IF	Citations
631	Accurate Determination of Interstrand Distances and Alignment in Amyloid Fibrils by Magic Angle Spinning NMR. Journal of Physical Chemistry B, 2010, 114, 13555-13561.	1.2	25
632	Determination of the Individual Roles of the Linker Residues in the Interdomain Motions of Calmodulin Using NMR Chemical Shifts. Journal of Molecular Biology, 2014, 426, 1826-1838.	2.0	25
633	Single Point Mutations Induce a Switch in the Molecular Mechanism of the Aggregation of the Alzheimerâ€™s Disease Associated Aî²₄₂ Peptide. ACS Chemical Biology, 2014, 9, 378-382.	1.6	25
634	Force generation by the growth of amyloid aggregates. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9524-9529.	3.3	25
635	A Rational Design Strategy for the Selective Activity Enhancement of a Molecular Chaperone toward a Target Substrate. Biochemistry, 2015, 54, 5103-5112.	1.2	25
636	Gradient-free determination of isoelectric points of proteins on chip. Physical Chemistry Chemical Physics, 2017, 19, 23060-23067.	1.3	25
637	Exploring the role of postâ€translational modifications in regulating Î±â€synuclein interactions by studying the effects of phosphorylation on nanobody binding. Protein Science, 2018, 27, 1262-1274.	3.1	25
638	Structural differences between toxic and nontoxic HypF-N oligomers. Chemical Communications, 2018, 54, 8637-8640.	2.2	25
639	Determination of intermediate state structures in the opening pathway of SARS-CoV-2 spike using cryo-electron microscopy. Chemical Science, 2021, 12, 9168-9175.	3.7	25
640	A dopamine metabolite stabilizes neurotoxic amyloid-Î² oligomers. Communications Biology, 2021, 4, 19.	2.0	25
641	Protein Folding: A Perspective from Theory and Experiment. , 1998, 37, 868.		25
642	Molecular dynamics ensemble refinement of the heterogeneous native state of NCBD using chemical shifts and NOEs. PeerJ, 2018, 6, e5125.	0.9	25
643	A Small Molecule Stabilizes the Disordered Native State of the Alzheimerâ€™s Aî² Peptide. ACS Chemical Neuroscience, 2022, 13, 1738-1745.	1.7	25
644	Structures of the Excited States of Phospholamban and Shifts in Their Populations upon Phosphorylation. Biochemistry, 2013, 52, 6684-6694.	1.2	24
645	Immunization with Î±â€synuclein/Grp94 reshapes peripheral immunity and suppresses microgliosis in a chronic Parkinsonism model. Glia, 2018, 66, 191-205.	2.5	24
646	Rapid Structural, Kinetic, and Immunochemical Analysis of Alpha-Synuclein Oligomers in Solution. Nano Letters, 2020, 20, 8163-8169.	4.5	24
647	Surface-Catalyzed Secondary Nucleation Dominates the Generation of Toxic IAPP Aggregates. Frontiers in Molecular Biosciences, 2021, 8, 757425.	1.6	24
648	Selective association of protein molecules followed by mass spectrometry. Protein Science, 1999, 8, 1368-1370.	3.1	23

#	Article	IF	Citations
649	Single-Molecule Measurements of Transient Biomolecular Complexes through Microfluidic Dilution. Analytical Chemistry, 2013, 85, 6855-6859.	3.2	23
650	Supersaturated proteins are enriched at synapses and underlie cell and tissue vulnerability in Alzheimer's disease. Heliyon, 2019, 5, e02589.	1.4	23
651	Therapeutic Strategies to Reduce the Toxicity of Misfolded Protein Oligomers. International Journal of Molecular Sciences, 2020, 21, 8651.	1.8	23
652	Assessing motor-related phenotypes of Caenorhabditis elegans with the wide field-of-view nematode tracking platform. Nature Protocols, 2020, 15, 2071-2106.	5.5	23
653	Modulation of the Interactions Between Î±-Synuclein and Lipid Membranes by Post-translational Modifications. Frontiers in Neurology, 2021, 12, 661117.	1.1	23
654	Dissection of multiâ€protein complexes using mass spectrometry: Subunit interactions in transthyretin and retinolâ€binding protein complexes. Proteins: Structure, Function and Bioinformatics, 1998, 33, 3-11.	1.5	23
655	Complete Assignment of Aromatic 1H Nuclear Magnetic Resonances of the Tyrosine Residues of Hen Lysozyme. FEBS Journal, 1978, 92, 99-103.	0.2	22
656	Identification using 1H NMR spectroscopy of slowly exchanging amide hydrogens of hen lysozyme in solution. FEBS Journal, 1984, 145, 389-395.	0.2	22
657	A glimpse at the organization of the protein universe. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5641-5642.	3.3	22
658	The statistical theory of allostery. Nature Chemical Biology, 2011, 7, 411-412.	3.9	22
659	A Rationally Designed Six-Residue Swap Generates Comparability in the Aggregation Behavior of Î±-Synuclein and Î²-Synuclein. Biochemistry, 2012, 51, 8771-8778.	1.2	22
660	The physical basis of protein misfolding disorders. Physics Today, 2015, 68, 36-41.	0.3	22
661	Identification and characterization of PKCÎ³, a kinase associated with SCA14, as an amyloidogenic protein. Human Molecular Genetics, 2015, 24, 525-539.	1.4	22
662	Structural Effects of Two Camelid Nanobodies Directed to Distinct C-Terminal Epitopes on Î±-Synuclein. Biochemistry, 2016, 55, 3116-3122.	1.2	22
663	The metastability of the proteome of spinal motor neurons underlies their selective vulnerability in ALS. Neuroscience Letters, 2019, 704, 89-94.	1.0	22
664	Complexity in Lipid Membrane Composition Induces Resilience to AÎ²₄₂ Aggregation. ACS Chemical Neuroscience, 2020, 11, 1347-1352.	1.7	22
665	Scaling analysis reveals the mechanism and rates of prion replication in vivo. Nature Structural and Molecular Biology, 2021, 28, 365-372.	3.6	22
666	2H NMR studies of metallocenes in host lattices. Journal of Inclusion Phenomena, 1987, 5, 65-68.	0.6	21

#	Article	IF	Citations
667	Comparison of Sequence-Based and Structure-Based Energy Functions for the Reversible Folding of a Peptide. Biophysical Journal, 2005, 88, 3158-3166.	0.2	21
668	Structural Comparison of the Two Alternative Transition States for Folding of TI I27. Biophysical Journal, 2006, 91, 263-275.	0.2	21
669	The dynamics of interleukinâ€8 and its interaction with human CXC receptor I peptide. Protein Science, 2014, 23, 464-480.	3.1	21
670	Structure of a Single-Chain Fv Bound to the 17 N-Terminal Residues of Huntingtin Provides Insights into Pathogenic Amyloid Formation and Suppression. Journal of Molecular Biology, 2015, 427, 2166-2178.	2.0	21
671	Absolute Quantification of Amyloid Propagons by Digital Microfluidics. Analytical Chemistry, 2017, 89, 12306-12313.	3.2	21
672	Identification of Small Molecule Inhibitors of Tau Aggregation by Targeting Monomeric Tau As a Potential Therapeutic Approach for Tauopathies. Current Alzheimer Research, 2015, 12, 814-28.	0.7	21
673	13C cross-polarization/magic angle spinning and2H NMR studies of the structure and dynamics of the (deoxycholic acid)2-ferrocene inclusion compound. Magnetic Resonance in Chemistry, 1990, 28, S37-S46.	1.1	20
674	Equilibrium Unfolding Studies of Horse Muscle Acylphosphatase. FEBS Journal, 1994, 225, 811-817.	0.2	20
675	Folding Lennard-Jones proteins by a contact potential. , 1999, 37, 544-553.		20
676	Using Sideâ€Chain Aromatic Proton Chemical Shifts for a Quantitative Analysis of Protein Structures. Angewandte Chemie - International Edition, 2011, 50, 9620-9623.	7.2	20
677	A Conformational Ensemble Derived Using NMR Methyl Chemical Shifts Reveals a Mechanical Clamping Transition That Gates the Binding of the HU Protein to DNA. Journal of the American Chemical Society, 2014, 136, 2204-2207.	6.6	20
678	Spatial Propagation of Protein Polymerization. Physical Review Letters, 2014, 112, 098101.	2.9	20
679	The Significance of the Location of Mutations for the Native-State Dynamics of Human Lysozyme. Biophysical Journal, 2016, 111, 2358-2367.	0.2	20
680	Inhibiting the Ca 2+ Influx Induced by Human CSF. Cell Reports, 2017, 21, 3310-3316.	2.9	20
681	Microfluidic Diffusion Platform for Characterizing the Sizes of Lipid Vesicles and the Thermodynamics of Proteinâ€“Lipid Interactions. Analytical Chemistry, 2018, 90, 3284-3290.	3.2	20
682	Looking at structure, stability, and evolution of proteins through the principal eigenvector of contact matrices and hydrophobicity profiles. Gene, 2005, 347, 219-230.	1.0	19
683	An accidental breach of a protein's natural defenses. Nature Structural and Molecular Biology, 2006, 13, 295-297.	3.6	19
684	The length distribution of frangible biofilaments. Journal of Chemical Physics, 2015, 143, 164901.	1.2	19

#	Article	IF	Citations
685	Structure-Free Validation of Residual Dipolar Coupling and Paramagnetic Relaxation Enhancement Measurements of Disordered Proteins. Biochemistry, 2015, 54, 6876-6886.	1.2	19
686	Using Pseudocontact Shifts and Residual Dipolar Couplings as Exact NMR Restraints for the Determination of Protein Structural Ensembles. Biochemistry, 2015, 54, 7470-7476.	1.2	19
687	Effect of molecular chaperones on aberrant protein oligomers in vitro: super-versus sub-stoichiometric chaperone concentrations. Biological Chemistry, 2016, 397, 401-415.	1.2	19
688	Amyloid-like Fibrils from an Î±-Helical Transmembrane Protein. Biochemistry, 2017, 56, 3225-3233.	1.2	19
689	Chemical and mechanistic analysis of photodynamic inhibition of Alzheimer's Î²-amyloid aggregation. Chemical Communications, 2019, 55, 1152-1155.	2.2	19
690	An intrinsically disordered motif regulates the interaction between the p47 adaptor and the p97 AAA+ ATPase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 26226-26236.	3.3	19
691	Proliferation of Tau 304â€“380 Fragment Aggregates through Autocatalytic Secondary Nucleation. ACS Chemical Neuroscience, 2021, 12, 4406-4415.	1.7	19
692	Recombinant amyloidogenic domain of ApoA-I: Analysis of its fibrillogenic potential. Biochemical and Biophysical Research Communications, 2006, 351, 223-228.	1.0	18
693	1H, 15N and 13C assignments of domain 5 of DictyosteliumÂdiscoideum gelation factor (ABP-120) in its native and 8M urea-denatured states. Biomolecular NMR Assignments, 2009, 3, 29-31.	0.4	18
694	Structure and Dynamics of GeoCyp: A Thermophilic Cyclophilin with a Novel Substrate Binding Mechanism That Functions Efficiently at Low Temperatures. Biochemistry, 2015, 54, 3207-3217.	1.2	18
695	Biophysical approaches for the study of interactions between molecular chaperones and protein aggregates. Chemical Communications, 2015, 51, 14425-14434.	2.2	18
696	Identification and Structural Characterization of an Intermediate in the Folding of the Measles Virus X Domain. Journal of Biological Chemistry, 2016, 291, 10886-10892.	1.6	18
697	Structural Characterization of the Early Events in the Nucleationâ€“Condensation Mechanism in a Protein Folding Process. Journal of the American Chemical Society, 2017, 139, 6899-6910.	6.6	18
698	Simultaneous NMR characterisation of multiple minima in the free energy landscape of an RNA UUCG tetraloop. Physical Chemistry Chemical Physics, 2017, 19, 2797-2804.	1.3	18
699	Enhancement of the Anti-Aggregation Activity of a Molecular Chaperone Using a Rationally Designed Post-Translational Modification. ACS Central Science, 2019, 5, 1417-1424.	5.3	18
700	Identifying A- and P-site locations on ribosome-protected mRNA fragments using Integer Programming. Scientific Reports, 2019, 9, 6256.	1.6	18
701	1H-NMR analysis of turkey egg-white lysozyme and comparison with hen egg-white lysozyme. FEBS Journal, 1993, 215, 255-266.	0.2	17
702	Towards quantitative predictions in cell biology using chemical properties of proteins. Molecular BioSystems, 2008, 4, 1170.	2.9	17

#	Article	IF	Citations
703	Enzymatic activity in disordered states of proteins. Current Opinion in Chemical Biology, 2010, 14, 671-675.	2.8	17
704	A non-natural variant of human lysozyme (I59T) mimics the in vitro behaviour of the I56T variant that is responsible for a form of familial amyloidosis. Protein Engineering, Design and Selection, 2010, 23, 499-506.	1.0	17
705	Nanobodies as Structural Probes of Protein Misfolding and Fibril Formation. Methods in Molecular Biology, 2012, 911, 533-558.	0.4	17
706	Mapping the Protein Fold Universe Using the CamTube Force Field in Molecular Dynamics Simulations. PLoS Computational Biology, 2015, 11, e1004435.	1.5	17
707	Alpha-2-Macroglobulin Is Acutely Sensitive to Freezing and Lyophilization: Implications for Structural and Functional Studies. PLoS ONE, 2015, 10, e0130036.	1.1	17
708	The importance of loop length in the folding of an immunoglobulin domain. Protein Engineering, Design and Selection, 2004, 17, 443-453.	1.0	16
709	Apomyoglobin reveals a random-nucleation mechanism in amyloid protofibril formation. Acta Histochemica, 2006, 108, 215-219.	0.9	16
710	Measuring the Kinetics of Amyloid Fibril Elongation Using Quartz Crystal Microbalances. Methods in Molecular Biology, 2012, 849, 101-119.	0.4	16
711	1H, 13C and 15N resonance assignments of human muscle acylphosphatase. Biomolecular NMR Assignments, 2012, 6, 27-29.	0.4	16
712	Archaeal MBF1 binds to 30S and 70S ribosomes via its helixâ€“turnâ€“helix domain. Biochemical Journal, 2014, 462, 373-384.	1.7	16
713	The influence of novel gemini surfactants containing cycloalkyl side-chains on the structural phases of DNA in solution. Colloids and Surfaces B: Biointerfaces, 2015, 131, 83-92.	2.5	16
714	Delivery of Native Proteins into C. elegans Using a Transduction Protocol Based on Lipid Vesicles. Scientific Reports, 2017, 7, 15045.	1.6	16
715	Increased Secondary Nucleation Underlies Accelerated Aggregation of the Four-Residue N-Terminally Truncated Aî²42 Species Aî²5â€“42. ACS Chemical Neuroscience, 2019, 10, 2374-2384.	1.7	16
716	A metastable subproteome underlies inclusion formation in muscle proteinopathies. Acta Neuropathologica Communications, 2019, 7, 197.	2.4	16
717	Making biological membrane resistant to the toxicity of misfolded protein oligomers: a lesson from trodusquemine. Nanoscale, 2020, 12, 22596-22614.	2.8	16
718	An open-source automated PEG precipitation assay to measure the relative solubility of proteins with low material requirement. Scientific Reports, 2021, 11, 21932.	1.6	16
719	Characterization of the structure and dynamics of amyloidogenic variants of human lysozyme by NMR spectroscopy. Protein Science, 2001, 10, 2525-2530.	3.1	15
720	Determination of the Transition State Ensemble for the Folding of Ubiquitin from a Combination of Î¦ and Î· Analyses. Journal of Molecular Biology, 2008, 377, 575-588.	2.0	15

#	Article	IF	Citations
721	Using Chemical Shifts to Determine Structural Changes in Proteins upon Complex Formation. Journal of Physical Chemistry B, 2011, 115, 9491-9494.	1.2	15
722	Fibrillogenic propensity of the GroEL apical domain: A Janusâ€faced minichaperone. FEBS Letters, 2012, 586, 1120-1127.	1.3	15
723	Protein self-assembly intermediates. Nature Chemical Biology, 2013, 9, 216-217.	3.9	15
724	A method of determining RNA conformational ensembles using structure-based calculations of residual dipolar couplings. Journal of Chemical Physics, 2013, 138, 215103.	1.2	15
725	Characterization of the Conformational Fluctuations in the Josephin Domain of Ataxin-3. Biophysical Journal, 2014, 107, 2932-2940.	0.2	15
726	Alzheimerâ€™s disease: addressing a twenty-first century plague. Rendiconti Lincei, 2015, 26, 251-262.	1.0	15
727	Structure and Dynamics of the Integrin LFA-1 I-Domain in the Inactive State Underlie its Inside-Out/Outside-In Signaling and Allosteric Mechanisms. Structure, 2015, 23, 745-753.	1.6	15
728	Automated Ex Situ Assays of Amyloid Formation on a Microfluidic Platform. Biophysical Journal, 2016, 110, 555-560.	0.2	15
729	A rationally designed bicyclic peptide remodels AÎ²42 aggregation in vitro and reduces its toxicity in a worm model of Alzheimerâ€™s disease. Scientific Reports, 2020, 10, 15280.	1.6	15
730	Systematic Activity Maturation of a Single-Domain Antibody with Non-canonical Amino Acids through Chemical Mutagenesis. Cell Chemical Biology, 2021, 28, 70-77.e5.	2.5	15
731	The binding of the small heat-shock protein Î±B-crystallin to fibrils of Î±-synuclein is driven by entropic forces. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
732	Cholesterol-rich naked mole-rat brain lipid membranes are susceptible to amyloid beta-induced damage in vitro. Aging, 2020, 12, 22266-22290.	1.4	15
733	The cellular modifier MOACâ€4/SERF drives amyloid formation through charge complementation. EMBO Journal, 2021, 40, e107568.	3.5	15
734	Characterisation of transition state structures for protein folding using 'high', 'medium' and 'low' Â-values. Protein Engineering, Design and Selection, 2008, 21, 215-222.	1.0	14
735	Identification of an RNA Polymerase III Regulator Linked to Disease-Associated Protein Aggregation. Molecular Cell, 2017, 65, 1096-1108.e6.	4.5	14
736	Sequential Release of Proteins from Structured Multishell Microcapsules. Biomacromolecules, 2017, 18, 3052-3059.	2.6	14
737	A Rationally Designed Hsp70 Variant Rescues the Aggregation-Associated Toxicity of Human IAPP in Cultured Pancreatic Islet Î²-Cells. International Journal of Molecular Sciences, 2018, 19, 1443.	1.8	14
738	Surface accessibility of aromatic residues in human lysozyme using photochemically induced dynamic nuclear polarization NMR spectroscopy. FEBS Letters, 1985, 185, 248-252.	1.3	13

#	Article	IF	Citations
739	Hot sandpiles. Europhysics Letters, 1996, 35, 481-486.	0.7	13
740	Molecular dynamics simulations from putative transition states of Î±â€spectrin SH3 domain. Proteins: Structure, Function and Bioinformatics, 2007, 69, 536-550.	1.5	13
741	A Relationship between the Aggregation Rates of Î±-Synuclein Variants and the Î²-Sheet Populations in Their Monomeric Forms. Journal of Physical Chemistry B, 2013, 117, 10737-10741.	1.2	13
742	Structure and Dynamics of Intrinsically Disordered Proteins. Advances in Experimental Medicine and Biology, 2015, 870, 35-48.	0.8	13
743	Chaperome screening leads to identification of Grp94/Gp96 and FKBP4/52 as modulators of the Î±â€synucleinâ€elicited immune response. FASEB Journal, 2016, 30, 564-577.	0.2	13
744	Cooperative Assembly of Hsp70 Subdomain Clusters. Biochemistry, 2018, 57, 3641-3649.	1.2	13
745	Determination of the conformational states of strychnine in solution using NMR residual dipolar couplings in a tensor-free approach. Methods, 2018, 148, 4-8.	1.9	13
746	Characterizing Individual Protein Aggregates by Infrared Nanospectroscopy and Atomic Force Microscopy. Journal of Visualized Experiments, 2019, , .	0.2	13
747	Amelioration of aggregate cytotoxicity by catalytic conversion of protein oligomers into amyloid fibrils. Nanoscale, 2020, 12, 18663-18672.	2.8	13
748	Biophysical studies of protein misfolding and aggregation inin vivomodels of Alzheimer's and Parkinson's diseases. Quarterly Reviews of Biophysics, 2020, 53, e22.	2.4	13
749	Kinetic analysis reveals that independent nucleation events determine the progression of polyglutamine aggregation in C. elegans. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
750	Quantitative Measurement of the Affinity of Toxic and Nontoxic Misfolded Protein Oligomers for Lipid Bilayers and of its Modulation by Lipid Composition and Trodusquemine. ACS Chemical Neuroscience, 2021, 12, 3189-3202.	1.7	13
751	Kinetic profiling of therapeutic strategies for inhibiting the formation of amyloid oligomers. Journal of Chemical Physics, 2022, 156, 164904.	1.2	13
752	Common sequence motifs of nascent chains engage the ribosome surface and trigger factor. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
753	The Generic Nature of Protein Folding and Misfolding. , 2006, , 21-41.		12
754	Analysis of structural order in amyloid fibrils. Nanotechnology, 2007, 18, 044031.	1.3	12
755	1H, 15N and 13C assignments of the dimeric ribosome binding domain of trigger factor from Escherichia coli. Biomolecular NMR Assignments, 2009, 3, 17-20.	0.4	12
756	Mutational Analysis of the Aggregation-Prone and Disaggregation-Prone Regions of Acylphosphatase. Journal of Molecular Biology, 2009, 387, 965-974.	2.0	12

#	Article	IF	Citations
757	Analysis of Sub-Ï„c and Supra-Ï„c Motions in Protein GÎ²1 Using Molecular Dynamics Simulations. Biophysical Journal, 2009, 97, 2513-2520.	0.2	12
758	Interactions in the native state of monellin, which play a protective role against aggregation. Molecular BioSystems, 2011, 7, 521-532.	2.9	12
759	A geometrical parametrization of C1â€²-C5â€² RNA ribose chemical shifts calculated by density functional theory. Journal of Chemical Physics, 2013, 139, 034101.	1.2	12
760	Conformational Effects of the A21G Flemish Mutation on the Aggregation of Amyloid Î² Peptide. Biological and Pharmaceutical Bulletin, 2015, 38, 1668-1672.	0.6	12
761	Analysis of the hierarchical structure of the B. subtilis transcriptional regulatory network. Molecular BioSystems, 2015, 11, 930-941.	2.9	12
762	Bacterial production and direct functional screening of expanded molecular libraries for discovering inhibitors of protein aggregation. Science Advances, 2019, 5, eaax5108.	4.7	12
763	Rationally Designed Antibodies as Research Tools to Study the Structureâ€“Toxicity Relationship of Amyloid-Î² Oligomers. International Journal of Molecular Sciences, 2020, 21, 4542.	1.8	12
764	Comparative Studies in the A30P and A53T Î±-Synuclein C. elegans Strains to Investigate the Molecular Origins of Parkinson's Disease. Frontiers in Cell and Developmental Biology, 2021, 9, 552549.	1.8	12
765	Facile Installation of Post-translational Modifications on the Tau Protein via Chemical Mutagenesis. ACS Chemical Neuroscience, 2021, 12, 557-561.	1.7	12
766	Calculation of the free energy barriers in the oligomerisation of Ab. Frontiers in Bioscience - Landmark, 2008, Volume, 5614.	3.0	12
767	Chemical shifts of aromatic protons in protein NMR spectra. FEBS Letters, 1983, 159, 132-136.	1.3	11
768	Assignment of resonances in the 1H NMR spectrum of human lysozyme. FEBS Journal, 1985, 153, 383-396.	0.2	11
769	Trapping folding intermediates. Nature, 1988, 335, 666-667.	13.7	11
770	Aromatic ring dynamics in crystalline molecular solids by one- and two-dimensional exchange spectroscopy. Magnetic Resonance in Chemistry, 1990, 28, 163-170.	1.1	11
771	A stochastic method for the reconstruction of protein structures from one-dimensional structural profiles. Gene, 2008, 422, 47-51.	1.0	11
772	Characterizing the First Steps of Amyloid Formation for the ccÎ² Peptide. Journal of Physical Chemistry B, 2008, 112, 9998-10004.	1.2	11
773	Solvent exposure of Tyr10 as a probe of structural differences between monomeric and aggregated forms of the amyloid-Î² peptide. Biochemical and Biophysical Research Communications, 2015, 468, 696-701.	1.0	11
774	Protein Aggregateâ€Ligand Binding Assays Based on Microfluidic Diffusional Separation. ChemBioChem, 2016, 17, 1920-1924.	1.3	11

#	Article	IF	Citations
775	Bifunctional fluorescent probes for detection of amyloid aggregates and reactive oxygen species. Royal Society Open Science, 2018, 5, 171399.	1.1	11
776	On-chip measurements of protein unfolding from direct observations of micron-scale diffusion. Chemical Science, 2018, 9, 3503-3507.	3.7	11
777	Lipid Homeostasis and Its Links With Protein Misfolding Diseases. Frontiers in Molecular Neuroscience, 2022, 15, 829291.	1.4	11
778	Correlation between the binding affinity and the conformational entropy of nanobody SARS-CoV-2 spike protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
779	Model of correlated evolution. Physical Review E, 1996, 54, 6053-6057.	0.8	10
780	Subdomain Architecture and Stability of a Giant Repeat Protein. Journal of Physical Chemistry B, 2013, 117, 13029-13037.	1.2	10
781	Oligomer-targeting with a conformational antibody fragment promotes toxicity in AÎ²-expressing flies. Acta Neuropathologica Communications, 2014, 2, 43.	2.4	10
782	Chaperoned amyloid proteins for immune manipulation: Î±â€Synuclein/Hsp70 shifts immunity toward a modulatory phenotype. Immunity, Inflammation and Disease, 2014, 2, 226-238.	1.3	10
783	Oxetane Grafts Installed Siteâ€Selectively on Native Disulfides to Enhance Protein Stability and Activity Inâ€…Vivo. Angewandte Chemie, 2017, 129, 15159-15163.	1.6	10
784	Probing the dynamic stalk region of the ribosome using solution NMR. Scientific Reports, 2019, 9, 13528.	1.6	10
785	Expression of the amyloid-Î² peptide in a single pair of C. elegans sensory neurons modulates the associated behavioural response. PLoS ONE, 2019, 14, e0217746.	1.1	10
786	A maximum caliber approach for continuum path ensembles. European Physical Journal B, 2021, 94, 1.	0.6	10
787	Accelerating Reaction Rates of Biomolecules by Using Shear Stress in Artificial Capillary Systems. Journal of the American Chemical Society, 2021, 143, 16401-16410.	6.6	10
788	Neuroserpin and transthyretin are extracellular chaperones that preferentially inhibit amyloid formation. Science Advances, 2021, 7, eabf7606.	4.7	10
789	A variable-temperature13C cross-polarization magic angle spinning NMR study of some unusual dynamic and phase properties of (Â±)-3,4-di-O-acetyl-1,2,5,6-tetra-O-benzyl-myo-inositol, â€˜jumping crystalsâ€™. Magnetic Resonance in Chemistry, 1992, 30, 606-615.	1.1	9
790	NMR and protein dynamics. International Journal of Quantum Chemistry, 1996, 59, 315-332.	1.0	9
791	Disordered flat phase and phase diagram for restricted solid-on-solid models of fcc (110) surfaces. Physical Review B, 1996, 53, 13169-13186.	1.1	9
792	Oleg Ptitsyn (1929-99). Nature, 1999, 400, 122-122.	13.7	9

#	Article	IF	Citations
793	Derivation of a solubility condition for proteins from an analysis of the competition between folding and aggregation. Molecular BioSystems, 2010, 6, 2490.	2.9	9
794	Structural Insights into the Calcium-Mediated Allosteric Transition in the C-Terminal Domain of Calmodulin from Nuclear Magnetic Resonance Measurements. Biochemistry, 2016, 55, 19-28.	1.2	9
795	Ultrasensitive Measurement of Ca²⁺ Influx into Lipid Vesicles Induced by Protein Aggregates. Angewandte Chemie, 2017, 129, 7858-7862.	1.6	9
796	Statistical Mechanics of Globular Oligomer Formation by Protein Molecules. Journal of Physical Chemistry B, 2018, 122, 11721-11730.	1.2	9
797	Using Tetracysteine-Tagged TDP-43 with a Biarsenical Dye To Monitor Real-Time Trafficking in a Cell Model of Amyotrophic Lateral Sclerosis. Biochemistry, 2019, 58, 4086-4095.	1.2	9
798	A Cell- and Tissue-Specific Weakness of the Protein Homeostasis System Underlies Brain Vulnerability to Protein Aggregation. IScience, 2020, 23, 100934.	1.9	9
799	The Amyloid Fibril-Forming Î²-Sheet Regions of Amyloid Î² and Î±-Synuclein Preferentially Interact with the Molecular Chaperone 14-3-3Î¶. Molecules, 2021, 26, 6120.	1.7	9
800	Ï€-Clamp-Mediated Homo- and Heterodimerization of Single-Domain Antibodies via Site-Specific Homobifunctional Conjugation. Journal of the American Chemical Society, 2022, 144, 13026-13031.	6.6	9
801	Quantitative approaches to defining normal and aberrant protein homeostasis. Faraday Discussions, 2009, 143, 277.	1.6	8
802	New opportunities for tensor-free calculations of residual dipolar couplings for the study of protein dynamics. Journal of Biomolecular NMR, 2014, 58, 233-238.	1.6	8
803	NMR characterization of the conformational fluctuations of the human lymphocyte functionâ€associated antigenâ€1 Iâ€domain. Protein Science, 2014, 23, 1596-1606.	3.1	8
804	The free energy landscape of the oncogene protein E7 of human papillomavirus type 16 reveals a complex interplay between ordered and disordered regions. Scientific Reports, 2019, 9, 5822.	1.6	8
805	A superposition free method for protein conformational ensemble analyses and local clustering based on a differential geometry representation of backbone. Proteins: Structure, Function and Bioinformatics, 2019, 87, 302-312.	1.5	8
806	New Frontiers for Machine Learning in Protein Science. Journal of Molecular Biology, 2021, 433, 167232.	2.0	8
807	Conformational Entropy as a Potential Liability of Computationally Designed Antibodies. Biomolecules, 2022, 12, 718.	1.8	8
808	Selective substitution of 2 H and 3 H into aromatic amino acids catalyzed by Raney nickel. FEBS Letters, 1979, 101, 329-332.	1.3	7
809	Nuclear Overhauser effects and the assignment of the proton NMR spectra of proteins. FEBS Letters, 1984, 176, 307-312.	1.3	7
810	Relaxation data in NMR structure determination: Model calculations for the lysozyme-Gd3+ complex. Proteins: Structure, Function and Bioinformatics, 1991, 10, 117-129.	1.5	7

#	Article	IF	Citations
811	Diffusion in disordered media as a process with memory. Physical Review E, 1996, 54, R1021-R1024.	0.8	7
812	Stochastic reconstruction of protein structures from effective connectivity profiles. PMC Biophysics, 2008, 1, 5.	2.2	7
813	Coarse-grained model for protein folding based on structural profiles. Physical Review E, 2011, 84, 041934.	0.8	7
814	Automated Behavioral Analysis of Large C. elegans Populations Using a Wide Field-of-view Tracking Platform. Journal of Visualized Experiments, 2018, , .	0.2	7
815	Differential Interactome and Innate Immune Response Activation of Two Structurally Distinct Misfolded Protein Oligomers. ACS Chemical Neuroscience, 2019, 10, 3464-3478.	1.7	7
816	Biophysical studies of protein misfolding and aggregation in in vivo models of Alzheimer's and Parkinson's diseases â€“ ERRATUM. Quarterly Reviews of Biophysics, 2020, 53, e13.	2.4	7
817	Distinct responses of human peripheral blood cells to different misfolded protein oligomers. Immunology, 2021, 164, 358-371.	2.0	7
818	A Brain-Permeable Aminosterol Regulates Cell Membranes to Mitigate the Toxicity of Diverse Pore-Forming Agents. ACS Chemical Neuroscience, 2022, 13, 1219-1231.	1.7	7
819	Production of15N-labelled hen egg white lysozyme usingAspergillus niger. Biotechnology Letters, 1992, 14, 897-902.	1.1	6
820	An optimal derivation of a potential for protein folding. Physica A: Statistical Mechanics and Its Applications, 1999, 262, 35-39.	1.2	6
821	Detection of non-native hydrophobic interactions in the denatured state of lysozyme by molecular dynamics simulations. Journal of Physics Condensed Matter, 2005, 17, S1617-S1626.	0.7	6
822	Efficient identification of nearâ€native conformations in ab initio protein structure prediction using structural profiles. Proteins: Structure, Function and Bioinformatics, 2010, 78, 249-258.	1.5	6
823	In support of the BMRB. Nature Structural and Molecular Biology, 2012, 19, 854-860.	3.6	6
824	Analysis of the performance of the CHESHIRE and YAPP methods at CASD-NMR round 3. Journal of Biomolecular NMR, 2015, 62, 503-509.	1.6	6
825	Reply to â€œComment on â€˜A Tensor-Free Method for the Structural and Dynamic Refinement of Proteins using Residual Dipolar Couplingsâ€™â€• Journal of Physical Chemistry B, 2015, 119, 8225-8226.	1.2	6
826	Application of Lysine-specific Labeling to Detect Transient Interactions Present During Human Lysozyme Amyloid Fibril Formation. Scientific Reports, 2017, 7, 15018.	1.6	6
827	A method of predicting the in vitro fibril formation propensity of AÎ²40 mutants based on their inclusion body levels in E. coli. Scientific Reports, 2019, 9, 3680.	1.6	6
828	Determination of the structural ensemble of the molten globule state of a protein by computer simulations. Proteins: Structure, Function and Bioinformatics, 2019, 87, 635-645.	1.5	6

#	Article	IF	Citations
829	Rationally Designed Bicyclic Peptides Prevent the Conversion of AÎ²42 Assemblies Into Fibrillar Structures. Frontiers in Neuroscience, 2021, 15, 623097.	1.4	6
830	Two human metabolites rescue a C. elegans model of Alzheimerâ€™s disease via a cytosolic unfolded protein response. Communications Biology, 2021, 4, 843.	2.0	6
831	Exogenous misfolded protein oligomers can cross the intestinal barrier and cause a disease phenotype in C. elegans. Scientific Reports, 2021, 11, 14391.	1.6	6
832	Dynamics and Control of Peptide Self-Assembly and Aggregation. Advances in Experimental Medicine and Biology, 2019, 1174, 1-33.	0.8	6
833	The Pathological G51D Mutation in Alpha-Synuclein Oligomers Confers Distinct Structural Attributes and Cellular Toxicity. Molecules, 2022, 27, 1293.	1.7	6
834	Identification of a Thyroid Hormone Derivative as a Pleiotropic Agent for the Treatment of Alzheimerâ€™s Disease. Pharmaceuticals, 2021, 14, 1330.	1.7	6
835	A31P MAS NMR study of cytidine 2â€²-phosphate bound to ribonuclease A in the crystalline state. FEBS Letters, 1987, 225, 183-187.	1.3	5
836	Initial denaturing conditions influence the slow folding phase of acylphosphatase associated with proline isomerization. Protein Science, 2000, 9, 1466-1473.	3.1	5
837	Assessment of the quality of energy functions for protein folding by using a criterion derived with the help of the noisy go model. Journal of Biological Physics, 2001, 27, 205-215.	0.7	5
838	Protein Structure Validation Using Side-Chain Chemical Shifts. Journal of Physical Chemistry B, 2012, 116, 4754-4759.	1.2	5
839	Probing the Residual Structure of the Low Populated Denatured State of ADA2h under Folding Conditions by Relaxation Dispersion Nuclear Magnetic Resonance Spectroscopy. Biochemistry, 2015, 54, 4611-4622.	1.2	5
840	A method for partitioning the information contained in a protein sequence between its structure and function. Proteins: Structure, Function and Bioinformatics, 2018, 86, 956-964.	1.5	5
841	Characterisation of the structural, dynamic and aggregation properties of the W64R amyloidogenic variant of human lysozyme. Biophysical Chemistry, 2021, 271, 106563.	1.5	5
842	The signal peptide of the amyloid precursor protein forms amyloid-like aggregates and enhances AÎ²42 aggregation. Cell Reports Physical Science, 2021, 2, 100599.	2.8	5
843	Are casein micelles extracellular condensates formed by liquidâ€liquid phase separation?. FEBS Letters, 2022, 596, 2072-2085.	1.3	5
844	Lysozyme Hydrolysis of Î²-Glycosides. ACS Symposium Series, 1990, , 377-388.	0.5	4
845	The Structurally Constrained Neutral Model of Protein Evolution. Biological and Medical Physics Series, 2007, , 75-112.	0.3	4
846	Protein dynamics under light control. Nature Chemical Biology, 2008, 4, 449-450.	3.9	4

#	Article	IF	Citations
847	Selenium-Enhanced Electron Microscopic Imaging of Different Aggregate Forms of a Segment of the Amyloid Î² Peptide in Cells. ACS Nano, 2012, 6, 4740-4747.	7.3	4
848	Dynamics and Timekeeping in Biological Systems. Annual Review of Biochemistry, 2014, 83, 159-164.	5.0	4
849	Principles of Protein Structural Ensemble Determination. Biophysical Journal, 2018, 114, 388a-389a.	0.2	4
850	Machine learning-aided protein identification from multidimensional signatures. Lab on A Chip, 2021, 21, 2922-2931.	3.1	4
851	Protein Folding: A Perspective from Theory and Experiment. , 1998, 37, 868.		4
852	Protein Folding and Misfolding: From Atoms to Organisms. , 2008, , 289-335.		4
853	Computational maturation of a single-domain antibody against AÎ²42 aggregation. Chemical Science, 2021, 12, 13940-13948.	3.7	4
854	NMR Spectroscopy and Protein Folding: Studies of Lysozyme and Î±â€Lactalbumin. Novartis Foundation Symposium, 1991, 161, 167-189.	1.2	4
855	Growth with memory. Europhysics Letters, 1997, 37, 505-510.	0.7	3
856	Protein stability and foldabilityâ€“designability complementarity. Physica A: Statistical Mechanics and Its Applications, 1998, 249, 576-580.	1.2	3
857	Functionalised fibrils for bio-nanotechnology. , 2006, , .		3
858	Excited-State Control of Protein Activity. Journal of Molecular Biology, 2011, 412, 153-154.	2.0	3
859	MD Simulations of Intrinsically Disordered Proteins with Replica-Averaged Chemical Shift Restraints. Biophysical Journal, 2014, 106, 481a.	0.2	3
860	An Environmentally Sensitive Fluorescent Dye as a Multidimensional Probe of Amyloid Formation. Journal of Physical Chemistry B, 2016, 120, 2087-2094.	1.2	3
861	Determination of a Structural Ensemble Representing the Dynamics of a G-Quadruplex DNA. Biochemistry, 2020, 59, 379-388.	1.2	3
862	Probing the unfolded protein response in long-lived naked mole-rats. Biochemical and Biophysical Research Communications, 2020, 529, 1151-1157.	1.0	3
863	Structural Characterization of Covalently Stabilized Human Cystatin C Oligomers. International Journal of Molecular Sciences, 2020, 21, 5860.	1.8	3
864	A mistranslation-prone transcriptome underlying polyglutamine expansion diseases. Nature Reviews Molecular Cell Biology, 2021, 22, 583-584.	16.1	3

#	Article	IF	Citations
865	Parallel and Sequential Pathways of Molecular Recognition of a Tandem-Repeat Protein and Its Intrinsically Disordered Binding Partner. Biomolecules, 2021, 11, 827.	1.8	3
866	A Practical Guide to the Simultaneous Determination of Protein Structure and Dynamics Using Metainference. Methods in Molecular Biology, 2019, 2022, 313-340.	0.4	3
867	Vulnerability of the spinal motor neuron presynaptic terminal sub-proteome in ALS. Neuroscience Letters, 2022, 778, 136614.	1.0	3
868	Identification of the epitopes of calcitonin geneâ€related peptide (CGRP) for two antiâ€CGRP monoclonal antibodies by 2D NMR. Protein Science, 1997, 6, 1945-1952.	3.1	2
869	Expression and characterization of the intact Nâ€terminal domain of streptokinase. Protein Science, 1999, 8, 443-446.	3.1	2
870	Early Nascent Chain Folding Events on the Ribosome. Israel Journal of Chemistry, 2010, 50, 99-108.	1.0	2
871	Asymmetric folding pathways and transient misfolding in a coarse-grained model of proteins. Europhysics Letters, 2011, 94, 48005.	0.7	2
872	Proteome Metastability in Health, Aging, and Disease. Biophysical Journal, 2014, 106, 59a.	0.2	2
873	Single-Molecule Characterisation of Alpha-Synuclein Oligomers. Biophysical Journal, 2014, 106, 268a.	0.2	2
874	Solution-State Nuclear Magnetic Resonance Spectroscopy and Protein Folding. Methods in Molecular Biology, 2011, 752, 97-120.	0.4	2
875	Competition between protein aggregation and protein complex formation. BMC Bioinformatics, 2008, 9, .	1.2	1
876	Network views of the cell. , 0, , 4-13.		1
877	Probing Protein Aggregation with Quartz Crystal Microbalances. Methods in Molecular Biology, 2011, 752, 137-145.	0.4	1
878	In Vivo Translation Rates Can Substantially Delay the Co-Translational Folding of the E. Coli Cytosolic Proteome. Biophysical Journal, 2013, 104, 578a.	0.2	1
879	Thermodynamics of an Intrinsically Disordered Protein by Atomistic Simulations. Biophysical Journal, 2013, 104, 55a.	0.2	1
880	The codon information index: a quantitative measure of the information provided by the codon bias. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P04031.	0.9	1
881	Structure and Dynamics of Alzheimer's Associated Amyloid-Beta Peptide. Biophysical Journal, 2019, 116, 437a.	0.2	1
882	Rational Design of Conformation-Specific Antibodies for Tau Oligomers. Biophysical Journal, 2020, 118, 370a-371a.	0.2	1

#	Article	IF	Citations
883	Sequence-based prediction and measurement of pH-dependent protein solubility. Biophysical Journal, 2022, 121, 350a.	0.2	1
884	Protein Folding and Aggregation and its Relationship to Disease. Biochemical Society Transactions, 2000, 28, A137-A137.	1.6	0
885	Introduction to the special issue of GENE. Gene, 2008, 422, vii.	1.0	0
886	Physical Principles of Protein Behavior in the Cell. Journal of Proteome Research, 2009, 8, 2615-2615.	1.8	0
887	Focus on Physical Principles of Protein Behavior in the Cell. Proteomics, 2010, 10, 4149-4150.	1.3	0
888	Quantitative approaches for characterising fibrillar protein nanostructures. Materials Research Society Symposia Proceedings, 2010, 1274, 1.	0.1	0
889	Characterization of Free Energy Landscapes of Proteins using NMR Spectroscopy. Biophysical Journal, 2013, 104, 45a.	0.2	0
890	Structure of a Misfolded Intermediate of a PDZ Domain. , 2014, , 463-474.		0
891	Elucidating the Structural Basis of Î±-Synuclein Fibrillation using Small Camelid Nanobodies. Biophysical Journal, 2014, 106, 257a.	0.2	0
892	Structural and Mechanistic Analyses of the Effects of Small Compounds on Amyloid Beta Self-Assembly. Biophysical Journal, 2014, 106, 269a.	0.2	0
893	Determination of the Individual Roles of the Linker Residues in the Inter-Domain Motions of Calmodulin using NMR Chemical Shifts. Biophysical Journal, 2014, 106, 636a.	0.2	0
894	Insights into the Inhibition Mechanism of Biomolecular Self-Assembly from Chemical Kinetics. Biophysical Journal, 2014, 106, 682a.	0.2	0
895	Conformational Equilibrium between the Sub States of the Acidic Denatured State of ACBP Determined by NMR Chemical Shifts and Metadynamics. Biophysical Journal, 2014, 106, 459a-460a.	0.2	0
896	The Computational Studies of Co-Translational Protein Folding. Biophysical Journal, 2015, 108, 515a.	0.2	0
897	The Physical Basis of the Amyloid Phenomenon. , 2017, , 237-249.		0
898	Optical Structural Analysis of Individual Î±â€Synuclein Oligomers. Angewandte Chemie, 2018, 130, 4980-4984.	1.6	0
899	Homage to Chris Dobson. Frontiers in Molecular Biosciences, 2019, 6, 137.	1.6	0
900	Chris Dobson (1949â€“2019). Nature Chemical Biology, 2020, 16, 105-105.	3.9	0

#	Article	IF	Citations
901	Unraveling the Physicochemical Determinants of Protein Liquid-liquid Phase Separation by Nanoscale Infrared Vibrational Spectroscopy. Bio-protocol, 2021, 11, e4122.	0.2	0
902	Structural investigation of the folding of an immunoglobulin domain on the ribosome using NMR Spectroscopy (LB197). FASEB Journal, 2014, 28, LB197.	0.2	0
903	Kinetic analysis of tau aggregation for drug discovery. Biophysical Journal, 2022, 121, 354a.	0.2	0