

Yang Zhang

List of Publications by Year in descending order

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135
papers

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159
all docs

159
docs citations

159
times ranked

37100
citing authors

#	ARTICLE	IF	CITATIONS
1	I-TASSER: a unified platform for automated protein structure and function prediction. <i>Nature Protocols</i> , 2010, 5, 725-738.	12.0	5,594
2	The I-TASSER Suite: protein structure and function prediction. <i>Nature Methods</i> , 2015, 12, 7-8.	19.0	4,923
3	I-TASSER server for protein 3D structure prediction. <i>BMC Bioinformatics</i> , 2008, 9, 40.	2.6	4,415
4	TM-align: a protein structure alignment algorithm based on the TM-score. <i>Nucleic Acids Research</i> , 2005, 33, 2302-2309.	14.5	2,634
5	I-TASSER server: new development for protein structure and function predictions. <i>Nucleic Acids Research</i> , 2015, 43, W174-W181.	14.5	1,897
6	Scoring function for automated assessment of protein structure template quality. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 57, 702-710.	2.6	1,697
7	Improving the Physical Realism and Structural Accuracy of Protein Models by a Two-Step Atomic-Level Energy Minimization. <i>Biophysical Journal</i> , 2011, 101, 2525-2534.	0.5	871
8	<i>Ab initio</i> protein structure assembly using continuous structure fragments and optimized knowledge-based force field. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1715-1735.	2.6	744
9	Protein-ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment. <i>Bioinformatics</i> , 2013, 29, 2588-2595.	4.1	739
10	LOMETS: A local meta-threading-server for protein structure prediction. <i>Nucleic Acids Research</i> , 2007, 35, 3375-3382.	14.5	734
11	How significant is a protein structure similarity with TM-score = 0.5?. <i>Bioinformatics</i> , 2010, 26, 889-895.	4.1	674
12	COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. <i>Nucleic Acids Research</i> , 2012, 40, W471-W477.	14.5	582
13	BioLiP: a semi-manually curated database for biologically relevant ligand-protein interactions. <i>Nucleic Acids Research</i> , 2012, 41, D1096-D1103.	14.5	568
14	Ab initio modeling of small proteins by iterative TASSER simulations. <i>BMC Biology</i> , 2007, 5, 17.	3.8	439
15	Progress and challenges in protein structure prediction. <i>Current Opinion in Structural Biology</i> , 2008, 18, 342-348.	5.7	437
16	COFACTOR: improved protein function prediction by combining structure, sequence and protein-protein interaction information. <i>Nucleic Acids Research</i> , 2017, 45, W291-W299.	14.5	424
17	Template-based modeling and free modeling by I-TASSER in CASP7. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 108-117.	2.6	410
18	I-TASSER: Fully automated protein structure prediction in CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 100-113.	2.6	384

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19	SPICKER: A clustering approach to identify near-native protein folds. <i>Journal of Computational Chemistry</i> , 2004, 25, 865-871.	3.3	380
20	MUSTER: Improving protein sequence profileâ€“profile alignments by using multiple sources of structure information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 547-556.	2.6	341
21	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, 7594-7599.	7.1	324
22	Atomic-Level Protein Structure Refinement Using Fragment-Guided Molecular Dynamics Conformation Sampling. <i>Structure</i> , 2011, 19, 1784-1795.	3.3	309
23	STRUM: structure-based prediction of protein stability changes upon single-point mutation. <i>Bioinformatics</i> , 2016, 32, 2936-2946.	4.1	275
24	Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. <i>Cell Reports Methods</i> , 2021, 1, 100014.	2.9	272
25	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, 1029-1034.	7.1	269
26	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.	8.8	261
27	TOUCHSTONE II: A New Approach to Ab Initio Protein Structure Prediction. <i>Biophysical Journal</i> , 2003, 85, 1145-1164.	0.5	243
28	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.	3.7	242
29	Protein structure prediction: when is it useful?. <i>Current Opinion in Structural Biology</i> , 2009, 19, 145-155.	5.7	234
30	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.	2.5	216
31	Toward optimal fragment generations for <i>ab initio</i> protein structure assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 229-239.	2.6	191
32	Deepâ€“learning contactâ€“map guided protein structure prediction in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1149-1164.	2.6	180
33	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.	6.1	174
34	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. <i>Scientific Reports</i> , 2013, 3, 2619.	3.3	171
35	A comprehensive assessment of sequence-based and template-based methods for protein contact prediction. <i>Bioinformatics</i> , 2008, 24, 924-931.	4.1	165
36	COACH-D: improved proteinâ€“ligand binding sites prediction with refined ligand-binding poses through molecular docking. <i>Nucleic Acids Research</i> , 2018, 46, W438-W442.	14.5	164

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37	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.	3.3	153
38	Development and large scale benchmark testing of the PROSPECTOR_3 threading algorithm. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 502-518.	2.6	152
39	DeepMSA: constructing deep multiple sequence alignment to improve contact prediction and fold-recognition for distant-homology proteins. <i>Bioinformatics</i> , 2020, 36, 2105-2112.	4.1	147
40	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. <i>Bioinformatics</i> , 2019, 35, 4647-4655.	4.1	142
41	Automated protein structure modeling in CASP9 by I-TASSER pipeline combined with QUARK-based <i>ab initio</i> folding and FGMD-based structure refinement. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 147-160.	2.6	139
42	Local energy landscape flattening: Parallel hyperbolic Monte Carlo sampling of protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 192-201.	2.6	130
43	MM-align: a quick algorithm for aligning multiple-chain protein complex structures using iterative dynamic programming. <i>Nucleic Acids Research</i> , 2009, 37, e83-e83.	14.5	126
44	Predicting the Effect of Mutations on Protein-Protein Binding Interactions through Structure-Based Interface Profiles. <i>PLoS Computational Biology</i> , 2015, 11, e1004494.	3.2	122
45	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.	4.2	119
46	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.	14.5	118
47	REMO: A new protocol to refine full atomic protein models from α traces by optimizing hydrogen-bonding networks. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 665-676.	2.6	112
48	BindProfX: Assessing Mutation-Induced Binding Affinity Change by Protein Interface Profiles with Pseudo-Counts. <i>Journal of Molecular Biology</i> , 2017, 429, 426-434.	4.2	107
49	3DRobot: automated generation of diverse and well-packed protein structure decoys. <i>Bioinformatics</i> , 2016, 32, 378-387.	4.1	104
50	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.	7.1	104
51	Recognizing Protein-Ligand Binding Sites by Global Structural Alignment and Local Geometry Refinement. <i>Structure</i> , 2012, 20, 987-997.	3.3	101
52	Interplay of I-TASSER and QUARK for template-based and <i>ab initio</i> protein structure prediction in CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 175-187.	2.6	98
53	Recognizing metal and acid radical ion-binding sites by integrating <i>ab initio</i> modeling with template-based transfers. <i>Bioinformatics</i> , 2016, 32, 3260-3269.	4.1	98
54	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.	2.6	96

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55	De novo design of protein peptides to block association of the SARS-CoV-2 spike protein with human ACE2. <i>Aging</i> , 2020, 12, 11263-11276.	3.1	89
56	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, 136-151.	2.6	86
57	Effects of SARS-CoV-2 mutations on protein structures and intraviral protein-protein interactions. <i>Journal of Medical Virology</i> , 2021, 93, 2132-2140.	5.0	85
58	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	80
59	ThreaDom: extracting protein domain boundary information from multiple threading alignments. <i>Bioinformatics</i> , 2013, 29, i247-i256.	4.1	79
60	Deep learning techniques have significantly impacted protein structure prediction and protein design. <i>Current Opinion in Structural Biology</i> , 2021, 68, 194-207.	5.7	77
61	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.	2.6	75
62	ANGLOR: A Composite Machine-Learning Algorithm for Protein Backbone Torsion Angle Prediction. <i>PLoS ONE</i> , 2008, 3, e3400.	2.5	75
63	EvoEF2: accurate and fast energy function for computational protein design. <i>Bioinformatics</i> , 2020, 36, 1135-1142.	4.1	73
64	Toward the solution of the protein structure prediction problem. <i>Journal of Biological Chemistry</i> , 2021, 297, 100870.	3.4	73
65	NeBcon: protein contact map prediction using neural network training coupled with naive Bayes classifiers. <i>Bioinformatics</i> , 2017, 33, 2296-2306.	4.1	71
66	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.	3.2	70
67	Mapping Monomeric Threading to Protein-Protein Structure Prediction. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 717-725.	5.4	67
68	Integration of QUARK and I-TASSER for Ab Initio Protein Structure Prediction in CASP11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 76-86.	2.6	63
69	Improving Protein Structure Prediction Using Multiple Sequence-Based Contact Predictions. <i>Structure</i> , 2011, 19, 1182-1191.	3.3	62
70	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. <i>Bioinformatics</i> , 2018, 34, 2209-2218.	4.1	62
71	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.	4.2	60
72	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.	4.2	58

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73	ATPbind: Accurate Proteinâ€™ ATP Binding Site Prediction by Combining Sequence-Profiling and Structure-Based Comparisons. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 501-510.	5.4	57
74	FASPR: an open-source tool for fast and accurate protein side-chain packing. <i>Bioinformatics</i> , 2020, 36, 3758-3765.	4.1	54
75	Protein structure prediction using deep learning distance and hydrogenâ€™ bonding restraints in <scp>CASP14</scp>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1734-1751.	2.6	53
76	Templateâ€™based protein structure prediction in <scp>CASP11</scp> and retrospect of <scp>Iâ€™TASSER</scp> in the last decade. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 233-246.	2.6	48
77	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. <i>PLoS Computational Biology</i> , 2019, 15, e1007411.	3.2	45
78	EDock: blind proteinâ€™ligand docking by replica-exchange monte carlo simulation. <i>Journal of Cheminformatics</i> , 2020, 12, 37.	6.1	45
79	An Evolution-Based Approach to De Novo Protein Design and Case Study on Mycobacterium tuberculosis. <i>PLoS Computational Biology</i> , 2013, 9, e1003298.	3.2	44
80	EvoDesign: de novo protein design based on structural and evolutionary profiles. <i>Nucleic Acids Research</i> , 2013, 41, W273-W280.	14.5	44
81	FUpred: detecting protein domains through deep-learning-based contact map prediction. <i>Bioinformatics</i> , 2020, 36, 3749-3757.	4.1	44
82	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. <i>Nature Communications</i> , 2021, 12, 5011.	12.8	44
83	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. <i>Scientific Reports</i> , 2013, 3, 1895.	3.3	43
84	SSIPE: accurately estimating proteinâ€™protein binding affinity change upon mutations using evolutionary profiles in combination with an optimized physical energy function. <i>Bioinformatics</i> , 2020, 36, 2429-2437.	4.1	42
85	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.	14.5	37
86	Potential of Three Ethnomedicinal Plants as Antisickling Agents. <i>Molecular Pharmaceutics</i> , 2017, 14, 172-182.	4.6	37
87	CGLFold: a contact-assisted<i>de novo</i> protein structure prediction using global exploration and loop perturbation sampling algorithm. <i>Bioinformatics</i> , 2020, 36, 2443-2450.	4.1	36
88	Computational Protein Design and Large-Scale Assessment by I-TASSER Structure Assembly Simulations. <i>Journal of Molecular Biology</i> , 2011, 407, 764-776.	4.2	34
89	Improving Protein Template Recognition by Using Small-Angle X-Ray Scattering Profiles. <i>Biophysical Journal</i> , 2011, 101, 2770-2781.	0.5	33
90	CR-I-TASSER: assemble protein structures from cryo-EM density maps using deep convolutional neural networks. <i>Nature Methods</i> , 2022, 19, 195-204.	19.0	33

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91	LabCaS: Labeling calpain substrate cleavage sites from amino acid sequence using conditional random fields. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 622-634.	2.6	29
92	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. <i>Genome Biology</i> , 2019, 20, 229.	8.8	28
93	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.	3.7	27
94	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.	3.7	27
95	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.	4.2	26
96	Exploring the speed and performance of molecular replacement with <i>AMPLE</i> using <i>QUARK</i> ab initio protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 338-343.	2.5	25
97	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.	14.5	25
98	Progressive assembly of multi-domain protein structures from cryo-EM density maps. <i>Nature Computational Science</i> , 2022, 2, 265-275.	8.0	25
99	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.	3.7	23
100	Protein inter-residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in <i>CASP14</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1911-1921.	2.6	23
101	Improving accuracy of protein contact prediction using balanced network deconvolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 485-496.	2.6	22
102	Underestimation-Assisted Global-Local Cooperative Differential Evolution and the Application to Protein Structure Prediction. <i>IEEE Transactions on Evolutionary Computation</i> , 2019, 24, 1-1.	10.0	22
103	MMpred: a distance-assisted multimodal conformation sampling for <i>de novo</i> protein structure prediction. <i>Bioinformatics</i> , 2021, 37, 4350-4356.	4.1	22
104	Artificial intelligence-based multi-objective optimization protocol for protein structure refinement. <i>Bioinformatics</i> , 2020, 36, 437-448.	4.1	21
105	Endoplasmic reticulum-associated degradation is required for nephrin maturation and kidney glomerular filtration function. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	21
106	Mechanism for DPY30 and ASH2L intrinsically disordered regions to modulate the MLL/SET1 activity on chromatin. <i>Nature Communications</i> , 2021, 12, 2953.	12.8	21
107	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.	3.7	20
108	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.	4.2	19

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109	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.	4.2	19
110	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.	4.1	19
111	Landscape of variable domain of heavy-chain-only antibody repertoire from alpaca. <i>Immunology</i> , 2020, 161, 53-65.	4.4	17
112	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, .	2.3	17
113	LOMETS3: integrating deep learning and profile alignment for advanced protein template recognition and function annotation. <i>Nucleic Acids Research</i> , 2022, 50, W454-W464.	14.5	17
114	Structure and Location of the Regulatory β^2 Subunits in the $(\beta^1\beta^2\beta^3)^4$ Phosphorylase Kinase Complex. <i>Journal of Biological Chemistry</i> , 2012, 287, 36651-36661.	3.4	16
115	Changing the Apoptosis Pathway through Evolutionary Protein Design. <i>Journal of Molecular Biology</i> , 2019, 431, 825-841.	4.2	16
116	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.	5.4	15
117	ADDRESS: A Database of Disease-associated Human Variants Incorporating Protein Structure and Folding Stabilities. <i>Journal of Molecular Biology</i> , 2021, 433, 166840.	4.2	15
118	DEMO2: Assemble multi-domain protein structures by coupling analogous template alignments with deep-learning inter-domain restraint prediction. <i>Nucleic Acids Research</i> , 2022, 50, W235-W245.	14.5	15
119	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. <i>Journal of Proteome Research</i> , 2015, 14, 3750-3761.	3.7	13
120	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, .	7.1	12
121	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	11
122	Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons. <i>Bioinformatics</i> , 2020, 36, 4383-4388.	4.1	10
123	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, 7060.	4.1	10
124	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.	2.8	9
125	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, 616-628.	2.3	9
126	Integrating Multimeric Threading With High-throughput Experiments for Structural Interactome of <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2021, 433, 166944.	4.2	9

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127	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. <i>IScience</i> , 2022, 25, 104425.	4.1	7
128	Approaches to <i>ab initio</i> molecular replacement of α -helical transmembrane proteins. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 985-996.	2.3	6
129	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.	2.6	4
130	Protein structural features predict responsiveness to pharmacological chaperone treatment for three lysosomal storage disorders. <i>PLoS Computational Biology</i> , 2021, 17, e1009370.	3.2	4
131	The structure of the large regulatory α subunit of phosphorylase kinase examined by modeling and hydrogen-deuterium exchange. <i>Protein Science</i> , 2018, 27, 472-484.	7.6	3
132	RTL8 promotes nuclear localization of UBQLN2 to subnuclear compartments associated with protein quality control. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 176.	5.4	3
133	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.	2.3	2
134	Function Prediction for G Protein-Coupled Receptors through Text Mining and Induction Matrix Completion. <i>ACS Omega</i> , 2019, 4, 3045-3054.	3.5	2
135	Accurate flexible refinement for atomic-level protein structure using cryo-EM density maps and deep learning. <i>Briefings in Bioinformatics</i> , 2022, , .	6.5	2