Yang Zhang

List of Publications by Citations

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	I-TASSER: a unified platform for automated protein structure and function prediction. *Nature Protocols*, **2010**, 5, 725-38	18.8	4448
139	I-TASSER server for protein 3D structure prediction. *BMC Bioinformatics*, **2008**, 9, 40	3.6	3560
138	The I-TASSER Suite: protein structure and function prediction. *Nature Methods*, **2015**, 12, 7-8	21.6	3430
137	TM-align: a protein structure alignment algorithm based on the TM-score. *Nucleic Acids Research*, **2005**, 33, 2302-9	20.1	1777
136	Scoring function for automated assessment of protein structure template quality. *Proteins: Structure, Function and Bioinformatics*, **2004**, 57, 702-10	4.2	1196
135	I-TASSER server: new development for protein structure and function predictions. *Nucleic Acids Research*, **2015**, 43, W174-81	20.1	1059
134	LOMETS: a local meta-threading-server for protein structure prediction. *Nucleic Acids Research*, **2007**, 35, 3375-82	20.1	626
133	Ab initio protein structure assembly using continuous structure fragments and optimized knowledge-based force field. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 1715-35	4.2	607
132	Improving the physical realism and structural accuracy of protein models by a two-step atomic-level energy minimization. *Biophysical Journal*, **2011**, 101, 2525-34	2.9	600
131	Protein-ligand binding site recognition using complementary binding-specific substructure comparison and sequence profile alignment. *Bioinformatics*, **2013**, 29, 2588-95	7.2	483
130	How significant is a protein structure similarity with TM-score = 0.5?. *Bioinformatics*, **2010**, 26, 889-95	7.2	455
129	COFACTOR: an accurate comparative algorithm for structure-based protein function annotation. *Nucleic Acids Research*, **2012**, 40, W471-7	20.1	448
128	Progress and challenges in protein structure prediction. *Current Opinion in Structural Biology*, **2008**, 18, 342-8	8.1	382
127	Ab initio modeling of small proteins by iterative TASSER simulations. *BMC Biology*, **2007**, 5, 17	7.3	378
126	Template-based modeling and free modeling by I-TASSER in CASP7. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 108-17	4.2	368
125	BioLiP: a semi-manually curated database for biologically relevant ligand-protein interactions. *Nucleic Acids Research*, **2013**, 41, D1096-103	20.1	348
124	I-TASSER: fully automated protein structure prediction in CASP8. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 100-13	4.2	326

123	SPICKER: a clustering approach to identify near-native protein folds. *Journal of Computational Chemistry*, **2004**, 25, 865-71	3.5	326
122	MUSTER: Improving protein sequence profile-profile alignments by using multiple sources of structure information. *Proteins: Structure, Function and Bioinformatics*, **2008**, 72, 547-56	4.2	301
121	Automated structure prediction of weakly homologous proteins on a genomic scale. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 7594-9	11.5	295
120	Atomic-level protein structure refinement using fragment-guided molecular dynamics conformation sampling. *Structure*, **2011**, 19, 1784-95	5.2	243
119	COFACTOR: improved protein function prediction by combining structure, sequence and protein-protein interaction information. *Nucleic Acids Research*, **2017**, 45, W291-W299	20.1	235
118	The protein structure prediction problem could be solved using the current PDB library. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 1029-34	11.5	235
117	TOUCHSTONE II: a new approach to ab initio protein structure prediction. *Biophysical Journal*, **2003**, 85, 1145-64	2.9	223
116	Protein structure prediction: when is it useful?. *Current Opinion in Structural Biology*, **2009**, 19, 145-55	8.1	212
115	STRUM: structure-based prediction of protein stability changes upon single-point mutation. *Bioinformatics*, **2016**, 32, 2936-46	7.2	190
114	A novel side-chain orientation dependent potential derived from random-walk reference state for protein fold selection and structure prediction. *PLoS ONE*, **2010**, 5, e15386	3.7	172
113	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. *Journal of Proteome Research*, **2020**, 19, 1351-1360	5.6	166
112	Toward optimal fragment generations for ab initio protein structure assembly. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 229-39	4.2	156
111	Development and large scale benchmark testing of the PROSPECTOR_3 threading algorithm. *Proteins: Structure, Function and Bioinformatics*, **2004**, 56, 502-18	4.2	137
110	A comprehensive assessment of sequence-based and template-based methods for protein contact prediction. *Bioinformatics*, **2008**, 24, 924-31	7.2	136
109	A comparative assessment and analysis of 20 representative sequence alignment methods for protein structure prediction. *Scientific Reports*, **2013**, 3, 2619	4.9	128
108	GPCR-I-TASSER: A Hybrid Approach to G Protein-Coupled Receptor Structure Modeling and the Application to the Human Genome. *Structure*, **2015**, 23, 1538-1549	5.2	121
107	Local energy landscape flattening: parallel hyperbolic Monte Carlo sampling of protein folding. *Proteins: Structure, Function and Bioinformatics*, **2002**, 48, 192-201	4.2	118
106	Automated protein structure modeling in CASP9 by I-TASSER pipeline combined with QUARK-based ab initio folding and FG-MD-based structure refinement. *Proteins: Structure, Function and Bioinformatics*, **2011**, 79 Suppl 10, 147-60	4.2	111

105	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, **2019**, 20, 244	18.3	111
104	Deep-learning contact-map guided protein structure prediction in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1149-1164	4.2	108
103	REMO: A new protocol to refine full atomic protein models from C-alpha traces by optimizing hydrogen-bonding networks. *Proteins: Structure, Function and Bioinformatics*, **2009**, 76, 665-76	4.2	97
102	Predicting the Effect of Mutations on Protein-Protein Binding Interactions through Structure-Based Interface Profiles. *PLoS Computational Biology*, **2015**, 11, e1004494	5	95
101	Interplay of I-TASSER and QUARK for template-based and ab initio protein structure prediction in CASP10. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82 Suppl 2, 175-87	4.2	91
100	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. *Bioinformatics*, **2019**, 35, 4647-4655	7.2	88
99	3DRobot: automated generation of diverse and well-packed protein structure decoys. *Bioinformatics*, **2016**, 32, 378-87	7.2	87
98	DockRMSD: an open-source tool for atom mapping and RMSD calculation of symmetric molecules through graph isomorphism. *Journal of Cheminformatics*, **2019**, 11, 40	8.6	81
97	Recognizing protein-ligand binding sites by global structural alignment and local geometry refinement. *Structure*, **2012**, 20, 987-97	5.2	80
96	COACH-D: improved protein-ligand binding sites prediction with refined ligand-binding poses through molecular docking. *Nucleic Acids Research*, **2018**, 46, W438-W442	20.1	77
95	ResQ: An Approach to Unified Estimation of B-Factor and Residue-Specific Error in Protein Structure Prediction. *Journal of Molecular Biology*, **2016**, 428, 693-701	6.5	76
94	LOMETS2: improved meta-threading server for fold-recognition and structure-based function annotation for distant-homology proteins. *Nucleic Acids Research*, **2019**, 47, W429-W436	20.1	76
93	MM-align: a quick algorithm for aligning multiple-chain protein complex structures using iterative dynamic programming. *Nucleic Acids Research*, **2009**, 37, e83	20.1	70
92	BindProfX: Assessing Mutation-Induced Binding Affinity Change by Protein Interface Profiles with Pseudo-Counts. *Journal of Molecular Biology*, **2017**, 429, 426-434	6.5	65
91	BSP-SLIM: a blind low-resolution ligand-protein docking approach using predicted protein structures. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 93-110	4.2	65
90	Ensembling multiple raw coevolutionary features with deep residual neural networks for contact-map prediction in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1082-1091	4.2	63
89	DeepMSA: constructing deep multiple sequence alignment to improve contact prediction and fold-recognition for distant-homology proteins. *Bioinformatics*, **2020**, 36, 2105-2112	7.2	60
88	Template-based and free modeling of I-TASSER and QUARK pipelines using predicted contact maps in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 136-151	4.2	58

87	ThreaDom: extracting protein domain boundary information from multiple threading alignments. *Bioinformatics*, **2013**, 29, i247-56	7.2	56
86	Recognizing metal and acid radical ion-binding sites by integrating ab initio modeling with template-based transferals. *Bioinformatics*, **2016**, 32, 3260-3269	7.2	56
85	Improving protein structure prediction using multiple sequence-based contact predictions. *Structure*, **2011**, 19, 1182-91	5.2	55
84	ANGLOR: a composite machine-learning algorithm for protein backbone torsion angle prediction. *PLoS ONE*, **2008**, 3, e3400	3.7	55
83	design of protein peptides to block association of the SARS-CoV-2 spike protein with human ACE2. *Aging*, **2020**, 12, 11263-11276	5.6	54
82	NeBcon: protein contact map prediction using neural network training coupled with naïve Bayes classifiers. *Bioinformatics*, **2017**, 33, 2296-2306	7.2	52
81	Mapping monomeric threading to protein-protein structure prediction. *Journal of Chemical Information and Modeling*, **2013**, 53, 717-25	6.1	49
80	Effects of SARS-CoV-2 mutations on protein structures and intraviral protein-protein interactions. *Journal of Medical Virology*, **2021**, 93, 2132-2140	19.7	48
79	Integration of QUARK and I-TASSER for Ab Initio Protein Structure Prediction in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 76-86	4.2	47
78	Template-based protein structure prediction in CASP11 and retrospect of I-TASSER in the last decade. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 233-46	4.2	42
77	Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. *Cell Reports Methods*, **2021**, 1,		40
76	An evolution-based approach to De Novo protein design and case study on Mycobacterium tuberculosis. *PLoS Computational Biology*, **2013**, 9, e1003298	5	39
75	EvoDesign: De novo protein design based on structural and evolutionary profiles. *Nucleic Acids Research*, **2013**, 41, W273-80	20.1	36
74	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. *Future Generation Computer Systems*, **2019**, 99, 73-85	7.5	35
73	EvoDesign: Designing Protein-Protein Binding Interactions Using Evolutionary Interface Profiles in Conjunction with an Optimized Physical Energy Function. *Journal of Molecular Biology*, **2019**, 431, 2467-2476	6.5	35
72	Ab Initio structure prediction for Escherichia coli: towards genome-wide protein structure modeling and fold assignment. *Scientific Reports*, **2013**, 3, 1895	4.9	34
71	EvoEF2: accurate and fast energy function for computational protein design. *Bioinformatics*, **2020**, 36, 1135-1142	7.2	33
70	MetaGO: Predicting Gene Ontology of Non-homologous Proteins Through Low-Resolution Protein Structure Prediction and Protein-Protein Network Mapping. *Journal of Molecular Biology*, **2018**, 430, 2256-2265	6.5	32

69	Computational protein design and large-scale assessment by I-TASSER structure assembly simulations. *Journal of Molecular Biology*, **2011**, 407, 764-76	6.5	32
68	I-TASSER-MR: automated molecular replacement for distant-homology proteins using iterative fragment assembly and progressive sequence truncation. *Nucleic Acids Research*, **2017**, 45, W429-W434	20.1	31
67	Assembling multidomain protein structures through analogous global structural alignments. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 15930-15938	11.5	30
66	ATPbind: Accurate Protein-ATP Binding Site Prediction by Combining Sequence-Profiling and Structure-Based Comparisons. *Journal of Chemical Information and Modeling*, **2018**, 58, 501-510	6.1	28
65	Improving protein template recognition by using small-angle x-ray scattering profiles. *Biophysical Journal*, **2011**, 101, 2770-81	2.9	28
64	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. *Bioinformatics*, **2018**, 34, 2209-2218	7.2	25
63	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. *PLoS Computational Biology*, **2019**, 15, e1007411	5	25
62	Potential of Three Ethnomedicinal Plants as Antisickling Agents. *Molecular Pharmaceutics*, **2017**, 14, 172-182	5.1	22
61	Exploring the speed and performance of molecular replacement with AMPLE using QUARK ab initio protein models. *Acta Crystallographica Section D: Biological Crystallography*, **2015**, 71, 338-43		21
60	SSIPe: accurately estimating protein-protein binding affinity change upon mutations using evolutionary profiles in combination with an optimized physical energy function. *Bioinformatics*, **2020**, 36, 2429-2437	7.2	21
59	LabCaS: labeling calpain substrate cleavage sites from amino acid sequence using conditional random fields. *Proteins: Structure, Function and Bioinformatics*, **2013**, 81, 622-34	4.2	20
58	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks. *PLoS Computational Biology*, **2021**, 17, e1008865	5	20
57	Structure and Protein Interaction-Based Gene Ontology Annotations Reveal Likely Functions of Uncharacterized Proteins on Human Chromosome 17. *Journal of Proteome Research*, **2018**, 17, 4186-4196	5.6	20
56	ThreaDomEx: a unified platform for predicting continuous and discontinuous protein domains by multiple-threading and segment assembly. *Nucleic Acids Research*, **2017**, 45, W400-W407	20.1	19
55	Improving accuracy of protein contact prediction using balanced network deconvolution. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 485-96	4.2	18
54	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. *Genome Biology*, **2019**, 20, 229	18.3	17
53	FASPR: an open-source tool for fast and accurate protein side-chain packing. *Bioinformatics*, **2020**, 36, 3758-3765	7.2	16
52	Deep learning techniques have significantly impacted protein structure prediction and protein design. *Current Opinion in Structural Biology*, **2021**, 68, 194-207	8.1	16

51	FUpred: detecting protein domains through deep-learning-based contact map prediction. *Bioinformatics*, **2020**, 36, 3749-3757	7.2	15
50	Identifying the Zoonotic Origin of SARS-CoV-2 by Modeling the Binding Affinity between the Spike Receptor-Binding Domain and Host ACE2. *Journal of Proteome Research*, **2020**, 19, 4844-4856	5.6	15
49	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
48	Structure and location of the regulatory □subunits in the (⍰4 phosphorylase kinase complex. *Journal of Biological Chemistry*, **2012**, 287, 36651-61	5.4	13
47	Underestimation-Assisted Global-Local Cooperative Differential Evolution and the Application to Protein Structure Prediction. *IEEE Transactions on Evolutionary Computation*, **2020**, 24, 536-550	15.6	12
46	EDock: blind protein-ligand docking by replica-exchange monte carlo simulation. *Journal of Cheminformatics*, **2020**, 12, 37	8.6	12
45	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018-2019 Additions to neXtProt and the CAFA3 Challenge. *Journal of Proteome Research*, **2019**, 18, 4154-4166	5.6	12
44	Changing the Apoptosis Pathway through Evolutionary Protein Design. *Journal of Molecular Biology*, **2019**, 431, 825-841	6.5	12
43	Artificial intelligence-based multi-objective optimization protocol for protein structure refinement. *Bioinformatics*, **2020**, 36, 437-448	7.2	12
42	Toward the solution of the protein structure prediction problem. *Journal of Biological Chemistry*, **2021**, 297, 100870	5.4	12
41	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. *Journal of Proteome Research*, **2015**, 14, 3750-61	5.6	11
40	Computational Design of Peptides to Block Binding of the SARS-CoV-2 Spike Protein to Human ACE2		11
39	Crystal structure of designed PX domain from cytokine-independent survival kinase and implications on evolution-based protein engineering. *Journal of Structural Biology*, **2015**, 191, 197-206	3.4	9
38	CGLFold: a contact-assisted de novo protein structure prediction using global exploration and loop perturbation sampling algorithm. *Bioinformatics*, **2020**, 36, 2443-2450	7.2	9
37	Using iterative fragment assembly and progressive sequence truncation to facilitate phasing and crystal structure determination of distantly related proteins. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 616-28	5.5	9
36	The Human DNA Mismatch Repair Protein MSH3 Contains Nuclear Localization and Export Signals That Enable Nuclear-Cytosolic Shuttling in Response to Inflammation. *Molecular and Cellular Biology*, **2020**, 40,	4.8	9
35	Computational design of SARS-CoV-2 spike glycoproteins to increase immunogenicity by T cell epitope engineering. *Computational and Structural Biotechnology Journal*, **2021**, 19, 518-529	6.8	9
34	Protein structure prediction using deep learning distance and hydrogen-bonding restraints in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1734-1751	4.2	9

33	A New Protocol for Atomic-Level Protein Structure Modeling and Refinement Using Low-to-Medium Resolution Cryo-EM Density Maps. *Journal of Molecular Biology*, **2020**, 432, 5365-5377	6.5	8
32	DAMpred: Recognizing Disease-Associated nsSNPs through Bayes-Guided Neural-Network Model Built on Low-Resolution Structure Prediction of Proteins and Protein-Protein Interactions. *Journal of Molecular Biology*, **2019**, 431, 2449-2459	6.5	7
31	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
30	Functions of Essential Genes and a Scale-Free Protein Interaction Network Revealed by Structure-Based Function and Interaction Prediction for a Minimal Genome. *Journal of Proteome Research*, **2021**, 20, 1178-1189	5.6	7
29	Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons. *Bioinformatics*, **2020**, 36, 4383-4388	7.2	6
28	Virtual Screening of Human Class-A GPCRs Using Ligand Profiles Built on Multiple Ligand-Receptor Interactions. *Journal of Molecular Biology*, **2020**, 432, 4872-4890	6.5	6
27	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. *Nature Communications*, **2021**, 12, 5011	17.4	6
26	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. *Briefings in Bioinformatics*, **2021**, 22,	13.4	5
25	Toward the Accuracy and Speed of Protein Side-Chain Packing: A Systematic Study on Rotamer Libraries. *Journal of Chemical Information and Modeling*, **2020**, 60, 410-420	6.1	5
24	Protein inter-residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1911-1921	4.2	4
23	Landscape of variable domain of heavy-chain-only antibody repertoire from alpaca. *Immunology*, **2020**, 161, 53-65	7.8	3
22	Approaches to ab initio molecular replacement of α-helical transmembrane proteins. *Acta Crystallographica Section D: Structural Biology*, **2017**, 73, 985-996	5.5	3
21	Rational Design of SARS-CoV-2 Spike Glycoproteins To Increase Immunogenicity By T Cell Epitope Engineering **2020**,		3
20	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks		3
19	Endoplasmic reticulum-associated degradation is required for nephrin maturation and kidney glomerular filtration function. *Journal of Clinical Investigation*, **2021**, 131,	15.9	3
18	ADDRESS: A Database of Disease-associated Human Variants Incorporating Protein Structure and Folding Stabilities. *Journal of Molecular Biology*, **2021**, 433, 166840	6.5	3
17	Integrating Multimeric Threading With High-throughput Experiments for Structural Interactome of Escherichia coli. *Journal of Molecular Biology*, **2021**, 433, 166944	6.5	3
16	Evolution of a chordate-specific mechanism for myoblast fusion		3

15	Decoding the link of microbiome niches with homologous sequences enables accurately targeted protein structure prediction. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	2
14	Progressive and accurate assembly of multi-domain protein structures from cryo-EM density maps **2020**,		2
13	Mechanism for DPY30 and ASH2L intrinsically disordered regions to modulate the MLL/SET1 activity on chromatin. *Nature Communications*, **2021**, 12, 2953	17.4	2
12	Identification of 13 Guanidinobenzoyl- or Aminidinobenzoyl-Containing Drugs to Potentially Inhibit TMPRSS2 for COVID-19 Treatment. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	2
11	MMpred: a distance-assisted multimodal conformation sampling for de novo protein structure prediction. *Bioinformatics*, **2021**,	7.2	2
10	MR-REX: molecular replacement by cooperative conformational search and occupancy optimization on low-accuracy protein models. *Acta Crystallographica Section D: Structural Biology*, **2018**, 74, 606-620	5.5	1
9	Effects of SARS-CoV-2 Mutations on Protein Structures and Intraviral Protein-Protein Interactions		1
8	Function Prediction for G Protein-Coupled Receptors through Text Mining and Induction Matrix Completion. *ACS Omega*, **2019**, 4, 3045-3054	3.9	1
7	Fitting Low-Resolution Protein Structures into Cryo-EM Density Maps by Multiobjective Optimization of Global and Local Correlations. *Journal of Physical Chemistry B*, **2021**, 125, 528-538	3.4	1
6	The structure of the large regulatory β subunit of phosphorylase kinase examined by modeling and hydrogen-deuterium exchange. *Protein Science*, **2018**, 27, 472-484	6.3	1
5	CR-I-TASSER: assemble protein structures from cryo-EM density maps using deep convolutional neural networks.. *Nature Methods*, **2022**, 19, 195-204	21.6	0
4	Protein structural features predict responsiveness to pharmacological chaperone treatment for three lysosomal storage disorders. *PLoS Computational Biology*, **2021**, 17, e1009370	5	0
3	Progressive assembly of multi-domain protein structures from cryo-EM density maps. *Nature Computational Science*, **2022**, 2, 265-275		0
2	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. *IScience*, **2022**, 25, 104425	6.1	0
1	RTL8 promotes nuclear localization of UBQLN2 to subnuclear compartments associated with protein quality control.. *Cellular and Molecular Life Sciences*, **2022**, 79, 176	10.3	