

Yang Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

140
papers

26,960
citations

55
h-index

159
g-index

159
ext. papers

33,457
ext. citations

8.1
avg, IF

8.06
L-index

#	Paper	IF	Citations
140	CR-I-TASSER: assemble protein structures from cryo-EM density maps using deep convolutional neural networks.. <i>Nature Methods</i> , 2022 , 19, 195-204	21.6	0
139	RTL8 promotes nuclear localization of UBQLN2 to subnuclear compartments associated with protein quality control.. <i>Cellular and Molecular Life Sciences</i> , 2022 , 79, 176	10.3	
138	Progressive assembly of multi-domain protein structures from cryo-EM density maps. <i>Nature Computational Science</i> , 2022 , 2, 265-275		0
137	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. <i>IScience</i> , 2022 , 25, 104425	6.1	0
136	Decoding the link of microbiome niches with homologous sequences enables accurately targeted protein structure prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
135	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	5
134	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks. <i>PLoS Computational Biology</i> , 2021 , 17, e1008865	5	20
133	Endoplasmic reticulum-associated degradation is required for nephrin maturation and kidney glomerular filtration function. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	3
132	ADDRESS: A Database of Disease-associated Human Variants Incorporating Protein Structure and Folding Stabilities. <i>Journal of Molecular Biology</i> , 2021 , 433, 166840	6.5	3
131	Integrating Multimeric Threading With High-throughput Experiments for Structural Interactome of Escherichia coli. <i>Journal of Molecular Biology</i> , 2021 , 433, 166944	6.5	3
130	Mechanism for DPY30 and ASH2L intrinsically disordered regions to modulate the MLL/SET1 activity on chromatin. <i>Nature Communications</i> , 2021 , 12, 2953	17.4	2
129	Deep learning techniques have significantly impacted protein structure prediction and protein design. <i>Current Opinion in Structural Biology</i> , 2021 , 68, 194-207	8.1	16
128	Identification of 13 Guanidinobenzoyl- or Aminidinobenzoyl-Containing Drugs to Potentially Inhibit TMPRSS2 for COVID-19 Treatment. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
127	MMpred: a distance-assisted multimodal conformation sampling for de novo protein structure prediction. <i>Bioinformatics</i> , 2021 ,	7.2	2
126	Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. <i>Cell Reports Methods</i> , 2021 , 1,		40
125	Effects of SARS-CoV-2 mutations on protein structures and intraviral protein-protein interactions. <i>Journal of Medical Virology</i> , 2021 , 93, 2132-2140	19.7	48
124	Computational design of SARS-CoV-2 spike glycoproteins to increase immunogenicity by T cell epitope engineering. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 518-529	6.8	9

123	Functions of Essential Genes and a Scale-Free Protein Interaction Network Revealed by Structure-Based Function and Interaction Prediction for a Minimal Genome. <i>Journal of Proteome Research</i> , 2021 , 20, 1178-1189	5.6	7
122	Fitting Low-Resolution Protein Structures into Cryo-EM Density Maps by Multiobjective Optimization of Global and Local Correlations. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 528-538	3.4	1
121	Toward the solution of the protein structure prediction problem. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100870	5.4	12
120	Protein structure prediction using deep learning distance and hydrogen-bonding restraints in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1734-1751	4.2	9
119	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. <i>Nature Communications</i> , 2021 , 12, 5011	17.4	6
118	Protein inter-residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in CASP14. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1911-1921	4.2	4
117	Protein structural features predict responsiveness to pharmacological chaperone treatment for three lysosomal storage disorders. <i>PLoS Computational Biology</i> , 2021 , 17, e1009370	5	0
116	Underestimation-Assisted Global-Local Cooperative Differential Evolution and the Application to Protein Structure Prediction. <i>IEEE Transactions on Evolutionary Computation</i> , 2020 , 24, 536-550	15.6	12
115	Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons. <i>Bioinformatics</i> , 2020 , 36, 4383-4388	7.2	6
114	EDock: blind protein-ligand docking by replica-exchange monte carlo simulation. <i>Journal of Cheminformatics</i> , 2020 , 12, 37	8.6	12
113	Landscape of variable domain of heavy-chain-only antibody repertoire from alpaca. <i>Immunology</i> , 2020 , 161, 53-65	7.8	3
112	Protein Structure and Sequence Reanalysis of 2019-nCoV Genome Refutes Snakes as Its Intermediate Host and the Unique Similarity between Its Spike Protein Insertions and HIV-1. <i>Journal of Proteome Research</i> , 2020 , 19, 1351-1360	5.6	166
111	Virtual Screening of Human Class-A GPCRs Using Ligand Profiles Built on Multiple Ligand-Receptor Interactions. <i>Journal of Molecular Biology</i> , 2020 , 432, 4872-4890	6.5	6
110	FUPred: detecting protein domains through deep-learning-based contact map prediction. <i>Bioinformatics</i> , 2020 , 36, 3749-3757	7.2	15
109	FASPR: an open-source tool for fast and accurate protein side-chain packing. <i>Bioinformatics</i> , 2020 , 36, 3758-3765	7.2	16
108	design of protein peptides to block association of the SARS-CoV-2 spike protein with human ACE2. <i>Aging</i> , 2020 , 12, 11263-11276	5.6	54
107	Rational Design of SARS-CoV-2 Spike Glycoproteins To Increase Immunogenicity By T Cell Epitope Engineering 2020 ,		3
106	Protein structure and sequence re-analysis of 2019-nCoV genome does not indicate snakes as its intermediate host or the unique similarity between its spike protein insertions and HIV-1 2020 ,		14

105	Progressive and accurate assembly of multi-domain protein structures from cryo-EM density maps 2020 ,		2
104	Toward the Accuracy and Speed of Protein Side-Chain Packing: A Systematic Study on Rotamer Libraries. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 410-420	6.1	5
103	CGLFold: a contact-assisted de novo protein structure prediction using global exploration and loop perturbation sampling algorithm. <i>Bioinformatics</i> , 2020 , 36, 2443-2450	7.2	9
102	DeepMSA: constructing deep multiple sequence alignment to improve contact prediction and fold-recognition for distant-homology proteins. <i>Bioinformatics</i> , 2020 , 36, 2105-2112	7.2	60
101	SSIPE: accurately estimating protein-protein binding affinity change upon mutations using evolutionary profiles in combination with an optimized physical energy function. <i>Bioinformatics</i> , 2020 , 36, 2429-2437	7.2	21
100	Identifying the Zoonotic Origin of SARS-CoV-2 by Modeling the Binding Affinity between the Spike Receptor-Binding Domain and Host ACE2. <i>Journal of Proteome Research</i> , 2020 , 19, 4844-4856	5.6	15
99	A New Protocol for Atomic-Level Protein Structure Modeling and Refinement Using Low-to-Medium Resolution Cryo-EM Density Maps. <i>Journal of Molecular Biology</i> , 2020 , 432, 5365-5377	6.5	8
98	EvoEF2: accurate and fast energy function for computational protein design. <i>Bioinformatics</i> , 2020 , 36, 1135-1142	7.2	33
97	Artificial intelligence-based multi-objective optimization protocol for protein structure refinement. <i>Bioinformatics</i> , 2020 , 36, 437-448	7.2	12
96	The Human DNA Mismatch Repair Protein MSH3 Contains Nuclear Localization and Export Signals That Enable Nuclear-Cytosolic Shuttling in Response to Inflammation. <i>Molecular and Cellular Biology</i> , 2020 , 40,	4.8	9
95	DockRMSD: an open-source tool for atom mapping and RMSD calculation of symmetric molecules through graph isomorphism. <i>Journal of Cheminformatics</i> , 2019 , 11, 40	8.6	81
94	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. <i>Bioinformatics</i> , 2019 , 35, 4647-4655	7.2	88
93	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. <i>Future Generation Computer Systems</i> , 2019 , 99, 73-85	7.5	35
92	EvoDesign: Designing Protein-Protein Binding Interactions Using Evolutionary Interface Profiles in Conjunction with an Optimized Physical Energy Function. <i>Journal of Molecular Biology</i> , 2019 , 431, 2467-2476	6.5	35
91	DAMPred: Recognizing Disease-Associated nsSNPs through Bayes-Guided Neural-Network Model Built on Low-Resolution Structure Prediction of Proteins and Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2019 , 431, 2449-2459	6.5	7
90	Ensembling multiple raw coevolutionary features with deep residual neural networks for contact-map prediction in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1082-1091	4.2	63
89	LOMETS2: improved meta-threading server for fold-recognition and structure-based function annotation for distant-homology proteins. <i>Nucleic Acids Research</i> , 2019 , 47, W429-W436	20.1	76
88	Assembling multidomain protein structures through analogous global structural alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 15930-15938	11.5	30

87	Deep-learning contact-map guided protein structure prediction in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1149-1164	4.2	108
86	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018-2019 Additions to neXtProt and the CAFA3 Challenge. <i>Journal of Proteome Research</i> , 2019 , 18, 4154-4166	5.6	12
85	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. <i>PLoS Computational Biology</i> , 2019 , 15, e1007411	5	25
84	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. <i>Genome Biology</i> , 2019 , 20, 229	18.3	17
83	Function Prediction for G Protein-Coupled Receptors through Text Mining and Induction Matrix Completion. <i>ACS Omega</i> , 2019 , 4, 3045-3054	3.9	1
82	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
81	Changing the Apoptosis Pathway through Evolutionary Protein Design. <i>Journal of Molecular Biology</i> , 2019 , 431, 825-841	6.5	12
80	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. <i>Bioinformatics</i> , 2018 , 34, 2209-2218	7.2	25
79	MetaGO: Predicting Gene Ontology of Non-homologous Proteins Through Low-Resolution Protein Structure Prediction and Protein-Protein Network Mapping. <i>Journal of Molecular Biology</i> , 2018 , 430, 2256-2265	6.5	32
78	ATPbind: Accurate Protein-ATP Binding Site Prediction by Combining Sequence-Profiling and Structure-Based Comparisons. <i>Journal of Chemical Information and Modeling</i> , 2018 , 58, 501-510	6.1	28
77	MR-REX: molecular replacement by cooperative conformational search and occupancy optimization on low-accuracy protein models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 606-620	5.5	1
76	COACH-D: improved protein-ligand binding sites prediction with refined ligand-binding poses through molecular docking. <i>Nucleic Acids Research</i> , 2018 , 46, W438-W442	20.1	77
75	The structure of the large regulatory β subunit of phosphorylase kinase examined by modeling and hydrogen-deuterium exchange. <i>Protein Science</i> , 2018 , 27, 472-484	6.3	1
74	Template-based and free modeling of I-TASSER and QUARK pipelines using predicted contact maps in CASP12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86 Suppl 1, 136-151	4.2	58
73	Structure and Protein Interaction-Based Gene Ontology Annotations Reveal Likely Functions of Uncharacterized Proteins on Human Chromosome 17. <i>Journal of Proteome Research</i> , 2018 , 17, 4186-4196	5.6	20
72	COFACTOR: improved protein function prediction by combining structure, sequence and protein-protein interaction information. <i>Nucleic Acids Research</i> , 2017 , 45, W291-W299	20.1	235
71	I-TASSER-MR: automated molecular replacement for distant-homology proteins using iterative fragment assembly and progressive sequence truncation. <i>Nucleic Acids Research</i> , 2017 , 45, W429-W434	20.1	31
70	ThreaDomEx: a unified platform for predicting continuous and discontinuous protein domains by multiple-threading and segment assembly. <i>Nucleic Acids Research</i> , 2017 , 45, W400-W407	20.1	19

69	NeBcon: protein contact map prediction using neural network training coupled with naïve Bayes classifiers. <i>Bioinformatics</i> , 2017 , 33, 2296-2306	7.2	52
68	BindProfX: Assessing Mutation-Induced Binding Affinity Change by Protein Interface Profiles with Pseudo-Counts. <i>Journal of Molecular Biology</i> , 2017 , 429, 426-434	6.5	65
67	Potential of Three Ethnomedicinal Plants as Antisickling Agents. <i>Molecular Pharmaceutics</i> , 2017 , 14, 172-182	5.82	22
66	Approaches to ab initio molecular replacement of helical transmembrane proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017 , 73, 985-996	5.5	3
65	ResQ: An Approach to Unified Estimation of B-Factor and Residue-Specific Error in Protein Structure Prediction. <i>Journal of Molecular Biology</i> , 2016 , 428, 693-701	6.5	76
64	STRUM: structure-based prediction of protein stability changes upon single-point mutation. <i>Bioinformatics</i> , 2016 , 32, 2936-46	7.2	190
63	3DRobot: automated generation of diverse and well-packed protein structure decoys. <i>Bioinformatics</i> , 2016 , 32, 378-87	7.2	87
62	Template-based protein structure prediction in CASP11 and retrospect of I-TASSER in the last decade. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 233-46	4.2	42
61	Integration of QUARK and I-TASSER for Ab Initio Protein Structure Prediction in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 76-86	4.2	47
60	Recognizing metal and acid radical ion-binding sites by integrating ab initio modeling with template-based transfers. <i>Bioinformatics</i> , 2016 , 32, 3260-3269	7.2	56
59	Using iterative fragment assembly and progressive sequence truncation to facilitate phasing and crystal structure determination of distantly related proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 616-28	5.5	9
58	GPCR-I-TASSER: A Hybrid Approach to G Protein-Coupled Receptor Structure Modeling and the Application to the Human Genome. <i>Structure</i> , 2015 , 23, 1538-1549	5.2	121
57	I-TASSER server: new development for protein structure and function predictions. <i>Nucleic Acids Research</i> , 2015 , 43, W174-81	20.1	1059
56	Exploring the speed and performance of molecular replacement with AMPLE using QUARK ab initio protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 338-43		21
55	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. <i>Journal of Proteome Research</i> , 2015 , 14, 3750-61	5.6	11
54	Crystal structure of designed PX domain from cytokine-independent survival kinase and implications on evolution-based protein engineering. <i>Journal of Structural Biology</i> , 2015 , 191, 197-206	3.4	9
53	Predicting the Effect of Mutations on Protein-Protein Binding Interactions through Structure-Based Interface Profiles. <i>PLoS Computational Biology</i> , 2015 , 11, e1004494	5	95
52	Improving accuracy of protein contact prediction using balanced network deconvolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 485-96	4.2	18

51	The I-TASSER Suite: protein structure and function prediction. <i>Nature Methods</i> , 2015 , 12, 7-8	21.6	3430
50	Interplay of I-TASSER and QUARK for template-based and ab initio protein structure prediction in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82 Suppl 2, 175-87	4.2	91
49	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. <i>Scientific Reports</i> , 2013 , 3, 2619	4.9	128
48	Protein-ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment. <i>Bioinformatics</i> , 2013 , 29, 2588-95	7.2	483
47	Mapping monomeric threading to protein-protein structure prediction. <i>Journal of Chemical Information and Modeling</i> , 2013 , 53, 717-25	6.1	49
46	Toward optimal fragment generations for ab initio protein structure assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 229-39	4.2	156
45	LabCaS: labeling calpain substrate cleavage sites from amino acid sequence using conditional random fields. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 622-34	4.2	20
44	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. <i>Scientific Reports</i> , 2013 , 3, 1895	4.9	34
43	An evolution-based approach to De Novo protein design and case study on Mycobacterium tuberculosis. <i>PLoS Computational Biology</i> , 2013 , 9, e1003298	5	39
42	EvoDesign: De novo protein design based on structural and evolutionary profiles. <i>Nucleic Acids Research</i> , 2013 , 41, W273-80	20.1	36
41	ThreaDom: extracting protein domain boundary information from multiple threading alignments. <i>Bioinformatics</i> , 2013 , 29, i247-56	7.2	56
40	BioLiP: a semi-manually curated database for biologically relevant ligand-protein interactions. <i>Nucleic Acids Research</i> , 2013 , 41, D1096-103	20.1	348
39	Recognizing protein-ligand binding sites by global structural alignment and local geometry refinement. <i>Structure</i> , 2012 , 20, 987-97	5.2	80
38	COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. <i>Nucleic Acids Research</i> , 2012 , 40, W471-7	20.1	448
37	BSP-SLIM: a blind low-resolution ligand-protein docking approach using predicted protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 93-110	4.2	65
36	Ab initio protein structure assembly using continuous structure fragments and optimized knowledge-based force field. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 1715-35	4.2	607
35	Structure and location of the regulatory β subunits in the β phosphorylase kinase complex. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36651-61	5.4	13
34	Improving the physical realism and structural accuracy of protein models by a two-step atomic-level energy minimization. <i>Biophysical Journal</i> , 2011 , 101, 2525-34	2.9	600

33	Improving protein template recognition by using small-angle x-ray scattering profiles. <i>Biophysical Journal</i> , 2011 , 101, 2770-81	2.9	28
32	Computational protein design and large-scale assessment by I-TASSER structure assembly simulations. <i>Journal of Molecular Biology</i> , 2011 , 407, 764-76	6.5	32
31	Improving protein structure prediction using multiple sequence-based contact predictions. <i>Structure</i> , 2011 , 19, 1182-91	5.2	55
30	Atomic-level protein structure refinement using fragment-guided molecular dynamics conformation sampling. <i>Structure</i> , 2011 , 19, 1784-95	5.2	243
29	Automated protein structure modeling in CASP9 by I-TASSER pipeline combined with QUARK-based ab initio folding and FG-MD-based structure refinement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011 , 79 Suppl 10, 147-60	4.2	111
28	I-TASSER: a unified platform for automated protein structure and function prediction. <i>Nature Protocols</i> , 2010 , 5, 725-38	18.8	4448
27	How significant is a protein structure similarity with TM-score = 0.5?. <i>Bioinformatics</i> , 2010 , 26, 889-95	7.2	455
26	A novel side-chain orientation dependent potential derived from random-walk reference state for protein fold selection and structure prediction. <i>PLoS ONE</i> , 2010 , 5, e15386	3.7	172
25	MM-align: a quick algorithm for aligning multiple-chain protein complex structures using iterative dynamic programming. <i>Nucleic Acids Research</i> , 2009 , 37, e83	20.1	70
24	Protein structure prediction: when is it useful?. <i>Current Opinion in Structural Biology</i> , 2009 , 19, 145-55	8.1	212
23	REMO: A new protocol to refine full atomic protein models from C-alpha traces by optimizing hydrogen-bonding networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 665-76	4.2	97
22	I-TASSER: fully automated protein structure prediction in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 77 Suppl 9, 100-13	4.2	326
21	I-TASSER server for protein 3D structure prediction. <i>BMC Bioinformatics</i> , 2008 , 9, 40	3.6	3560
20	Progress and challenges in protein structure prediction. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 342-8	8.1	382
19	A comprehensive assessment of sequence-based and template-based methods for protein contact prediction. <i>Bioinformatics</i> , 2008 , 24, 924-31	7.2	136
18	MUSTER: Improving protein sequence profile-profile alignments by using multiple sources of structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 72, 547-56	4.2	301
17	ANGLOR: a composite machine-learning algorithm for protein backbone torsion angle prediction. <i>PLoS ONE</i> , 2008 , 3, e3400	3.7	55
16	Ab initio modeling of small proteins by iterative TASSER simulations. <i>BMC Biology</i> , 2007 , 5, 17	7.3	378

15	Template-based modeling and free modeling by I-TASSER in CASP7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69 Suppl 8, 108-17	4.2	368
14	LOMETS: a local meta-threading-server for protein structure prediction. <i>Nucleic Acids Research</i> , 2007 , 35, 3375-82	20.1	626
13	TM-align: a protein structure alignment algorithm based on the TM-score. <i>Nucleic Acids Research</i> , 2005 , 33, 2302-9	20.1	1777
12	The protein structure prediction problem could be solved using the current PDB library. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 1029-34	11.5	235
11	Automated structure prediction of weakly homologous proteins on a genomic scale. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 7594-9	11.5	295
10	Development and large scale benchmark testing of the PROSPECTOR_3 threading algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 56, 502-18	4.2	137
9	Scoring function for automated assessment of protein structure template quality. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 702-10	4.2	1196
8	SPICKER: a clustering approach to identify near-native protein folds. <i>Journal of Computational Chemistry</i> , 2004 , 25, 865-71	3.5	326
7	TOUCHSTONE II: a new approach to ab initio protein structure prediction. <i>Biophysical Journal</i> , 2003 , 85, 1145-64	2.9	223
6	Local energy landscape flattening: parallel hyperbolic Monte Carlo sampling of protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002 , 48, 192-201	4.2	118
5	Computational Design of Peptides to Block Binding of the SARS-CoV-2 Spike Protein to Human ACE2		11
4	Effects of SARS-CoV-2 Mutations on Protein Structures and Intraviral Protein-Protein Interactions		1
3	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks		3
2	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
1	Evolution of a chordate-specific mechanism for myoblast fusion		3