

Feng Ding

List of Publications by Year in descending order

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Version: 2024-02-01

168
papers

9,858
citations

28190

55
h-index

43802

91
g-index

178
all docs

178
docs citations

178
times ranked

9801
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated minimization of steric clashes in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 261-270.	1.5	372
2	Eris: an automated estimator of protein stability. <i>Nature Methods</i> , 2007, 4, 466-467.	9.0	355
3	Ab Initio Folding of Proteins with All-Atom Discrete Molecular Dynamics. <i>Structure</i> , 2008, 16, 1010-1018.	1.6	287
4	Topological determinants of protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8637-8641.	3.3	278
5	Implications of peptide assemblies in amyloid diseases. <i>Chemical Society Reviews</i> , 2017, 46, 6492-6531.	18.7	262
6	Community-wide assessment of GPCR structure modelling and ligand docking: GPCR Dock 2008. <i>Nature Reviews Drug Discovery</i> , 2009, 8, 455-463.	21.5	260
7	Ab initio RNA folding by discrete molecular dynamics: From structure prediction to folding mechanisms. <i>Rna</i> , 2008, 14, 1164-1173.	1.6	258
8	Mechanism for the α -helix to α -hairpin transition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 220-228.	1.5	252
9	<i>RNA-Puzzles</i> : A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	1.6	241
10	iFoldRNA: three-dimensional RNA structure prediction and folding. <i>Bioinformatics</i> , 2008, 24, 1951-1952.	1.8	200
11	Molecular Dynamics Simulation of Amyloid \hat{I}^2 Dimer Formation. <i>Biophysical Journal</i> , 2004, 87, 2310-2321.	0.2	194
12	Discrete Molecular Dynamics: An Efficient And Versatile Simulation Method For Fine Protein Characterization. <i>Journal of Physical Chemistry B</i> , 2012, 116, 8375-8382.	1.2	179
13	Emergence of Protein Fold Families through Rational Design. <i>PLoS Computational Biology</i> , 2006, 2, e85.	1.5	177
14	Engineered allosteric activation of kinases in living cells. <i>Nature Biotechnology</i> , 2010, 28, 743-747.	9.4	177
15	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	1.6	161
16	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	1.6	158
17	Molecular Dynamics Simulation of the SH3 Domain Aggregation Suggests a Generic Amyloidogenesis Mechanism. <i>Journal of Molecular Biology</i> , 2002, 324, 851-857.	2.0	157
18	Modeling Backbone Flexibility Improves Protein Stability Estimation. <i>Structure</i> , 2007, 15, 1567-1576.	1.6	147

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19	Direct Molecular Dynamics Observation of Protein Folding Transition State Ensemble. <i>Biophysical Journal</i> , 2002, 83, 3525-3532.	0.2	133
20	Inhibition of amyloid beta toxicity in zebrafish with a chaperone-gold nanoparticle dual strategy. <i>Nature Communications</i> , 2019, 10, 3780.	5.8	132
21	Dynamical roles of metal ions and the disulfide bond in Cu, Zn superoxide dismutase folding and aggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 19696-19701.	3.3	131
22	Folding Trp-Cage to NMR Resolution Native Structure Using a Coarse-Grained Protein Model. <i>Biophysical Journal</i> , 2005, 88, 147-155.	0.2	130
23	Direct observation of a single nanoparticle's ubiquitin corona formation. <i>Nanoscale</i> , 2013, 5, 9162.	2.8	116
24	Rational design of a ligand-controlled protein conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6800-6804.	3.3	111
25	Multiscale Modeling of Nucleosome Dynamics. <i>Biophysical Journal</i> , 2007, 92, 1457-1470.	0.2	104
26	Stabilizing Off-pathway Oligomers by Polyphenol Nanoassemblies for IAPP Aggregation Inhibition. <i>Scientific Reports</i> , 2016, 6, 19463.	1.6	104
27	On the significance of an RNA tertiary structure prediction. <i>Rna</i> , 2010, 16, 1340-1349.	1.6	103
28	Graphene quantum dots against human IAPP aggregation and toxicity <i>in vivo</i> . <i>Nanoscale</i> , 2018, 10, 19995-20006.	2.8	100
29	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	1.6	100
30	Inhibition of hIAPP Amyloid Aggregation and Pancreatic β -Cell Toxicity by OH-Terminated PAMAM Dendrimer. <i>Small</i> , 2016, 12, 1615-1626.	5.2	99
31	Chemical and Biophysical Signatures of the Protein Corona in Nanomedicine. <i>Journal of the American Chemical Society</i> , 2022, 144, 9184-9205.	6.6	98
32	Molecular Origin of Polyglutamine Aggregation in Neurodegenerative Diseases. <i>PLoS Computational Biology</i> , 2005, 1, e30.	1.5	92
33	Discrete molecular dynamics. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2011, 1, 80-92.	6.2	91
34	Protein folding: Then and now. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 4-19.	1.4	88
35	Mitigation of Amyloidosis with Nanomaterials. <i>Advanced Materials</i> , 2020, 32, e1901690.	11.1	87
36	Polyglutamine Induced Misfolding of Huntingtin Exon1 is Modulated by the Flanking Sequences. <i>PLoS Computational Biology</i> , 2010, 6, e1000772.	1.5	86

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37	Rapid Flexible Docking Using a Stochastic Rotamer Library of Ligands. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 1623-1632.	2.5	80
38	Structural and Dynamic Determinants of Protein-Peptide Recognition. <i>Structure</i> , 2011, 19, 1837-1845.	1.6	79
39	Direct Observation of Protein Folding, Aggregation, and a Prion-like Conformational Conversion. <i>Journal of Biological Chemistry</i> , 2005, 280, 40235-40240.	1.6	77
40	Three-dimensional RNA structure refinement by hydroxyl radical probing. <i>Nature Methods</i> , 2012, 9, 603-608.	9.0	77
41	Discrete molecular dynamics simulations of peptide aggregation. <i>Physical Review E</i> , 2004, 69, 041908.	0.8	74
42	Local Unfolding of Cu, Zn Superoxide Dismutase Monomer Determines the Morphology of Fibrillar Aggregates. <i>Journal of Molecular Biology</i> , 2012, 421, 548-560.	2.0	74
43	Simple but predictive protein models. <i>Trends in Biotechnology</i> , 2005, 23, 450-455.	4.9	73
44	Topological Determinants of Protein Domain Swapping. <i>Structure</i> , 2006, 14, 5-14.	1.6	73
45	Fast complementation of split fluorescent protein triggered by DNA hybridization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2052-2056.	3.3	73
46	Reconstruction of the src-SH3 Protein Domain Transition State Ensemble using Multiscale Molecular Dynamics Simulations. <i>Journal of Molecular Biology</i> , 2005, 350, 1035-1050.	2.0	72
47	Graphene oxide inhibits hIAPP amyloid fibrillation and toxicity in insulin-producing NIT-1 cells. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 94-100.	1.3	70
48	Native-like RNA Tertiary Structures Using a Sequence-Encoded Cleavage Agent and Refinement by Discrete Molecular Dynamics. <i>Journal of the American Chemical Society</i> , 2009, 131, 2541-2546.	6.6	65
49	Harnessing a Physiologic Mechanism for siRNA Delivery With Mimetic Lipoprotein Particles. <i>Molecular Therapy</i> , 2012, 20, 1582-1589.	3.7	65
50	Star Polymers Reduce Islet Amyloid Polypeptide Toxicity via Accelerated Amyloid Aggregation. <i>Biomacromolecules</i> , 2017, 18, 4249-4260.	2.6	65
51	New Insights into FAK Signaling and Localization Based on Detection of a FAT Domain Folding Intermediate. <i>Structure</i> , 2004, 12, 2161-2171.	1.6	62
52	β -barrel Oligomers as Common Intermediates of Peptides Self-Assembling into Cross- β Aggregates. <i>Scientific Reports</i> , 2018, 8, 10353.	1.6	62
53	Competitive Binding of Natural Amphiphiles with Graphene Derivatives. <i>Scientific Reports</i> , 2013, 3, 2273.	1.6	61
54	Folding of Cu, Zn Superoxide Dismutase and Familial Amyotrophic Lateral Sclerosis. <i>Journal of Molecular Biology</i> , 2003, 334, 515-525.	2.0	59

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55	Scaling Behavior and Structure of Denatured Proteins. <i>Structure</i> , 2005, 13, 1047-1054.	1.6	58
56	Mitigating Human IAPP Amyloidogenesis In Vivo with Chiral Silica Nanoribbons. <i>Small</i> , 2018, 14, e1802825.	5.2	57
57	Contrasting effects of nanoparticle-protein attraction on amyloid aggregation. <i>RSC Advances</i> , 2015, 5, 105489-105498.	1.7	56
58	Inhibition of IAPP aggregation by insulin depends on the insulin oligomeric state regulated by zinc ion concentration. <i>Scientific Reports</i> , 2015, 5, 8240.	1.6	50
59	Cofibrillization of Pathogenic and Functional Amyloid Proteins with Gold Nanoparticles against Amyloidogenesis. <i>Biomacromolecules</i> , 2017, 18, 4316-4322.	2.6	50
60	Amyloid Self-Assembly of hIAPP8 ²⁰ via the Accumulation of Helical Oligomers, Helix to Sheet Transition, and Formation of Barrel Intermediates. <i>Small</i> , 2019, 15, e1805166.	5.2	49
61	Interaction of firefly luciferase and silver nanoparticles and its impact on enzyme activity. <i>Nanotechnology</i> , 2013, 24, 345101.	1.3	47
62	Amphiphilic surface chemistry of fullereneols is necessary for inhibiting the amyloid aggregation of alpha-synuclein NACore. <i>Nanoscale</i> , 2019, 11, 11933-11945.	2.8	47
63	Accelerated Amyloid Beta Pathogenesis by Bacterial Amyloid FapC. <i>Advanced Science</i> , 2020, 7, 2001299.	5.6	47
64	Novel application of a perturbed photonic crystal: High-quality filter. <i>Applied Physics Letters</i> , 1997, 71, 2889-2891.	1.5	46
65	Gaia: automated quality assessment of protein structure models. <i>Bioinformatics</i> , 2011, 27, 2209-2215.	1.8	44
66	Nucleation of β -rich oligomers and β -barrels in the early aggregation of human islet amyloid polypeptide. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2019, 1865, 434-444.	1.8	44
67	Spontaneous formation of β -sheet nano-barrels during the early aggregation of Alzheimer's amyloid beta. <i>Nano Today</i> , 2021, 38, 101125.	6.2	44
68	Structural and Thermodynamic Effects of Post-translational Modifications in Mutant and Wild Type Cu, Zn Superoxide Dismutase. <i>Journal of Molecular Biology</i> , 2011, 408, 555-567.	2.0	43
69	Computational approaches to understanding protein aggregation in neurodegeneration. <i>Journal of Molecular Cell Biology</i> , 2014, 6, 104-115.	1.5	43
70	NanoEHS beyond toxicity - focusing on biocorona. <i>Environmental Science: Nano</i> , 2017, 4, 1433-1454.	2.2	43
71	Distinct oligomerization and fibrillization dynamics of amyloid core sequences of amyloid-beta and islet amyloid polypeptide. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 28414-28423.	1.3	43
72	Active Nuclear Receptors Exhibit Highly Correlated AF-2 Domain Motions. <i>PLoS Computational Biology</i> , 2008, 4, e1000111.	1.5	42

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73	Effect of fullerene surface chemistry on nanoparticle binding-induced protein misfolding. <i>Nanoscale</i> , 2014, 6, 8340-8349.	2.8	41
74	Identifying weak interdomain interactions that stabilize the supertertiary structure of the N-terminal tandem PDZ domains of PSD-95. <i>Nature Communications</i> , 2018, 9, 3724.	5.8	41
75	Understanding Effects of PAMAM Dendrimer Size and Surface Chemistry on Serum Protein Binding with Discrete Molecular Dynamics Simulations. <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 11704-11715.	3.2	41
76	The Length Dependence of the PolyQ-mediated Protein Aggregation. <i>Journal of Biological Chemistry</i> , 2007, 282, 25487-25492.	1.6	40
77	PAMAM Dendrimers and Graphene: Materials for Removing Aromatic Contaminants from Water. <i>Environmental Science & Technology</i> , 2015, 49, 4490-4497.	4.6	40
78	Islet Amyloid Polypeptide Promotes Amyloid-Beta Aggregation by Binding-Induced Helix-Unfolding of the Amyloidogenic Core. <i>ACS Chemical Neuroscience</i> , 2018, 9, 967-975.	1.7	39
79	Profiling the Serum Protein Corona of Fibrillar Human Islet Amyloid Polypeptide. <i>ACS Nano</i> , 2018, 12, 6066-6078.	7.3	39
80	Multiple Folding Pathways of the SH3 Domain. <i>Biophysical Journal</i> , 2004, 87, 521-533.	0.2	38
81	Modulating protein amyloid aggregation with nanomaterials. <i>Environmental Science: Nano</i> , 2017, 4, 1772-1783.	2.2	38
82	Incorporating Backbone Flexibility in MedusaDock Improves Ligand-Binding Pose Prediction in the CSAR2011 Docking Benchmark. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 1871-1879.	2.5	37
83	Binding of cytoskeletal proteins with silver nanoparticles. <i>RSC Advances</i> , 2013, 3, 22002.	1.7	36
84	Submillisecond Elastic Recoil Reveals Molecular Origins of Fibrin Fiber Mechanics. <i>Biophysical Journal</i> , 2013, 104, 2671-2680.	0.2	35
85	Nanoscale inhibition of polymorphic and ambidextrous IAPP amyloid aggregation with small molecules. <i>Nano Research</i> , 2018, 11, 3636-3647.	5.8	35
86	A structural model reveals energy transduction in dynein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18540-18545.	3.3	34
87	Effects of Protein Corona on IAPP Amyloid Aggregation, Fibril Remodelling, and Cytotoxicity. <i>Scientific Reports</i> , 2017, 7, 2455.	1.6	34
88	Graphene quantum dots rescue protein dysregulation of pancreatic β -cells exposed to human islet amyloid polypeptide. <i>Nano Research</i> , 2019, 12, 2827-2834.	5.8	34
89	Amyloid Aggregation under the Lens of Liquid-Liquid Phase Separation. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 368-378.	2.1	34
90	Synthesis and in vitro properties of iron oxide nanoparticles grafted with brushed phosphorylcholine and polyethylene glycol. <i>Polymer Chemistry</i> , 2016, 7, 1931-1944.	1.9	32

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91	Amyloidosis inhibition, a new frontier of the protein corona. <i>Nano Today</i> , 2020, 35, 100937.	6.2	32
92	Robust and Generic RNA Modeling Using Inferred Constraints: A Structure for the Hepatitis C Virus IRES Pseudoknot Domain. <i>Biochemistry</i> , 2010, 49, 4931-4933.	1.2	31
93	Structural Basis for μ -Opioid Receptor Binding and Activation. <i>Structure</i> , 2011, 19, 1683-1690.	1.6	30
94	Thermostability and reversibility of silver nanoparticle-protein binding. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 1728-1739.	1.3	30
95	Parallel Folding Pathways in the SH3 Domain Protein. <i>Journal of Molecular Biology</i> , 2007, 373, 1348-1360.	2.0	29
96	N-terminal strands of filamin Ig domains act as a conformational switch under biological forces. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 12-24.	1.5	29
97	iFold: a platform for interactive folding simulations of proteins. <i>Bioinformatics</i> , 2006, 22, 2693-2694.	1.8	27
98	Promotion or Inhibition of Islet Amyloid Polypeptide Aggregation by Zinc Coordination Depends on Its Relative Concentration. <i>Biochemistry</i> , 2015, 54, 7335-7344.	1.2	27
99	Structures and dynamics of β -barrel oligomer intermediates of amyloid-beta ₁₆₋₂₂ aggregation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 1687-1697.	1.4	27
100	Single-Molecular Heteroamyloidosis of Human Islet Amyloid Polypeptide. <i>Nano Letters</i> , 2019, 19, 6535-6546.	4.5	27
101	Hybrid Dynamics Simulation Engine for Metalloproteins. <i>Biophysical Journal</i> , 2012, 103, 767-776.	0.2	26
102	Nanosilver Mitigates Biofilm Formation via FapC Amyloidosis Inhibition. <i>Small</i> , 2020, 16, e1906674.	5.2	26
103	G Protein Mono-ubiquitination by the Rsp5 Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2009, 284, 8940-8950.	1.6	25
104	Inhibition of Amyloid Aggregation and Toxicity with Janus Iron Oxide Nanoparticles. <i>Chemistry of Materials</i> , 2021, 33, 6484-6500.	3.2	25
105	Physical and toxicological profiles of human IAPP amyloids and plaques. <i>Science Bulletin</i> , 2019, 64, 26-35.	4.3	24
106	Misfolding and Self-Assembly Dynamics of Microtubule-Binding Repeats of the Alzheimer-Related Protein Tau. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2916-2925.	2.5	24
107	Fidelity of the Protein Structure Reconstruction from Inter-Residue Proximity Constraints. <i>Journal of Physical Chemistry B</i> , 2007, 111, 7432-7438.	1.2	23
108	Elevated amyloidoses of human IAPP and amyloid beta by lipopolysaccharide and their mitigation by carbon quantum dots. <i>Nanoscale</i> , 2020, 12, 12317-12328.	2.8	23

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109	Dynamic Protein Corona of Gold Nanoparticles with an Evolving Morphology. <i>ACS Applied Materials & Interfaces</i> , 2021, 13, 58238-58251.	4.0	23
110	Mechanistic Insights from Discrete Molecular Dynamics Simulations of Pesticide–Nanoparticle Interactions. <i>Environmental Science & Technology</i> , 2017, 51, 8396-8404.	4.6	22
111	Ultrasmall Molybdenum Disulfide Quantum Dots Cage Alzheimer’s Amyloid Beta to Restore Membrane Fluidity. <i>ACS Applied Materials & Interfaces</i> , 2021, 13, 29936-29948.	4.0	22
112	A Framework of Paracellular Transport via Nanoparticles–Induced Endothelial Leakiness. <i>Advanced Science</i> , 2021, 8, e2102519.	5.6	22
113	Structure–Function Relationship of PAMAM Dendrimers as Robust Oil Dispersants. <i>Environmental Science & Technology</i> , 2014, 48, 12868-12875.	4.6	21
114	A Thermodynamics Model for the Emergence of a Stripe–Like Binary SAM on a Nanoparticle Surface. <i>Small</i> , 2015, 11, 4894-4899.	5.2	21
115	Probing the modulated formation of gold nanoparticles–beta-lactoglobulin corona complexes and their applications. <i>Nanoscale</i> , 2017, 9, 17758-17769.	2.8	21
116	Zinc-coordination and C-peptide complexation: a potential mechanism for the endogenous inhibition of IAPP aggregation. <i>Chemical Communications</i> , 2017, 53, 9394-9397.	2.2	21
117	Probing protein aggregation using discrete molecular dynamics. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 4795.	3.0	21
118	Predicting Binding Affinity of CSAR Ligands Using Both Structure-Based and Ligand-Based Approaches. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 1915-1922.	2.5	20
119	Brushed polyethylene glycol and phosphorylcholine for grafting nanoparticles against protein binding. <i>Polymer Chemistry</i> , 2016, 7, 6875-6879.	1.9	20
120	CSAR Benchmark of Flexible MedusaDock in Affinity Prediction and Nativelike Binding Pose Selection. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1042-1052.	2.5	20
121	New Models of Tetrahymena Telomerase RNA from Experimentally Derived Constraints and Modeling. <i>Journal of the American Chemical Society</i> , 2012, 134, 20070-20080.	6.6	19
122	Thermo- and pH-responsive fibrillization of squid suckerin A1H1 peptide. <i>Nanoscale</i> , 2020, 12, 6307-6317.	2.8	19
123	RNA Tertiary Structure Analysis by 2–Hydroxyl Molecular Interference. <i>Biochemistry</i> , 2014, 53, 6825-6833.	1.2	17
124	Probing Interdomain Linkers and Protein Supertertiary Structure In Vitro and in Live Cells with Fluorescent Protein Resonance Energy Transfer. <i>Journal of Molecular Biology</i> , 2021, 433, 166793.	2.0	17
125	Labeling native bacterial RNA in live cells. <i>Cell Research</i> , 2014, 24, 894-897.	5.7	15
126	Structure modeling of RNA using sparse NMR constraints. <i>Nucleic Acids Research</i> , 2017, 45, 12638-12647.	6.5	15

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127	Human Plasma Protein Corona of A β Amyloid and Its Impact on Islet Amyloid Polypeptide Cross-Seeding. <i>Biomacromolecules</i> , 2020, 21, 988-998.	2.6	15
128	Ensemble switching unveils a kinetic rheostat mechanism of the eukaryotic thiamine pyrophosphate riboswitch. <i>Rna</i> , 2021, 27, 771-790.	1.6	15
129	Statistical Analysis of SHAPE-Directed RNA Secondary Structure Modeling. <i>Biochemistry</i> , 2013, 52, 596-599.	1.2	14
130	Direct Observation of β -Barrel Intermediates in the Self-Assembly of Toxic SOD1 ^{G38R} and Absence in Nontoxic Glycine Mutants. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 966-975.	2.5	14
131	Graphene quantum dots obstruct the membrane axis of Alzheimer's amyloid beta. <i>Physical Chemistry Chemical Physics</i> , 2021, 24, 86-97.	1.3	14
132	Discrete Molecular Dynamics Simulation of Biomolecules. <i>Biological and Medical Physics Series</i> , 2012, , 55-73.	0.3	13
133	β -Crystallin Chaperone Inhibits A β Aggregation by Capping the β -Sheet-Rich Oligomers and Fibrils. <i>Journal of Physical Chemistry B</i> , 2020, 124, 10138-10146.	1.2	13
134	Identifying Importance of Amino Acids for Protein Folding from Crystal Structures. <i>Methods in Enzymology</i> , 2003, 374, 616-638.	0.4	12
135	Lysophosphatidylcholine modulates the aggregation of human islet amyloid polypeptide. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 30627-30635.	1.3	12
136	The Membrane Axis of Alzheimer's Nanomedicine. <i>Advanced NanoBiomed Research</i> , 2021, 1, 2000040.	1.7	12
137	Out-of-Equilibrium Biophysical Chemistry: The Case for Multidimensional, Integrated Single-Molecule Approaches. <i>Journal of Physical Chemistry B</i> , 2021, 125, 10404-10418.	1.2	9
138	Integrative structural dynamics probing of the conformational heterogeneity in synaptosomal-associated protein 25. <i>Cell Reports Physical Science</i> , 2021, 2, 100616.	2.8	9
139	Hydrophobic/Hydrophilic Ratio of Amphiphilic Helix Mimetics Determines the Effects on Islet Amyloid Polypeptide Aggregation. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1760-1770.	2.5	9
140	Structural and energetic determinants of tyrosylprotein sulfotransferase sulfation specificity. <i>Bioinformatics</i> , 2014, 30, 2302-2309.	1.8	7
141	Computational Evaluation of Protein Stability Change upon Mutations. <i>Methods in Molecular Biology</i> , 2010, 634, 189-201.	0.4	7
142	Deviation from the Unimolecular Micelle Paradigm of PAMAM Dendrimers Induced by Strong Interligand Interactions. <i>Journal of Physical Chemistry C</i> , 2015, 119, 19475-19484.	1.5	6
143	SAMase of Bacteriophage T3 Inactivates <i>Escherichia coli</i> 's Methionine S-Adenosyltransferase by Forming Heteropolymers. <i>MBio</i> , 2021, 12, e0124221.	1.8	5
144	Morphological Determinants of Carbon Nanomaterial-Induced Amyloid Peptide Self-Assembly. <i>Frontiers in Chemistry</i> , 2020, 8, 160.	1.8	4

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145	A buried glutamate in the cross- β core renders β -endorphin fibrils reversible. <i>Nanoscale</i> , 2021, 13, 19593-19603.	2.8	4
146	Multiscale Modeling of RNA Structure and Dynamics. <i>Nucleic Acids and Molecular Biology</i> , 2012, , 167-184.	0.2	3
147	The capricious electrostatic force: Revealing the signaling pathway in integrin β 2-I domain. <i>Journal of Theoretical and Computational Chemistry</i> , 2018, 17, 1840001.	1.8	3
148	A hidden aggregation-prone structure in the heart of hypoxia inducible factor prolyl hydroxylase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 611-623.	1.5	2
149	Amyloidosis: Mitigation of Amyloidosis with Nanomaterials (Adv. Mater. 18/2020). <i>Advanced Materials</i> , 2020, 32, 2070146.	11.1	2
150	Nonnative Energetic Frustrations in Protein Folding at Residual Level: A Simulation Study of Homologous Immunoglobulin-like β -Sandwich Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1515.	1.8	1
151	Peptide Self-Assembly: Amyloid Self-Assembly of hAPP8 β 20 via the Accumulation of Helical Oligomers, β -Helix to β -Sheet Transition, and Formation of β -Barrel Intermediates (Small 18/2019). <i>Small</i> , 2019, 15, 1970093.	5.2	1
152	Substoichiometric Inhibition of Insulin against IAPP Aggregation Is Attenuated by the Incompletely Processed N-Terminus of proIAPP. <i>ACS Chemical Neuroscience</i> , 2022, 13, 2006-2016.	1.7	1
153	Rational Design of a Ligand-Controlled Protein Conformational Switch. <i>Biophysical Journal</i> , 2013, 104, 18a-19a.	0.2	0
154	Striped Nanoparticles: A Thermodynamics Model for the Emergence of a Stripe-like Binary SAM on a Nanoparticle Surface (Small 37/2015). <i>Small</i> , 2015, 11, 4798-4798.	5.2	0
155	Multiscale Modeling of Dendrimers for Biological Applications. <i>Biophysical Journal</i> , 2016, 110, 546a.	0.2	0
156	Brushed Polyethylene Glycol and Phosphorylcholine as Promising Grafting Agents against Protein Binding. <i>Biophysical Journal</i> , 2017, 112, 350a.	0.2	0
157	Mesoscopic Properties and Molecular Mechanisms of IAPP Amyloid Inhibition and Remodeling with Small Molecules. <i>Biophysical Journal</i> , 2017, 112, 340a.	0.2	0
158	Dynamic Equilibrium of the TPP Riboswitch as Observed by MFD FRET. <i>Biophysical Journal</i> , 2017, 112, 368a.	0.2	0
159	Oligomerization and Fibrillization Dynamics of Amyloid Peptides and BETA-Barrel Oligomer Intermediates. <i>Biophysical Journal</i> , 2018, 114, 227a-228a.	0.2	0
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