Yaoqi Zhou

List of Publications by Year
in descending order

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243 papers	14,447 citations	16437 64 h-index	28275 105 g-index
299 all docs	299 docs citations	299 times ranked	11815 citing authors

#	Article	IF	Citations
1	Self-Inhibitory Peptides Targeting the Neisseria gonorrhoeae MtrCDE Efflux Pump Increase Antibiotic Susceptibility. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0154221.	1.4	2
2	Design and Evaluation of a Novel Peptideâ€“Drug Conjugate Covalently Targeting SARS-CoV-2 Papain-like Protease. Journal of Medicinal Chemistry, 2022, 65, 876-884.	2.9	26
3	SPOT-Contact-LM: improving single-sequence-based prediction of protein contact map using a transformer language model. Bioinformatics, 2022, 38, 1888-1894.	1.8	25
4	High-throughput split-protein profiling by combining transposon mutagenesis and regulated protein-protein interactions with deep sequencing. International Journal of Biological Macromolecules, 2022, 203, 543-552.	3.6	0
5	Probing RNA structures and functions by solvent accessibility: an overview from experimental and computational perspectives. Briefings in Bioinformatics, 2022, 23, .	3.2	13
6	Reaching alignment-profile-based accuracy in predicting protein secondary and tertiary structural properties without alignment. Scientific Reports, 2022, 12, 7607.	1.6	14
7	Computational Prediction of N- and O-Linked Glycosylation Sites for Human and Mouse Proteins. Methods in Molecular Biology, 2022, , 177-186.	0.4	1
8	Predicting RNA distance-based contact maps by integrated deep learning on physics-inferred secondary structure and evolutionary-derived mutational coupling. Bioinformatics, 2022, 38, 3900-3910.	1.8	14
9	EVLncRNAs 2.0: an updated database of manually curated functional long non-coding RNAs validated by low-throughput experiments. Nucleic Acids Research, 2021, 49, D86-D91.	6.5	42
10	Single-sequence and profile-based prediction of RNA solvent accessibility using dilated convolutional neural network. Bioinformatics, 2021, 36, 5169-5176.	1.8	21
11	DescribePROT: database of amino acid-level protein structure and function predictions. Nucleic Acids Research, 2021, 49, D298-D308.	6.5	46
12	Improved RNA secondary structure and tertiary base-pairing prediction using evolutionary profile, mutational coupling and two-dimensional transfer learning. Bioinformatics, 2021, 37, 2589-2600.	1.8	47
13	Argonaute proteins: structures and their endonuclease activity. Molecular Biology Reports, 2021, 48, 4837-4849.	1.0	18
14	RNA Backbone Torsion and Pseudotorsion Angle Prediction Using Dilated Convolutional Neural Networks. Journal of Chemical Information and Modeling, 2021, 61, 2610-2622.	2.5	12
15	Pairing a high-resolution statistical potential with a nucleobase-centric sampling algorithm for improving RNA model refinement. Nature Communications, 2021, 12, 2777.	5.8	33
16	RNAcmap: a fully automatic pipeline for predicting contact maps of RNAs by evolutionary coupling analysis. Bioinformatics, 2021, 37, 3494-3500.	1.8	27
17	SPOT-1D-Single: improving the single-sequence-based prediction of protein secondary structure, backbone angles, solvent accessibility and half-sphere exposures using a large training set and ensembled deep learning. Bioinformatics, 2021, 37, 3464-3472.	1.8	22
18	From â€œDark Matterâ€• to â€œStarâ€• Insight Into the Regulation Mechanisms of Plant Functional Long Non-Coding RNAs. Frontiers in Plant Science, 2021, 12, 650926.	1.7	17

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19	De novo protein design by an energy function based on series expansion in distance and orientation dependence. Bioinformatics, 2021, 38, 86-93.	1.8	8
20	Structure-aware proteinâ€“protein interaction site prediction using deep graph convolutional network. Bioinformatics, 2021, 38, 125-132.	1.8	64
21	Repurposing clinically approved drugs for COVID-19 treatment targeting SARS-CoV-2 papain-like protease. International Journal of Biological Macromolecules, 2021, 188, 137-146.	3.6	32
22	SPOT-1D2: Improving Protein Secondary Structure Prediction using High Sequence Identity Training Set and an Ensemble of Recurrent and Residual-convolutional Neural Networks. , 2021, , .		1
23	DeepANIS: Predicting antibody paratope from concatenated CDR sequences by integrating bidirectional long-short-term memory and transformer neural networks. , 2021, , .		1
24	Identifying molecular recognition features in intrinsically disordered regions of proteins by transfer learning. Bioinformatics, 2020, 36, 1107-1113.	1.8	37
25	Getting to Know Your Neighbor: Protein Structure Prediction Comes of Age with Contextual Machine Learning. Journal of Computational Biology, 2020, 27, 796-814.	0.8	15
26	DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. Journal of Molecular Biology, 2020, 432, 3379-3387.	2.0	46
27	Recent advances in glycoinformatic platforms for glycomics and glycoproteomics. Current Opinion in Structural Biology, 2020, 62, 56-69.	2.6	74
28	Accurate inference of the full base-pairing structure of RNA by deep mutational scanning and covariation-induced deviation of activity. Nucleic Acids Research, 2020, 48, 1451-1465.	6.5	15
29	All-Atom Knowledge-Based Potential for RNA Structure Discrimination Based on the Distance-Scaled Finite Ideal-Gas Reference State. Journal of Computational Biology, 2020, 27, 856-867.	0.8	15
30	DNA sequence repeats identify numerous Type I restrictionâ€“modification systems that are potential epigenetic regulators controlling phaseâ€“variable regulons; phasevarions. FASEB Journal, 2020, 34, 1038-1051.	0.2	29
31	SPOTâ€Fold: Fragmentâ€Free Protein Structure Prediction Guided by Predicted Backbone Structure and Contact Map. Journal of Computational Chemistry, 2020, 41, 745-750.	1.5	9
32	Systematic Analysis of REBASE Identifies Numerous Type I Restriction-Modification Systems with Duplicated, Distinct hsdS Specificity Genes That Can Switch System Specificity by Recombination. MSystems, 2020, 5, .	1.7	17
33	Moraxella catarrhalis phase-variable loci show differences in expression during conditions relevant to disease. PLoS ONE, 2020, 15, e0234306.	1.1	5
34	Interplay of hydrophobic and hydrophilic interactions in sequence-dependent cell penetration of spontaneous membrane-translocating peptides revealed by bias-exchange metadynamics simulations. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183402.	1.4	10
35	GM-DockZn: a geometry matching-based docking algorithm for zinc proteins. Bioinformatics, 2020, 36, 4004-4011.	1.8	7
36	DLIGAND2: an improved knowledge-based energy function for proteinâ€“ligand interactions using the distance-scaled, finite, ideal-gas reference state. Journal of Cheminformatics, 2019, 11, 52.	2.8	35

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37	Improved fragment sampling for ab initio protein structure prediction using deep neural networks. Nature Machine Intelligence, 2019, 1, 347-355.	8.3	25
38	Assessment of predicted enzymatic activity of Î±â€•N â€acetylglucosaminidase variants of unknown significance for CAGI 2016. Human Mutation, 2019, 40, 1519-1529.	1.1	10
39	Predicting functional long non-coding RNAs validated by low throughput experiments. RNA Biology, 2019, 16, 1555-1564.	1.5	6
40	Nucleotide Sugar Transporter SLC35 Family Structure and Function. Computational and Structural Biotechnology Journal, 2019, 17, 1123-1134.	1.9	53
41	SPOT-Peptide: Template-Based Prediction of Peptide-Binding Proteins and Peptide-Binding Sites. Journal of Chemical Information and Modeling, 2019, 59, 924-930.	2.5	19
42	Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge. Human Mutation, 2019, 40, 1392-1399.	1.1	16
43	Assessment of methods for predicting the effects of PTEN and TPMT protein variants. Human Mutation, 2019, 40, 1495-1506.	1.1	16
44	SPRINT-Gly: predictingN-andO-linked glycosylation sites of human and mouse proteins by using sequence and predicted structural properties. Bioinformatics, 2019, 35, 4140-4146.	1.8	48
45	Different effects of cholesterol on membrane permeation of arginine and tryptophan revealed by bias-exchange metadynamics simulations. Journal of Chemical Physics, 2019, 150, 084106.	1.2	13
46	Experimentally Validated Plant lncRNAs in EVLncRNAs Database. Methods in Molecular Biology, 2019, 1933, 431-437.	0.4	5
47	SPOT-Disorder2: Improved Protein Intrinsic Disorder Prediction by Ensembled Deep Learning. Genomics, Proteomics and Bioinformatics, 2019, 17, 645-656.	3.0	106
48	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	15
49	RNA secondary structure prediction using an ensemble of two-dimensional deep neural networks and transfer learning. Nature Communications, 2019, 10, 5407.	5.8	214
50	RegSNPs-intron: a computational framework for predicting pathogenic impact of intronic single nucleotide variants. Genome Biology, 2019, 20, 254.	3.8	52
51	Reactivation of Dihydroorotate Dehydrogenase-Driven Pyrimidine Biosynthesis Restores Tumor Growth of Respiration-Deficient Cancer Cells. Cell Metabolism, 2019, 29, 399-416.e10.	7.2	190
52	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. Bioinformatics, 2019, 35, 2403-2410.	1.8	145
53	Selfâ€derived structureâ€disrupting peptides targeting methionine aminopeptidase in pathogenic bacteria: a new strategy to generate antimicrobial peptides. FASEB Journal, 2019, 33, 2095-2104.	0.2	7
54	Sixty-five years of the long march in protein secondary structure prediction: the final stretch?. Briefings in Bioinformatics, 2018, 19, bbw129.	3.2	168

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55	SPIN2: Predicting sequence profiles from protein structures using deep neural networks. Proteins: Structure, Function and Bioinformatics, 2018, 86, 629-633.	1.5	62
56	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
57	Transcriptome profiling of lentil (Lens culinaris) through the first 24 hours of Ascochyta lentis infection reveals key defence response genes. BMC Genomics, 2018, 19, 108.	1.2	53
58	A survey of Type III restriction-modification systems reveals numerous, novel epigenetic regulators controlling phase-variable regulons; phasevarions. Nucleic Acids Research, 2018, 46, 3532-3542.	6.5	43
59	Quantitative mapping of genetic similarity in human heritable diseases by shared mutations. Human Mutation, 2018, 39, 292-301.	1.1	8
60	Structure-based prediction of proteinâ€“ peptide binding regions using Random Forest. Bioinformatics, 2018, 34, 477-484.	1.8	62
61	Bâ€factor profile prediction for RNA flexibility using support vector machines. Journal of Computational Chemistry, 2018, 39, 407-411.	1.5	13
62	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
63	Singleâ€sequenceâ€based prediction of protein secondary structures and solvent accessibility by deep wholeâ€sequence learning. Journal of Computational Chemistry, 2018, 39, 2210-2216.	1.5	84
64	YesU from Bacillus subtilis preferentially binds fucosylated glycans. Scientific Reports, 2018, 8, 13139.	1.6	7
65	Predicting lysineâ€malonylation sites of proteins using sequence and predicted structural features. Journal of Computational Chemistry, 2018, 39, 1757-1763.	1.5	30
66	Bias-Exchange Metadynamics Simulation of Membrane Permeation of 20 Amino Acids. International Journal of Molecular Sciences, 2018, 19, 885.	1.8	14
67	Grid-based prediction of torsion angle probabilities of protein backbone and its application to discrimination of protein intrinsic disorder regions and selection of model structures. BMC Bioinformatics, 2018, 19, 29.	1.2	17
68	Detecting Proline and Non-Proline Cis Isomers in Protein Structures from Sequences Using Deep Residual Ensemble Learning. Journal of Chemical Information and Modeling, 2018, 58, 2033-2042.	2.5	13
69	Computational Prediction of Carbohydrateâ€Binding Proteins and Binding Sites. Current Protocols in Protein Science, 2018, 94, e75.	2.8	5
70	Molecular Dynamics Simulations of Human Antimicrobial Peptide LL-37 in Model POPC and POPG Lipid Bilayers. International Journal of Molecular Sciences, 2018, 19, 1186.	1.8	45
71	Accurate prediction of protein contact maps by coupling residual two-dimensional bidirectional long short-term memory with convolutional neural networks. Bioinformatics, 2018, 34, 4039-4045.	1.8	155
72	Improving protein disorder prediction by deep bidirectional long short-term memory recurrent neural networks. Bioinformatics, 2017, 33, 685-692.	1.8	235

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73	LRFragLib: an effective algorithm to identify fragments for de novo protein structure prediction. Bioinformatics, 2017, 33, 677-684.	1.8	10
74	A heuristic for the time constrained asymmetric linear sum assignment problem. Journal of Combinatorial Optimization, 2017, 33, 551-566.	0.8	4
75	regSNPs-splicing: a tool for prioritizing synonymous single-nucleotide substitution. Human Genetics, 2017, 136, 1279-1289.	1.8	27
76	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. Bioinformatics, 2017, 33, 2842-2849.	1.8	300
77	Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. Human Mutation, 2017, 38, 1042-1050.	1.1	13
78	SPOT-ligand 2: improving structure-based virtual screening by binding-homology search on an expanded structural template library. Bioinformatics, 2017, 33, 1238-1240.	1.8	18
79	Systems-level understanding of ethanol-induced stresses and adaptation in E. coli. Scientific Reports, 2017, 7, 44150.	1.6	43
80	Real-time reliable determination of binding kinetics of DNA hybridization using a multi-channel graphene biosensor. Nature Communications, 2017, 8, 14902.	5.8	303
81	Testers wanted for article search tool. Nature, 2017, 549, 31-31.	13.7	2
82	Investigating DNA-, RNA-, and protein-based features as a means to discriminate pathogenic synonymous variants. Human Mutation, 2017, 38, 1336-1347.	1.1	37
83	DisBind: A database of classified functional binding sites in disordered and structured regions of intrinsically disordered proteins. BMC Bioinformatics, 2017, 18, 206.	1.2	9
84	Fast and Accurate Accessible Surface Area Prediction Without a Sequence Profile. Methods in Molecular Biology, 2017, 1484, 127-136.	0.4	7
85	Genome-scale characterization of RNA tertiary structures and their functional impact by RNA solvent accessibility prediction. Rna, 2017, 23, 14-22.	1.6	28
86	Intrinsic Disorder and Semi-disorder Prediction by SPINE-D. Methods in Molecular Biology, 2017, 1484, 159-174.	0.4	8
87	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. Methods in Molecular Biology, 2017, 1484, 55-63.	0.4	137
88	ExonImpact: Prioritizing Pathogenic Alternative Splicing Events. Human Mutation, 2017, 38, 16-24.	1.1	12
89	Structural signatures of thermal adaptation of bacterial ribosomal RNA, transfer RNA, and messenger RNA. PLoS ONE, 2017, 12, e0184722.	1.1	15
90	Investigation the Possibility of Using Peptides with a Helical Repeating Pattern of Hydro-Phobic and Hydrophilic Residues to Inhibit IL-10. PLoS ONE, 2016, 11, e0153939.	1.1	14

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91	s<scp>DFIRE</scp>: Sequenceâ€specific statistical energy function for protein structure prediction by decoy selections. Journal of Computational Chemistry, 2016, 37, 1119-1124.	1.5	16
92	SPOTâ€Ligand: Fast and effective structureâ€based virtual screening by binding homology search according to ligand and receptor similarity. Journal of Computational Chemistry, 2016, 37, 1734-1739.	1.5	15
93	Sequenceâ€based prediction of proteinâ€“peptide binding sites using support vector machine. Journal of Computational Chemistry, 2016, 37, 1223-1229.	1.5	81
94	Infectivity of Plasmodium falciparum in Malaria-Naive Individuals Is Related to Knob Expression and Cytoadherence of the Parasite. Infection and Immunity, 2016, 84, 2689-2696.	1.0	14
95	Effective protein conformational sampling based on predicted torsion angles. Journal of Computational Chemistry, 2016, 37, 976-980.	1.5	2
96	Optimal secretion of alkali-tolerant xylanase in Bacillus subtilis by signal peptide screening. Applied Microbiology and Biotechnology, 2016, 100, 8745-8756.	1.7	35
97	Predicting the errors of predicted local backbone angles and non-local solvent- accessibilities of proteins by deep neural networks. Bioinformatics, 2016, 32, 3768-3773.	1.8	25
98	Sequence-Based Prediction of Proteinâ€“Carbohydrate Binding Sites Using Support Vector Machines. Journal of Chemical Information and Modeling, 2016, 56, 2115-2122.	2.5	59
99	Natural protein sequences are more intrinsically disordered than random sequences. Cellular and Molecular Life Sciences, 2016, 73, 2949-2957.	2.4	37
100	EASE-MM: Sequence-Based Prediction of Mutation-Induced Stability Changes with Feature-Based Multiple Models. Journal of Molecular Biology, 2016, 428, 1394-1405.	2.0	101
101	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	1.8	79
102	Fast and accurate non-sequential protein structure alignment using a new asymmetric linear sum assignment heuristic. Bioinformatics, 2016, 32, 370-377.	1.8	19
103	DDIG-in: detecting disease-causing genetic variations due to frameshifting indels and nonsense mutations employing sequence and structural properties at nucleotide and protein levels. Bioinformatics, 2015, 31, 1599-1606.	1.8	52
104	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. Scientific Reports, 2015, 5, 11476.	1.6	290
105	Advancing the Accuracy of Protein Fold Recognition by Utilizing Profiles From Hidden Markov Models. IEEE Transactions on Nanobioscience, 2015, 14, 761-772.	2.2	34
106	Predicting DNA-Binding Proteins and Binding Residues by Complex Structure Prediction and Application to Human Proteome. PLoS ONE, 2014, 9, e96694.	1.1	32
107	Direct prediction of profiles of sequences compatible with a protein structure by neural networks with fragment-based local and energy-based nonlocal profiles. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2565-2573.	1.5	46
108	Impact of human pathogenic micro-insertions and micro-deletions on post-transcriptional regulation. Human Molecular Genetics, 2014, 23, 3024-3034.	1.4	27

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109	Predicting backbone CÎ± angles and dihedrals from protein sequences by stacked sparse autoâ€encoder deep neural network. Journal of Computational Chemistry, 2014, 35, 2040-2046.	1.5	133
110	LEAP: Highly accurate prediction of protein loop conformations by integrating coarseâ€grained sampling and optimized energy scores with allâ€atom refinement of backbone and side chains. Journal of Computational Chemistry, 2014, 35, 335-341.	1.5	34
111	Carbohydrate-binding protein identification by coupling structural similarity searching with binding affinity prediction. Journal of Computational Chemistry, 2014, 35, 2177-2183.	1.5	20
112	Prediction and validation of the unexplored RNAâ€binding protein atlas of the human proteome. Proteins: Structure, Function and Bioinformatics, 2014, 82, 640-647.	1.5	22
113	Accurate single-sequence prediction of solvent accessible surface area using local and global features. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3170-3176.	1.5	50
114	SPOT-Seq-RNA: Predicting Proteinâ€“RNA Complex Structure and RNA-Binding Function by Fold Recognition and Binding Affinity Prediction. Methods in Molecular Biology, 2014, 1137, 119-130.	0.4	39
115	DDIG-in: discriminating between disease-associated and neutral non-frameshifting micro-indels. Genome Biology, 2013, 14, R23.	13.9	63
116	Structural insights into the histone H1-nucleosome complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19390-19395.	3.3	178
117	The Role of Semidisorder in Temperature Adaptation of Bacterial FlgM Proteins. Biophysical Journal, 2013, 105, 2598-2605.	0.2	5
118	Energy Functions in De Novo Protein Design: Current Challenges and Future Prospects. Annual Review of Biophysics, 2013, 42, 315-335.	4.5	75
119	Intrinsically Semi-disordered State and Its Role in Induced Folding and Protein Aggregation. Cell Biochemistry and Biophysics, 2013, 67, 1193-1205.	0.9	57
120	Prediction of RNA binding proteins comes of age from low resolution to high resolution. Molecular BioSystems, 2013, 9, 2417.	2.9	37
121	SPINE-D: Accurate Prediction of Short and Long Disordered Regions by a Single Neural-Network Based Method. Journal of Biomolecular Structure and Dynamics, 2012, 29, 799-813.	2.0	150
122	BEST: Improved Prediction of B-Cell Epitopes from Antigen Sequences. PLoS ONE, 2012, 7, e40104.	1.1	79
123	Templateâ€based structure prediction and classification of transcription factors in Arabidopsis thaliana. Protein Science, 2012, 21, 828-838.	3.1	11
124	A new sizeâ€independent score for pairwise protein structure alignment and its application to structure classification and nucleicâ€acid binding prediction. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2080-2088.	1.5	69
125	SPINE X: Improving protein secondary structure prediction by multistep learning coupled with prediction of solvent accessible surface area and backbone torsion angles. Journal of Computational Chemistry, 2012, 33, 259-267.	1.5	209
126	Characterizing the Existing and Potential Structural Space of Proteins by Large-Scale Multiple Loop Permutations. Journal of Molecular Biology, 2011, 408, 585-595.	2.0	24

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127	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	2.0	131
128	Editorial [Hot Topic: Machine Learning Models in Protein Bioinformatics (Guest Editors: Lukasz) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 70	0.7	7
129	Small Open Reading Frames: Current Prediction Techniques and Future Prospect. Current Protein and Peptide Science, 2011, 12, 503-507.	0.7	38
130	Trends in template/fragment-free protein structure prediction. Theoretical Chemistry Accounts, 2011, 128, 3-16.	0.5	48
131	In-silico prediction of disorder content using hybrid sequence representation. BMC Bioinformatics, 2011, 12, 245.	1.2	45
132	Protein side chain modeling with orientationâ€dependent atomic force fields derived by series expansions. Journal of Computational Chemistry, 2011, 32, 1680-1686.	1.5	35
133	Highly accurate and high-resolution function prediction of RNA binding proteins by fold recognition and binding affinity prediction. RNA Biology, 2011, 8, 988-996.	1.5	53
134	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. Bioinformatics, 2011, 27, 2076-2082.	1.8	288
135	Structure-based prediction of RNA-binding domains and RNA-binding sites and application to structural genomics targets. Nucleic Acids Research, 2011, 39, 3017-3025.	6.5	100
136	Improving computational protein design by using structureâ€derived sequence profile. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2338-2348.	1.5	23
137	Fluctuations of backbone torsion angles obtained from NMRâ€determined structures and their prediction. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3353-3362.	1.5	27
138	Structure-based prediction of DNA-binding proteins by structural alignment and a volume-fraction corrected DFIRE-based energy function. Bioinformatics, 2010, 26, 1857-1863.	1.8	81
139	Predicting Continuous Local Structure and the Effect of Its Substitution for Secondary Structure in Fragment-Free Protein Structure Prediction. Structure, 2009, 17, 1515-1527.	1.6	108
140	Improving the prediction accuracy of residue solvent accessibility and realâ€value backbone torsion angles of proteins by guidedâ€learning through a twoâ€layer neural network. Proteins: Structure, Function and Bioinformatics, 2009, 74, 847-856.	1.5	125
141	Consensus scoring for enriching nearâ€native structures from proteinâ€“protein docking decoys. Proteins: Structure, Function and Bioinformatics, 2009, 75, 397-403.	1.5	36
142	Predicting residueâ€“residue contact maps by a twoâ€layer, integrated neuralâ€network method. Proteins: Structure, Function and Bioinformatics, 2009, 76, 176-183.	1.5	38
143	Refining nearâ€native proteinâ€“protein docking decoys by local resampling and energy minimization. Proteins: Structure, Function and Bioinformatics, 2009, 76, 309-316.	1.5	10
144	An allâ€atom knowledgeâ€based energy function for proteinâ€DNA threading, docking decoy discrimination, and prediction of transcriptionâ€factor binding profiles. Proteins: Structure, Function and Bioinformatics, 2009, 76, 718-730.	1.5	46

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145	The dual role of a loop with low loop contact distance in folding and domain swapping. Protein Science, 2009, 11, 1695-1701.	3.1	20
146	Distance-scaled, finite ideal-gas reference state improves structure-derived potentials of mean force for structure selection and stability prediction. Protein Science, 2009, 11, 2714-2726.	3.1	836
147	Exploring the Molecular Design of Protein Interaction Sites with Molecular Dynamics Simulations and Free Energy Calculations. Biochemistry, 2009, 48, 399-414.	1.2	47
148	Assessing secondary structure assignment of protein structures by using pairwise sequenceâ€alignment benchmarks. Proteins: Structure, Function and Bioinformatics, 2008, 71, 61-67.	1.5	32
149	Realâ€value prediction of backbone torsion angles. Proteins: Structure, Function and Bioinformatics, 2008, 72, 427-433.	1.5	66
150	Specific interactions for ab initio folding of protein terminal regions with secondary structures. Proteins: Structure, Function and Bioinformatics, 2008, 72, 793-803.	1.5	219
151	Ab initio folding of terminal segments with secondary structures reveals the fine difference between two closely related allâ€atom statistical energy functions. Protein Science, 2008, 17, 1212-1219.	3.1	131
152	Folding processes of the B domain of protein A to the native state observed in all-atom ab initio folding simulations. Journal of Chemical Physics, 2008, 128, 235105.	1.2	35
153	Folding mechanisms of individual Î²-hairpins in a GÅ•model of Pin1 WW domain by all-atom molecular dynamics simulations. Journal of Chemical Physics, 2008, 128, 225103.	1.2	20
154	SP5: Improving Protein Fold Recognition by Using Torsion Angle Profiles and Profile-Based Gap Penalty Model. PLoS ONE, 2008, 3, e2325.	1.1	68
155	Temperature-Dependent Folding Pathways of Pin1 WW Domain: An All-Atom Molecular Dynamics Simulation of a GÅ•Model. Biophysical Journal, 2007, 93, 2152-2161.	0.2	23
156	Real-SPINE: An integrated system of neural networks for real-value prediction of protein structural properties. Proteins: Structure, Function and Bioinformatics, 2007, 68, 76-81.	1.5	79
157	Fold recognition by concurrent use of solvent accessibility and residue depth. Proteins: Structure, Function and Bioinformatics, 2007, 68, 636-645.	1.5	87
158	The helix-coil transition revisited. Proteins: Structure, Function and Bioinformatics, 2007, 69, 58-68.	1.5	15
159	A simple reference state makes a significant improvement in nearâ€native selections from structurally refined docking decoys. Proteins: Structure, Function and Bioinformatics, 2007, 69, 244-253.	1.5	59
160	DDOMAIN: Dividing structures into domains using a normalized domain-domain interaction profile. Protein Science, 2007, 16, 947-955.	3.1	67
161	Fast and Accurate Method for Identifying High-Quality Protein-Interaction Modules by Clique Merging and Its Application to Yeast. Journal of Proteome Research, 2006, 5, 801-807.	1.8	22
162	QBES: Predicting real values of solvent accessibility from sequences by efficient, constrained energy optimization. Proteins: Structure, Function and Bioinformatics, 2006, 63, 961-966.	1.5	18

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163	Achieving 80% ten-fold cross-validated accuracy for secondary structure prediction by large-scale training. Proteins: Structure, Function and Bioinformatics, 2006, 66, 838-845.	1.5	114
164	What is a Desirable Statistical Energy Function for Proteins and How Can It Be Obtained?. Cell Biochemistry and Biophysics, 2006, 46, 165-174.	0.9	50
165	Cooperativity inScapharca dimeric hemoglobin: Simulation of binding intermediates and elucidation of the role of interfacial water. Rendiconti Lincei, 2006, 17, 191-211.	1.0	0
166	Protein binding site prediction using an empirical scoring function. Nucleic Acids Research, 2006, 34, 3698-3707.	6.5	223
167	Uneven size distribution of mammalian genes in the number of tissues expressed and in the number of co-expressed genes. Human Molecular Genetics, 2006, 15, 1313-1318.	1.4	4
168	SCUD: Fast structure clustering of decoys using reference state to remove overall rotation. Journal of Computational Chemistry, 2005, 26, 1189-1192.	1.5	16
169	Docking prediction using biological information, ZDOCK sampling technique, and clustering guided by the DFIRE statistical energy function. Proteins: Structure, Function and Bioinformatics, 2005, 60, 314-318.	1.5	34
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