Kresten Lindorff-Larsen

List of Publications by Year
in descending order

161 papers	20,479 citations	41344 49 h-index	12597 132 g-index
234 all docs	234 docs citations	234 times ranked	18743 citing authors

#	Article	IF	Citations
1	The role of water coordination in the pH-dependent gating of hAQP10. Biochimica Et Biophysica Acta - Biomembranes, 2022, 1864, 183809.	2.6	3
2	Transient exposure of a buried phosphorylation site in an autoinhibited protein. Biophysical Journal, 2022, 121, 91-101.	0.5	8
3	Double Mutant of Chymotrypsin Inhibitor 2 Stabilized through Increased Conformational Entropy. Biochemistry, 2022, 61, 160-170.	2.5	6
4	Predicting and interpreting large-scale mutagenesis data using analyses of protein stability and conservation. Cell Reports, 2022, 38, 110207.	6.4	62
5	Co-evolution of drug resistance and broadened substrate recognition in HIV protease variants isolated from an Escherichia coli genetic selection system. Biochemical Journal, 2022, 479, 479-501.	3.7	1
6	Mg2+-dependent conformational equilibria in CorA and an integrated view on transport regulation. ELife, 2022, 11, .	6.0	10
7	Conformational ensembles of intrinsically disordered proteins and flexible multidomain proteins. Biochemical Society Transactions, 2022, 50, 541-554.	3.4	49
8	Improving Martini 3 for Disordered and Multidomain Proteins. Journal of Chemical Theory and Computation, 2022, 18, 2033-2041.	5.3	54
9	Disease-linked mutations cause exposure of a protein quality control degron. Structure, 2022, 30, 1245-1253.e5.	3.3	14
10	Properdin oligomers adopt rigid extended conformations supporting function. ELife, 2021, 10, .	6.0	10
11	Linking thermodynamics and measurements of protein stability. Protein Engineering, Design and Selection, 2021, 34, .	2.1	13
12	Interplay of folded domains and the disordered low-complexity domain in mediating hnRNPA1 phase separation. Nucleic Acids Research, 2021, 49, 2931-2945.	14.5	81
13	Charge Interactions in a Highly Charge-Depleted Protein. Journal of the American Chemical Society, 2021, 143, 2500-2508.	13.7	15
14	Understanding the Origins of Loss of Protein Function by Analyzing the Effects of Thousands of Variants on Activity and Abundance. Molecular Biology and Evolution, 2021, 38, 3235-3246.	8.9	65
15	Multiplexed assays reveal effects of missense variants in MSH2 and cancer predisposition. PLoS Genetics, 2021, 17, e1009496.	3.5	13
16	Mapping the degradation pathway of a disease-linked aspartoacylase variant. PLoS Genetics, 2021, 17, e1009539.	3.5	12
17	Refinement of Î±-Synuclein Ensembles Against SAXS Data: Comparison of Force Fields and Methods. Frontiers in Molecular Biosciences, 2021, 8, 654333.	3.5	51
18	Conformational Ensembles of Noncoding Elements in the SARS-CoV-2 Genome from Molecular Dynamics Simulations. Journal of the American Chemical Society, 2021, 143, 8333-8343.	13.7	17

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19	Cryo-EM reveals the architecture of placental malaria VAR2CSA and provides molecular insight into chondroitin sulfate binding. Nature Communications, 2021, 12, 2956.	12.8	30
20	Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. Frontiers in Molecular Biosciences, 2021, 8, 676235.	3.5	6
21	Order and disorderâ€"An integrative structure of the full-length human growth hormone receptor. Science Advances, 2021, 7, .	10.3	25
22	Fitting Side-Chain NMR Relaxation Data Using Molecular Simulations. Journal of Chemical Theory and Computation, 2021, 17, 5262-5275.	5.3	23
23	Synergistic stabilization of a double mutant in chymotrypsin inhibitor 2 from a library screen in E. coli. Communications Biology, 2021, 4, 980.	4.4	13
24	Insight into Calcium-Binding Motifs of Intrinsically Disordered Proteins. Biomolecules, 2021, 11, 1173.	4.0	16
25	On the Potential of Machine Learning to Examine the Relationship Between Sequence, Structure, Dynamics and Function of Intrinsically Disordered Proteins. Journal of Molecular Biology, 2021, 433, 167196.	4.2	51
26	Force Field Effects in Simulations of Flexible Peptides with Varying Polyproline II Propensity. Journal of Chemical Theory and Computation, 2021, 17, 6634-6646.	5.3	24
27	Computational and Experimental Assessment of Backbone Templates for Computational Redesign of the Thioredoxin Fold. Journal of Physical Chemistry B, 2021, 125, 11141-11149.	2.6	5
28	Architecture and assembly dynamics of the essential mitochondrial chaperone complex TIM9Â·10Â·12. Structure, 2021, 29, 1065-1073.e4.	3.3	10
29	Structural and functional variation of chitin-binding domains of a lytic polysaccharide monooxygenase from Cellvibrio japonicus. Journal of Biological Chemistry, 2021, 297, 101084.	3.4	16
30	DEER-PREdict: Software for efficient calculation of spin-labeling EPR and NMR data from conformational ensembles. PLoS Computational Biology, 2021, 17, e1008551.	3.2	47
31	A dual-reporter system for investigating and optimizing protein translation and folding in E. coli. Nature Communications, 2021, 12, 6093.	12.8	12
32	Refining conformational ensembles of flexible proteins against small-angle x-ray scattering data. Biophysical Journal, 2021, 120, 5124-5135.	0.5	24
33	Accurate model of liquidâ€"liquid phase behavior of intrinsically disordered proteins from optimization of single-chain properties. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	151
34	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
35	Novel HARS2 missense variants identified in individuals with sensorineural hearing impairment and Perrault syndrome. European Journal of Medical Genetics, 2020, 63, 103733.	1.3	9
36	Protein Dynamics Enables Phosphorylation of Buried Residues in Cdk2/Cyclin-A-Bound p27. Biophysical Journal, 2020, 119, 2010-2018.	0.5	21

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37	Classifying disease-associated variants using measures of protein activity and stability. , 2020, , 91-107.		21
38	Co-Chaperones in Targeting and Delivery of Misfolded Proteins to the 26S Proteasome. Biomolecules, 2020, 10, 1141.	4.0	29
39	Global analysis of protein stability by temperature and chemical denaturation. Analytical Biochemistry, 2020, 605, 113863.	2.4	20
40	Structural basis of client specificity in mitochondrial membrane-protein chaperones. Science Advances, 2020, 6, .	10.3	21
41	Integrating NMR and simulations reveals motions in the UUCG tetraloop. Nucleic Acids Research, 2020, 48, 5839-5848.	14.5	31
42	Protein destabilization and degradation as a mechanism for hereditary disease. , 2020, , 111-125.		5
43	What Will Computational Modeling Approaches Have to Say in the Era of Atomistic Cryo-EM Data?. Journal of Chemical Information and Modeling, 2020, 60, 2410-2412.	5.4	15
44	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution. PLoS Computational Biology, 2020, 16, e1007870.	3.2	76
45	Integrating Molecular Simulation and Experimental Data: A Bayesian/Maximum Entropy Reweighting Approach. Methods in Molecular Biology, 2020, 2112, 219-240.	0.9	129
46	Computing, Analyzing, and Comparing the Radius of Gyration and Hydrodynamic Radius in Conformational Ensembles of Intrinsically Disordered Proteins. Methods in Molecular Biology, 2020, 2141, 429-445.	0.9	24
47	How to learn from inconsistencies: Integrating molecular simulations with experimental data. Progress in Molecular Biology and Translational Science, 2020, 170, 123-176.	1.7	76
48	Folliculin variants linked to Birt-Hogg-DubÃ© syndrome are targeted for proteasomal degradation. PLoS Genetics, 2020, 16, e1009187.	3.5	16
49	Structure and dynamics of a nanodisc by integrating NMR, SAXS and SANS experiments with molecular dynamics simulations. ELife, 2020, 9, .	6.0	49
50	Title is missing!. , 2020, 16, e1007870.		0
51	Title is missing!. , 2020, 16, e1007870.		0
52	Title is missing!. , 2020, 16, e1007870.		0
53	Title is missing!. , 2020, 16, e1007870.		0
54	Promoting transparency and reproducibility in enhanced molecular simulations. Nature Methods, 2019, 16, 670-673.	19.0	655

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55	Structural Basis for Properdin Oligomerization and Convertase Stimulation in the Human Complement System. Frontiers in Immunology, 2019, 10, 2007.	4.8	47
56	Bayesian-Maximum-Entropy Reweighting of IDP Ensembles Based on NMR Chemical Shifts. Entropy, 2019, 21, 898.	2.2	35
57	PSX, Proteinâ€“Solvent Exchange: software for calculation of deuterium-exchange effects in small-angle neutron scattering measurements from protein coordinates. Journal of Applied Crystallography, 2019, 52, 1427-1436.	4.5	5
58	Allosteric modulation of the sarcoplasmic reticulum Ca2+ATPase by thapsigarginviadecoupling of functional motions. Physical Chemistry Chemical Physics, 2019, 21, 21991-21995.	2.8	7
59	Biophysical and Mechanistic Models for Disease-Causing Protein Variants. Trends in Biochemical Sciences, 2019, 44, 575-588.	7.5	143
60	Substrate-induced conformational dynamics of the dopamine transporter. Nature Communications, 2019, 10, 2714.	12.8	46
61	Fitting Corrections to an RNA Force Field Using Experimental Data. Journal of Chemical Theory and Computation, 2019, 15, 3425-3431.	5.3	54
62	Side chain to main chain hydrogen bonds stabilize a polyglutamine helix in a transcription factor. Nature Communications, 2019, 10, 2034.	12.8	78
63	Molecular dynamics-guided discovery of an ago-allosteric modulator for GPR40/FFAR1. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7123-7128.	7.1	35
64	Dissecting the statistical properties of the linear extrapolation method of determining protein stability. Protein Engineering, Design and Selection, 2019, 32, 471-479.	2.1	5
65	Barnaba: software for analysis of nucleic acid structures and trajectories. Rna, 2019, 25, 219-231.	3.5	50
66	Toward mechanistic models for genotypeâ€“phenotype correlations in phenylketonuria using protein stability calculations. Human Mutation, 2019, 40, 444-457.	2.5	56
67	Protein stability and degradation in health and disease. Advances in Protein Chemistry and Structural Biology, 2019, 114, 61-83.	2.3	31
68	Computational and cellular studies reveal structural destabilization and degradation of MLH1 variants in Lynch syndrome. ELife, 2019, 8, .	6.0	49
69	Dynamic activation and regulation of the mitogen-activated protein kinase p38. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4655-4660.	7.1	52
70	Structural heterogeneity and dynamics in protein evolution and design. Current Opinion in Structural Biology, 2018, 48, 157-163.	5.7	42
71	Gs protein peptidomimetics as allosteric modulators of the Î²2-adrenergic receptor. RSC Advances, 2018, 8, 2219-2228.	3.6	9
72	On the Calculation of SAXS Profiles of Folded and Intrinsically Disordered Proteins from Computer Simulations. Journal of Molecular Biology, 2018, 430, 2521-2539.	4.2	64

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73	Role of protein dynamics in transmembrane receptor signalling. Current Opinion in Structural Biology, 2018, 48, 74-82.	5.7	26
74	Structural Basis of Membrane Protein Chaperoning through the Mitochondrial Intermembrane Space. Cell, 2018, 175, 1365-1379.e25.	28.9	87
75	Random Mutagenesis Analysis of the Influenza A M2 Proton Channel Reveals Novel Resistance Mutants. Biochemistry, 2018, 57, 5957-5968.	2.5	11
76	A Robust Proton Flux (pHlux) Assay for Studying the Function and Inhibition of the Influenza A M2 Proton Channel. Biochemistry, 2018, 57, 5949-5956.	2.5	15
77	Cancer Mutations of the Tumor Suppressor SPOP Disrupt the Formation of Active, Phase-Separated Compartments. Molecular Cell, 2018, 72, 19-36.e8.	9.7	286
78	Frequency adaptive metadynamics for the calculation of rare-event kinetics. Journal of Chemical Physics, 2018, 149, 072309.	3.0	54
79	Conformational ensembles of RNA oligonucleotides from integrating NMR and molecular simulations. Science Advances, 2018, 4, eaar8521.	10.3	99
80	Biophysical experiments and biomolecular simulations: A perfect match?. Science, 2018, 361, 355-360.	12.6	205
81	Enhancing coevolution-based contact prediction by imposing structural self-consistency of the contacts. Scientific Reports, 2018, 8, 11112.	3.3	3
82	Monte Carlo Sampling of Protein Folding by Combining an All-Atom Physics-Based Model with a Native State Bias. Journal of Physical Chemistry B, 2018, 122, 11174-11185.	2.6	3
83	Editorial overview: Theory and simulation: Interpreting experimental data at the molecular level. Current Opinion in Structural Biology, 2018, 49, iv-v.	5.7	4
84	How well do force fields capture the strength of salt bridges in proteins?. PeerJ, 2018, 6, e4967.	2.0	58
85	Molecular dynamics ensemble refinement of the heterogeneous native state of NCBD using chemical shifts and NOEs. PeerJ, 2018, 6, e5125.	2.0	25
86	Diversityâ€Oriented Peptide Stapling: A Third Generation Copperâ€Catalysed Azideâ€“Alkyne Cycloaddition Stapling and Functionalisation Strategy. Chemistry - A European Journal, 2017, 23, 3490-3495.	3.3	21
87	Conformational Rigidity and Protein Dynamics at Distinct Timescales Regulate PTP1B Activity and Allostery. Molecular Cell, 2017, 65, 644-658.e5.	9.7	96
88	A phosphorylation-motif for tuneable helix stabilisation in intrinsically disordered proteins â€“ Lessons from the sodium proton exchanger 1 (NHE1). Cellular Signalling, 2017, 37, 40-51.	3.6	34
89	Biomolecular conformational changes and ligand binding: from kinetics to thermodynamics. Chemical Science, 2017, 8, 6466-6473.	7.4	51
90	Blocking protein quality control to counter hereditary cancers. Genes Chromosomes and Cancer, 2017, 56, 823-831.	2.8	23

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91	An Efficient Method for Estimating the Hydrodynamic Radius of Disordered Protein Conformations. Biophysical Journal, 2017, 113, 550-557.	0.5	110
92	Mapping the Universe of RNA Tetraloop Folds. Biophysical Journal, 2017, 113, 257-267.	0.5	37
93	Predicting the impact of Lynch syndrome-causing missense mutations from structural calculations. PLoS Genetics, 2017, 13, e1006739.	3.5	90
94	A combined computational and structural model of the full-length human prolactin receptor. Nature Communications, 2016, 7, 11578.	12.8	52
95	Picosecond to Millisecond Structural Dynamics in Human Ubiquitin. Journal of Physical Chemistry B, 2016, 120, 8313-8320.	2.6	93
96	DNA-binding protects p53 from interactions with cofactors involved in transcription-independent functions. Nucleic Acids Research, 2016, 44, gkw770.	14.5	40
97	Computational Redesign of Thioredoxin Is Hypersensitive toward Minor Conformational Changes in the Backbone Template. Journal of Molecular Biology, 2016, 428, 4361-4377.	4.2	21
98	Understanding singleâ€pass transmembrane receptor signaling from a structural viewpointâ€”what are we missing?. FEBS Journal, 2016, 283, 4424-4451.	4.7	49
99	Structure of the Bacterial Cytoskeleton Protein Bactofilin by NMR Chemical Shifts and Sequence Variation. Biophysical Journal, 2016, 110, 2342-2348.	0.5	15
100	A Soluble, Folded Protein without Charged Amino Acid Residues. Biochemistry, 2016, 55, 3949-3956.	2.5	34
101	The Role of Protein Loops and Linkers in Conformational Dynamics and Allostery. Chemical Reviews, 2016, 116, 6391-6423.	47.7	302
102	Topological constraints and modular structure in the folding and functional motions of GlpG, an intramembrane protease. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2098-2103.	7.1	21
103	A Monte Carlo Study of the Early Steps of Functional Amyloid Formation. PLoS ONE, 2016, 11, e0146096.	2.5	9
104	Mapping transiently formed and sparsely populated conformations on a complex energy landscape. ELife, 2016, 5, .	6.0	63
105	Bioinformatics analysis identifies several intrinsically disordered human E3 ubiquitin-protein ligases. PeerJ, 2016, 4, e1725.	2.0	24
106	Comparing Molecular Dynamics Force Fields in the Essential Subspace. PLoS ONE, 2015, 10, e0121114.	2.5	80
107	ENCORE: Software for Quantitative Ensemble Comparison. PLoS Computational Biology, 2015, 11, e1004415.	3.2	64
108	Structure of a Functional Amyloid Protein Subunit Computed Using Sequence Variation. Journal of the American Chemical Society, 2015, 137, 22-25.	13.7	98

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109	Interaction Networks in Protein Folding via Atomic-Resolution Experiments and Long-Time-Scale Molecular Dynamics Simulations. Journal of the American Chemical Society, 2015, 137, 6506-6516.	13.7	76
110	Exploiting Hydrophobicity for Efficient Production of Transmembrane Helices for Structure Determination by NMR Spectroscopy. Analytical Chemistry, 2015, 87, 9126-9131.	6.5	11
111	A Two-step Protein Quality Control Pathway for a Misfolded DJ-1 Variant in Fission Yeast. Journal of Biological Chemistry, 2015, 290, 21141-21153.	3.4	22
112	Combining Experiments and Simulations Using the Maximum Entropy Principle. PLoS Computational Biology, 2014, 10, e1003406.	3.2	167
113	Communication Routes in ARID Domains between Distal Residues in Helix 5 and the DNA-Binding Loops. PLoS Computational Biology, 2014, 10, e1003744.	3.2	40
114	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.	7.1	33
115	Conformational Changes and Free Energies in a Proline Isomerase. Journal of Chemical Theory and Computation, 2014, 10, 4169-4174.	5.3	46
116	Robust Estimation of Diffusion-Optimized Ensembles for Enhanced Sampling. Journal of Chemical Theory and Computation, 2014, 10, 543-553.	5.3	12
117	Probabilistic Determination of Native State Ensembles of Proteins. Journal of Chemical Theory and Computation, 2014, 10, 3484-3491.	5.3	38
118	Atomistic Description of the Folding of a Dimeric Protein. Journal of Physical Chemistry B, 2013, 117, 12935-12942.	2.6	45
119	A Sticky Cage can Slow Down Folding. Biophysical Journal, 2013, 104, 964-965.	0.5	1
120	PHAISTOS: A framework for Markov chain Monte Carlo simulation and inference of protein structure. Journal of Computational Chemistry, 2013, 34, 1697-1705.	3.3	35
121	Variational Optimization of an All-Atom Implicit Solvent Force Field To Match Explicit Solvent Simulation Data. Journal of Chemical Theory and Computation, 2013, 9, 5641-5652.	5.3	46
122	Atomic-level description of ubiquitin folding. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5915-5920.	7.1	281
123	Protein Structure Validation and Refinement Using Amide Proton Chemical Shifts Derived from Quantum Mechanics. PLoS ONE, 2013, 8, e84123.	2.5	21
124	Protein folding kinetics and thermodynamics from atomistic simulation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17845-17850.	7.1	262
125	Systematic Validation of Protein Force Fields against Experimental Data. PLoS ONE, 2012, 7, e32131.	2.5	570
126	Paths of long-range communication in the E2 enzymes of family 3: a molecular dynamics investigation. Physical Chemistry Chemical Physics, 2012, 14, 12515.	2.8	33

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127	Structure and Dynamics of an Unfolded Protein Examined by Molecular Dynamics Simulation. Journal of the American Chemical Society, 2012, 134, 3787-3791.	13.7	222
128	Evaluating the Effects of Cutoffs and Treatment of Long-range Electrostatics in Protein Folding Simulations. PLoS ONE, 2012, 7, e39918.	2.5	83
129	How Robust Are Protein Folding Simulations with Respect to Force Field Parameterization?. Biophysical Journal, 2011, 100, L47-L49.	0.5	725
130	How Fast-Folding Proteins Fold. Science, 2011, 334, 517-520.	12.6	1,609
131	Computational Design and Experimental Testing of the Fastest-Folding Î²-Sheet Protein. Journal of Molecular Biology, 2011, 405, 43-48.	4.2	106
132	Atomic-Level Characterization of the Structural Dynamics of Proteins. Science, 2010, 330, 341-346.	12.6	1,583
133	Improved sideâ€chain torsion potentials for the Amber ff99SB protein force field. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1950-1958.	2.6	4,694
134	Principles of conduction and hydrophobic gating in K ⁺ channels. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5833-5838.	7.1	298
135	Reply to Domene and Furini: Distinguishing knock-on and vacancy diffusion mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, .	7.1	0
136	Millisecond-scale molecular dynamics simulations on Anton. , 2009, , .		238
137	Long-timescale molecular dynamics simulations of protein structure and function. Current Opinion in Structural Biology, 2009, 19, 120-127.	5.7	671
138	Automated Event Detection and Activity Monitoring in Long Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2009, 5, 2595-2605.	5.3	47
139	Similarity Measures for Protein Ensembles. PLoS ONE, 2009, 4, e4203.	2.5	65
140	Experimental Parameterization of an Energy Function for the Simulation of Unfolded Proteins. Biophysical Journal, 2008, 94, 182-192.	0.5	70
141	Microsecond Molecular Dynamics Simulation Shows Effect of Slow Loop Dynamics on Backbone Amide Order Parameters of Proteinsâ€. Journal of Physical Chemistry B, 2008, 112, 6155-6158.	2.6	188
142	Detection of initiation sites in protein folding of the four helix bundle ACBP by chemical shift analysis. FEBS Letters, 2007, 581, 4965-4971.	2.8	47
143	Conformational Fluctuations Affect Protein Alignment in Dilute Liquid Crystal Media. Journal of the American Chemical Society, 2006, 128, 4371-4376.	13.7	26
144	Structure of the Regulatory Apparatus of a Calcium-dependent Protein Kinase (CDPK): A Novel Mode of Calmodulin-target Recognition. Journal of Molecular Biology, 2006, 357, 400-410.	4.2	64

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145	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.	2.6	38
146	BPPred: A Web-based computational tool for predicting biophysical parameters of proteins. Protein Science, 2006, 16, 125-134.	7.6	55
147	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.	7.1	136
148	Simultaneous determination of protein structure and dynamics. Nature, 2005, 433, 128-132.	27.8	641
149	Protein folding and the organization of the protein topology universe. Trends in Biochemical Sciences, 2005, 30, 13-19.	7.5	101
150	Interpreting Dynamically-Averaged Scalar Couplings in Proteins. Journal of Biomolecular NMR, 2005, 32, 273-280.	2.8	46
151	Transition State Contact Orders Correlate with Protein Folding Rates. Journal of Molecular Biology, 2005, 352, 495-500.	4.2	64
152	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.	13.7	658
153	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.	4.2	90
154	Transition states for protein folding have native topologies despite high structural variability. Nature Structural and Molecular Biology, 2004, 11, 443-449.	8.2	88
155	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.	13.7	155
156	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.	2.6	41
157	Parallel protein-unfolding pathways revealed and mapped. Nature Structural and Molecular Biology, 2003, 10, 658-662.	8.2	153
158	Calculation of Mutational Free Energy Changes in Transition States for Protein Folding. Biophysical Journal, 2003, 85, 1207-1214.	0.5	31
159	Surprisingly high stability of barley lipid transfer protein, LTP1, towards denaturant, heat and proteases. FEBS Letters, 2001, 488, 145-148.	2.8	126
160	Barley Lipid Transfer Protein, LTP1, Contains a New Type of Lipid-like Post-translational Modification*. Journal of Biological Chemistry, 2001, 276, 33547-33553.	3.4	36
161	Thiol Alkylation below Neutral pH. Analytical Biochemistry, 2000, 286, 308-310.	2.4	29