

Yaoqi Zhou

List of Publications by Year in descending order

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243
papers

14,447
citations

18887

64
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32181

105
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all docs

299
docs citations

299
times ranked

13364
citing authors

#	ARTICLE	IF	CITATIONS
1	Distance-scaled, finite ideal-gas reference state improves structure-derived potentials of mean force for structure selection and stability prediction. <i>Protein Science</i> , 2009, 11, 2714-2726.	3.1	836
2	Real-time reliable determination of binding kinetics of DNA hybridization using a multi-channel graphene biosensor. <i>Nature Communications</i> , 2017, 8, 14902.	5.8	303
3	Capturing non-local interactions by long short-term memory bidirectional recurrent neural networks for improving prediction of protein secondary structure, backbone angles, contact numbers and solvent accessibility. <i>Bioinformatics</i> , 2017, 33, 2842-2849.	1.8	300
4	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. <i>Scientific Reports</i> , 2015, 5, 11476.	1.6	290
5	Improving protein fold recognition and template-based modeling by employing probabilistic-based matching between predicted one-dimensional structural properties of query and corresponding native properties of templates. <i>Bioinformatics</i> , 2011, 27, 2076-2082.	1.8	288
6	A Knowledge-Based Energy Function for Protein~Ligand, Protein~Protein, and Protein~DNA Complexes. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 2325-2335.	2.9	264
7	Improving protein disorder prediction by deep bidirectional long short-term memory recurrent neural networks. <i>Bioinformatics</i> , 2017, 33, 685-692.	1.8	235
8	Protein binding site prediction using an empirical scoring function. <i>Nucleic Acids Research</i> , 2006, 34, 3698-3707.	6.5	223
9	Specific interactions for ab initio folding of protein terminal regions with secondary structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 793-803.	1.5	219
10	RNA secondary structure prediction using an ensemble of two-dimensional deep neural networks and transfer learning. <i>Nature Communications</i> , 2019, 10, 5407.	5.8	214
11	Fold recognition by combining sequence profiles derived from evolution and from depth-dependent structural alignment of fragments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 321-328.	1.5	211
12	Interpreting the folding kinetics of helical proteins. <i>Nature</i> , 1999, 401, 400-403.	13.7	209
13	SPINE X: Improving protein secondary structure prediction by multistep learning coupled with prediction of solvent accessible surface area and backbone torsion angles. <i>Journal of Computational Chemistry</i> , 2012, 33, 259-267.	1.5	209
14	The distance fluctuation criterion for melting: Comparison of square-well and Morse potential models for clusters and homopolymers. <i>Journal of Chemical Physics</i> , 2002, 116, 2323-2329.	1.2	204
15	Reactivation of Dihydroorotate Dehydrogenase-Driven Pyrimidine Biosynthesis Restores Tumor Growth of Respiration-Deficient Cancer Cells. <i>Cell Metabolism</i> , 2019, 29, 399-416.e10.	7.2	190
16	Equilibrium thermodynamics of homopolymers and clusters: Molecular dynamics and Monte Carlo simulations of systems with square-well interactions. <i>Journal of Chemical Physics</i> , 1997, 107, 10691-10708.	1.2	189
17	Single-body residue-level knowledge-based energy score combined with sequence-profile and secondary structure information for fold recognition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 1005-1013.	1.5	180
18	Structural insights into the histone H1-nucleosome complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19390-19395.	3.3	178

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19	First-Order Disorder-to-Order Transition in an Isolated Homopolymer Model. <i>Physical Review Letters</i> , 1996, 77, 2822-2825.	2.9	177
20	A physical reference state unifies the structure-derived potential of mean force for protein folding and binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 93-101.	1.5	176
21	Folding Rate Prediction Using Total Contact Distance. <i>Biophysical Journal</i> , 2002, 82, 458-463.	0.2	171
22	Sixty-five years of the long march in protein secondary structure prediction: the final stretch?. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw129.	3.2	168
23	Folding thermodynamics of a model three-helix-bundle protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 14429-14432.	3.3	158
24	Accurate prediction of protein contact maps by coupling residual two-dimensional bidirectional long short-term memory with convolutional neural networks. <i>Bioinformatics</i> , 2018, 34, 4039-4045.	1.8	155
25	Native proteins are surface-molten solids: application of the lindemann criterion for the solid versus liquid state 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 285, 1371-1375.	2.0	154
26	An accurate, residue-level, pair potential of mean force for folding and binding based on the distance-scaled, ideal-gas reference state. <i>Protein Science</i> , 2004, 13, 400-411.	3.1	153
27	SPINE-D: Accurate Prediction of Short and Long Disordered Regions by a Single Neural-Network Based Method. <i>Journal of Biomolecular Structure and Dynamics</i> , 2012, 29, 799-813.	2.0	150
28	Improving prediction of protein secondary structure, backbone angles, solvent accessibility and contact numbers by using predicted contact maps and an ensemble of recurrent and residual convolutional neural networks. <i>Bioinformatics</i> , 2019, 35, 2403-2410.	1.8	145
29	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. <i>Methods in Molecular Biology</i> , 2017, 1484, 55-63.	0.4	137
30	Predicting backbone ϕ angles and dihedrals from protein sequences by stacked sparse auto-encoder deep neural network. <i>Journal of Computational Chemistry</i> , 2014, 35, 2040-2046.	1.5	133
31	Chemical association in simple models of molecular and ionic fluids. <i>Journal of Chemical Physics</i> , 1989, 91, 3618-3623.	1.2	132
32	Ab initio folding of terminal segments with secondary structures reveals the fine difference between two closely related all-atom statistical energy functions. <i>Protein Science</i> , 2008, 17, 1212-1219.	3.1	131
33	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	2.0	131
34	Improving the prediction accuracy of residue solvent accessibility and real-value backbone torsion angles of proteins by guided-learning through a two-layer neural network. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 847-856.	1.5	125
35	Quantifying the effect of burial of amino acid residues on protein stability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 315-322.	1.5	116
36	Achieving 80% ten-fold cross-validated accuracy for secondary structure prediction by large-scale training. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 838-845.	1.5	114

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37	Accurate and efficient loop selections by the DFIRE-based all-atom statistical potential. <i>Protein Science</i> , 2004, 13, 391-399.	3.1	112
38	Title is missing!. <i>Nature</i> , 1999, 401, 400-403.	13.7	109
39	Predicting Continuous Local Structure and the Effect of Its Substitution for Secondary Structure in Fragment-Free Protein Structure Prediction. <i>Structure</i> , 2009, 17, 1515-1527.	1.6	108
40	The calorimetric criterion for a two-state process revisited. <i>Protein Science</i> , 1999, 8, 1064-1074.	3.1	107
41	SPOT-Disorder2: Improved Protein Intrinsic Disorder Prediction by Ensembled Deep Learning. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 645-656.	3.0	106
42	Folding of a model three-helix bundle protein: a thermodynamic and kinetic analysis 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 293, 917-951.	2.0	103
43	Chemical association in simple models of molecular and ionic fluids. II. Thermodynamic properties. <i>Journal of Chemical Physics</i> , 1992, 96, 1504-1506.	1.2	102
44	Chemical association in simple models of molecular and ionic fluids. III. The cavity function. <i>Journal of Chemical Physics</i> , 1992, 96, 1507-1515.	1.2	102
45	EASE-MM: Sequence-Based Prediction of Mutation-Induced Stability Changes with Feature-Based Multiple Models. <i>Journal of Molecular Biology</i> , 2016, 428, 1394-1405.	2.0	101
46	Structure-based prediction of RNA-binding domains and RNA-binding sites and application to structural genomics targets. <i>Nucleic Acids Research</i> , 2011, 39, 3017-3025.	6.5	100
47	Ion solvation dynamics in an interaction-site model solvent. <i>Chemical Physics</i> , 1991, 152, 201-220.	0.9	93
48	SPEM: improving multiple sequence alignment with sequence profiles and predicted secondary structures. <i>Bioinformatics</i> , 2005, 21, 3615-3621.	1.8	92
49	Fluids inside a pore—an integral-equation approach. <i>Molecular Physics</i> , 1989, 66, 767-789.	0.8	91
50	Fold recognition by concurrent use of solvent accessibility and residue depth. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 636-645.	1.5	87
51	Single-sequence-based prediction of protein secondary structures and solvent accessibility by deep whole-sequence learning. <i>Journal of Computational Chemistry</i> , 2018, 39, 2210-2216.	1.5	84
52	Structure-based prediction of DNA-binding proteins by structural alignment and a volume-fraction corrected DFIRE-based energy function. <i>Bioinformatics</i> , 2010, 26, 1857-1863.	1.8	81
53	Sequence-based prediction of protein-peptide binding sites using support vector machine. <i>Journal of Computational Chemistry</i> , 2016, 37, 1223-1229.	1.5	81
54	Real-SPINE: An integrated system of neural networks for real-value prediction of protein structural properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 76-81.	1.5	79

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55	BEST: Improved Prediction of B-Cell Epitopes from Antigen Sequences. PLoS ONE, 2012, 7, e40104.	1.1	79
56	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	1.8	79
57	Predicting the topology of transmembrane helical proteins using mean burial propensity and a hidden-Markov-model-based method. Protein Science, 2003, 12, 1547-1555.	3.1	77
58	SPARKS 2 and SP3 servers in CASP6. Proteins: Structure, Function and Bioinformatics, 2005, 61, 152-156.	1.5	76
59	Energy Functions in De Novo Protein Design: Current Challenges and Future Prospects. Annual Review of Biophysics, 2013, 42, 315-335.	4.5	75
60	EVLncRNAs: a manually curated database for long non-coding RNAs validated by low-throughput experiments. Nucleic Acids Research, 2018, 46, D100-D105.	6.5	75
61	Recent advances in glycoinformatic platforms for glycomics and glycoproteomics. Current Opinion in Structural Biology, 2020, 62, 56-69.	2.6	74
62	Stability scale and atomic solvation parameters extracted from 1023 mutation experiments. Proteins: Structure, Function and Bioinformatics, 2002, 49, 483-492.	1.5	73
63	A new size-independent score for pairwise protein structure alignment and its application to structure classification and nucleic acid binding prediction. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2080-2088.	1.5	69
64	Criticality of charged systems. I. The restricted primitive model. Journal of Chemical Physics, 1995, 102, 5785-5795.	1.2	68
65	SP5: Improving Protein Fold Recognition by Using Torsion Angle Profiles and Profile-Based Gap Penalty Model. PLoS ONE, 2008, 3, e2325.	1.1	68
66	DDOMAIN: Dividing structures into domains using a normalized domain-domain interaction profile. Protein Science, 2007, 16, 947-955.	3.1	67
67	Accurate Single-Sequence Prediction of Protein Intrinsic Disorder by an Ensemble of Deep Recurrent and Convolutional Architectures. Journal of Chemical Information and Modeling, 2018, 58, 2369-2376.	2.5	67
68	Real-time prediction of backbone torsion angles. Proteins: Structure, Function and Bioinformatics, 2008, 72, 427-433.	1.5	66
69	Structure-aware protein-protein interaction site prediction using deep graph convolutional network. Bioinformatics, 2021, 38, 125-132.	1.8	64
70	Assembly and Kinetic Folding Pathways of a Tetrameric β^2 -Sheet Complex: Molecular Dynamics Simulations on Simplified Off-Lattice Protein Models. Biophysical Journal, 2004, 86, 31-49.	0.2	63
71	DDIG-in: discriminating between disease-associated and neutral non-frameshifting micro-indels. Genome Biology, 2013, 14, R23.	13.9	63
72	SPIN2: Predicting sequence profiles from protein structures using deep neural networks. Proteins: Structure, Function and Bioinformatics, 2018, 86, 629-633.	1.5	62

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73	Structure-based prediction of proteinâ€ peptide binding regions using Random Forest. <i>Bioinformatics</i> , 2018, 34, 477-484.	1.8	62
74	A simple reference state makes a significant improvement in nearâ€native selections from structurally refined docking decoys. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 244-253.	1.5	59
75	Sequence-Based Prediction of Proteinâ€Carbohydrate Binding Sites Using Support Vector Machines. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 2115-2122.	2.5	59
76	Intrinsically Semi-disordered State and Its Role in Induced Folding and Protein Aggregation. <i>Cell Biochemistry and Biophysics</i> , 2013, 67, 1193-1205.	0.9	57
77	Temperature Dependence of the Distribution of the First Passage Time:â€ Results from Discontinuous Molecular Dynamics Simulations of an All-Atom Model of the Second Î²-Hairpin Fragment of Protein G. <i>Journal of the American Chemical Society</i> , 2003, 125, 6300-6305.	6.6	56
78	Highly accurate and high-resolution function prediction of RNA binding proteins by fold recognition and binding affinity prediction. <i>RNA Biology</i> , 2011, 8, 988-996.	1.5	53
79	Transcriptome profiling of lentil (<i>Lens culinaris</i>) through the first 24 hours of <i>Ascochyta lentis</i> infection reveals key defence response genes. <i>BMC Genomics</i> , 2018, 19, 108.	1.2	53
80	Nucleotide Sugar Transporter SLC35 Family Structure and Function. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1123-1134.	1.9	53
81	DDIG-in: detecting disease-causing genetic variations due to frameshifting indels and nonsense mutations employing sequence and structural properties at nucleotide and protein levels. <i>Bioinformatics</i> , 2015, 31, 1599-1606.	1.8	52
82	RegSNPs-intron: a computational framework for predicting pathogenic impact of intronic single nucleotide variants. <i>Genome Biology</i> , 2019, 20, 254.	3.8	52
83	Role of hydrophilic and hydrophobic contacts in folding of the second Î²-hairpin fragment of protein G: Molecular dynamics simulation studies of an all-atom model. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 154-162.	1.5	51
84	What is a Desirable Statistical Energy Function for Proteins and How Can It Be Obtained?. <i>Cell Biochemistry and Biophysics</i> , 2006, 46, 165-174.	0.9	50
85	Accurate single-sequence prediction of solvent accessible surface area using local and global features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3170-3176.	1.5	50
86	Trends in template/fragment-free protein structure prediction. <i>Theoretical Chemistry Accounts</i> , 2011, 128, 3-16.	0.5	48
87	SPRINT-Gly: predicting <i>N</i> - and <i>O</i> -linked glycosylation sites of human and mouse proteins by using sequence and predicted structural properties. <i>Bioinformatics</i> , 2019, 35, 4140-4146.	1.8	48
88	Exploring the Molecular Design of Protein Interaction Sites with Molecular Dynamics Simulations and Free Energy Calculations. <i>Biochemistry</i> , 2009, 48, 399-414.	1.2	47
89	Improved RNA secondary structure and tertiary base-pairing prediction using evolutionary profile, mutational coupling and two-dimensional transfer learning. <i>Bioinformatics</i> , 2021, 37, 2589-2600.	1.8	47
90	An allâ€atom knowledgeâ€based energy function for proteinâ€DNA threading, docking decoy discrimination, and prediction of transcriptionâ€factor binding profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 718-730.	1.5	46

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91	Direct prediction of profiles of sequences compatible with a protein structure by neural networks with fragment-based local and energy-based nonlocal profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2565-2573.	1.5	46
92	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. <i>Journal of Molecular Biology</i> , 2020, 432, 3379-3387.	2.0	46
93	DescribePROT: database of amino acid-level protein structure and function predictions. <i>Nucleic Acids Research</i> , 2021, 49, D298-D308.	6.5	46
94	The role of sidechain packing and native contact interactions in folding: Discontinuous molecular dynamics folding simulations of an all-atom GÅ model of fragment B of Staphylococcal protein A. <i>Journal of Chemical Physics</i> , 2002, 117, 8983-8995.	1.2	45
95	In-silico prediction of disorder content using hybrid sequence representation. <i>BMC Bioinformatics</i> , 2011, 12, 245.	1.2	45
96	Molecular Dynamics Simulations of Human Antimicrobial Peptide LL-37 in Model POPC and POPG Lipid Bilayers. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1186.	1.8	45
97	Systems-level understanding of ethanol-induced stresses and adaptation in <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 44150.	1.6	43
98	A survey of Type III restriction-modification systems reveals numerous, novel epigenetic regulators controlling phase-variable regulons; phasevarions. <i>Nucleic Acids Research</i> , 2018, 46, 3532-3542.	6.5	43
99	EVLncRNAs 2.0: an updated database of manually curated functional long non-coding RNAs validated by low-throughput experiments. <i>Nucleic Acids Research</i> , 2021, 49, D86-D91.	6.5	42
100	The Dependence of All-Atom Statistical Potentials on Structural Training Database. <i>Biophysical Journal</i> , 2004, 86, 3349-3358.	0.2	41
101	Phase Separation of Ionic Fluids: An Extended Ebeling-Grigo Approach. <i>The Journal of Physical Chemistry</i> , 1996, 100, 1415-1419.	2.9	39
102	SPOT-Seq-RNA: Predicting Protein-RNA Complex Structure and RNA-Binding Function by Fold Recognition and Binding Affinity Prediction. <i>Methods in Molecular Biology</i> , 2014, 1137, 119-130.	0.4	39
103	Predicting residue-residue contact maps by a two-layer, integrated neural network method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 176-183.	1.5	38
104	Small Open Reading Frames: Current Prediction Techniques and Future Prospect. <i>Current Protein and Peptide Science</i> , 2011, 12, 503-507.	0.7	38
105	Prediction of RNA binding proteins comes of age from low resolution to high resolution. <i>Molecular BioSystems</i> , 2013, 9, 2417.	2.9	37
106	Natural protein sequences are more intrinsically disordered than random sequences. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 2949-2957.	2.4	37
107	Investigating DNA-, RNA-, and protein-based features as a means to discriminate pathogenic synonymous variants. <i>Human Mutation</i> , 2017, 38, 1336-1347.	1.1	37
108	Identifying molecular recognition features in intrinsically disordered regions of proteins by transfer learning. <i>Bioinformatics</i> , 2020, 36, 1107-1113.	1.8	37

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109	Nonlocal integral equation approximations. I. The zeroth order (hydrostatic) approximation with applications. <i>Journal of Chemical Physics</i> , 1990, 92, 5533-5543.	1.2	36
110	Cooperativity in Scapharca Dimeric Hemoglobin: Simulation of Binding Intermediates and Elucidation of the Role of Interfacial Water. <i>Journal of Molecular Biology</i> , 2003, 326, 593-606.	2.0	36
111	Consensus scoring for enriching near-native structures from protein docking decoys. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 397-403.	1.5	36
112	Analytical approach to molecular liquids. IV. Solvation dynamics and electron transfer reactions. <i>Journal of Chemical Physics</i> , 1989, 91, 4885-4890.	1.2	35
113	Folding processes of the B domain of protein A to the native state observed in all-atom <i>ab initio</i> folding simulations. <i>Journal of Chemical Physics</i> , 2008, 128, 235105.	1.2	35
114	Protein side chain modeling with orientation-dependent atomic force fields derived by series expansions. <i>Journal of Computational Chemistry</i> , 2011, 32, 1680-1686.	1.5	35
115	Optimal secretion of alkali-tolerant xylanase in <i>Bacillus subtilis</i> by signal peptide screening. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8745-8756.	1.7	35
116	DLIGAND2: an improved knowledge-based energy function for protein-ligand interactions using the distance-scaled, finite, ideal-gas reference state. <i>Journal of Cheminformatics</i> , 2019, 11, 52.	2.8	35
117	Thermodynamic perturbation theory for fused hard-sphere and hard-disk chain fluids. <i>Journal of Chemical Physics</i> , 1995, 103, 2688-2695.	1.2	34
118	Docking prediction using biological information, ZDOCK sampling technique, and clustering guided by the DFIRE statistical energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 314-318.	1.5	34
119	LEAP: Highly accurate prediction of protein loop conformations by integrating coarse-grained sampling and optimized energy scores with all-atom refinement of backbone and side chains. <i>Journal of Computational Chemistry</i> , 2014, 35, 335-341.	1.5	34
120	Advancing the Accuracy of Protein Fold Recognition by Utilizing Profiles From Hidden Markov Models. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 761-772.	2.2	34
121	Critical nucleation size in the folding of small apparently two-state proteins. <i>Protein Science</i> , 2004, 13, 1173-1181.	3.1	33
122	Pairing a high-resolution statistical potential with a nucleobase-centric sampling algorithm for improving RNA model refinement. <i>Nature Communications</i> , 2021, 12, 2777.	5.8	33
123	Assessing secondary structure assignment of protein structures by using pairwise sequence alignment benchmarks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 61-67.	1.5	32
124	Predicting DNA-Binding Proteins and Binding Residues by Complex Structure Prediction and Application to Human Proteome. <i>PLoS ONE</i> , 2014, 9, e96694.	1.1	32
125	Repurposing clinically approved drugs for COVID-19 treatment targeting SARS-CoV-2 papain-like protease. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 137-146.	3.6	32
126	Thermodynamics and stability of a \hat{A} -sheet complex: Molecular dynamics simulations on simplified off-lattice protein models. <i>Protein Science</i> , 2004, 13, 40-53.	3.1	31

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127	Note on standard free energy of transfer and partitioning of ionic species between two fluid phases. <i>Journal of Chemical Physics</i> , 1988, 89, 3836-3839.	1.2	30
128	Predicting lysineâ€™malonylation sites of proteins using sequence and predicted structural features. <i>Journal of Computational Chemistry</i> , 2018, 39, 1757-1763.	1.5	30
129	DNA sequence repeats identify numerous Type I restrictionâ€™modification systems that are potential epigenetic regulators controlling phaseâ€™variable regulons; phasevarions. <i>FASEB Journal</i> , 2020, 34, 1038-1051.	0.2	29
130	The theory of semipermeable vesicles and membranes: An integralâ€™equation approach. I. General formalism and application to a hardâ€™sphere mixture. <i>Journal of Chemical Physics</i> , 1988, 89, 7010-7019.	1.2	28
131	Fluids inside a poreâ€™an integral-equation approach. <i>Molecular Physics</i> , 1989, 66, 791-796.	0.8	28
132	Protein Motions at Zero-Total Angular Momentum: The Importance of Long-Range Correlations. <i>Biophysical Journal</i> , 2000, 79, 2902-2908.	0.2	28
133	Genome-scale characterization of RNA tertiary structures and their functional impact by RNA solvent accessibility prediction. <i>Rna</i> , 2017, 23, 14-22.	1.6	28
134	The hard-sphere fluid: New exact results with applications. <i>Journal of Statistical Physics</i> , 1988, 52, 1389-1412.	0.5	27
135	Fluctuations of backbone torsion angles obtained from NMRâ€™determined structures and their prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3353-3362.	1.5	27
136	Impact of human pathogenic micro-insertions and micro-deletions on post-transcriptional regulation. <i>Human Molecular Genetics</i> , 2014, 23, 3024-3034.	1.4	27
137	regSNPs-splicing: a tool for prioritizing synonymous single-nucleotide substitution. <i>Human Genetics</i> , 2017, 136, 1279-1289.	1.8	27
138	RNAcmap: a fully automatic pipeline for predicting contact maps of RNAs by evolutionary coupling analysis. <i>Bioinformatics</i> , 2021, 37, 3494-3500.	1.8	27
139	Thermodynamics of an All-Atom Off-Lattice Model of the Fragment B of Staphylococcal Protein A:â€™ Implication for the Origin of the Cooperativity of Protein Folding. <i>Journal of Physical Chemistry B</i> , 2002, 106, 1481-1485.	1.2	26
140	Design and Evaluation of a Novel Peptideâ€™Drug Conjugate Covalently Targeting SARS-CoV-2 Papain-like Protease. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 876-884.	2.9	26
141	Predicting the errors of predicted local backbone angles and non-local solvent- accessibilities of proteins by deep neural networks. <i>Bioinformatics</i> , 2016, 32, 3768-3773.	1.8	25
142	Improved fragment sampling for ab initio protein structure prediction using deep neural networks. <i>Nature Machine Intelligence</i> , 2019, 1, 347-355.	8.3	25
143	SPOT-Contact-LM: improving single-sequence-based prediction of protein contact map using a transformer language model. <i>Bioinformatics</i> , 2022, 38, 1888-1894.	1.8	25
144	Characterizing the Existing and Potential Structural Space of Proteins by Large-Scale Multiple Loop Permutations. <i>Journal of Molecular Biology</i> , 2011, 408, 585-595.	2.0	24

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145	The theory of semipermeable vesicles and membranes: An integral equation approach. II. Donnan equilibrium. <i>Journal of Chemical Physics</i> , 1988, 89, 7020-7029.	1.2	23
146	Criticality of charged systems. II. The binary mixture of hard spheres and ions. <i>Journal of Chemical Physics</i> , 1995, 102, 5796-5802.	1.2	23
147	Folding Thermodynamics of Model Four-Strand Antiparallel β^2 -Sheet Proteins. <i>Biophysical Journal</i> , 2002, 82, 646-659.	0.2	23
148	Temperature-Dependent Folding Pathways of Pin1 WW Domain: An All-Atom Molecular Dynamics Simulation of a GÅ-Model. <i>Biophysical Journal</i> , 2007, 93, 2152-2161.	0.2	23
149	Improving computational protein design by using structure-derived sequence profile. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2338-2348.	1.5	23
150	Outer-sphere electron-transfer reactions in model molecular solvents: the mean spherical approximation. <i>Chemical Physics</i> , 1991, 152, 185-200.	0.9	22
151	Fast and Accurate Method for Identifying High-Quality Protein-Interaction Modules by Clique Merging and Its Application to Yeast. <i>Journal of Proteome Research</i> , 2006, 5, 801-807.	1.8	22
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