Chengxin Zhang

List of Publications by Year
in descending order

51	4,004	218677	189892
papers	citations	26 h-index	50 g-index

62	62	62	5389
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	COFACTOR: improved protein function prediction by combining structure, sequence and proteinâ€“protein interaction information. Nucleic Acids Research, 2017, 45, W291-W299.	14.5	424
2	Porous hypercrosslinked polymer-TiO2-graphene composite photocatalysts for visible-light-driven CO2 conversion. Nature Communications, 2019, 10, 676.	12.8	278
3	Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. Cell Reports Methods, 2021, 1, 100014.	2.9	272
4	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
5	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.	3.7	242
6	A novel metalporphyrin-based microporous organic polymer with high CO₂ uptake and efficient chemical conversion of CO₂ under ambient conditions. Journal of Materials Chemistry A, 2017, 5, 1509-1515.	10.3	186
7	PyMod 2.0: improvements in protein sequence-structure analysis and homology modeling within PyMOL. Bioinformatics, 2017, 33, 444-446.	4.1	183
8	Deepâ€learning contactâ€map guided protein structure prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1149-1164.	2.6	180
9	Controlling Monomer Feeding Rate to Achieve Highly Crystalline Covalent Triazine Frameworks. Advanced Materials, 2019, 31, e1807865.	21.0	158
10	DeepMSA: constructing deep multiple sequence alignment to improve contact prediction and fold-recognition for distant-homology proteins. Bioinformatics, 2020, 36, 2105-2112.	4.1	147
11	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. Bioinformatics, 2019, 35, 4647-4655.	4.1	142
12	Layered microporous polymers by solvent knitting method. Science Advances, 2017, 3, e1602610.	10.3	135
13	LOMETS2: improved meta-threading server for fold-recognition and structure-based function annotation for distant-homology proteins. Nucleic Acids Research, 2019, 47, W429-W436.	14.5	118
14	BindProfX: Assessing Mutation-Induced Binding Affinity Change by Protein Interface Profiles with Pseudo-Counts. Journal of Molecular Biology, 2017, 429, 426-434.	4.2	107
15	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.	7.1	104
16	Ensembling multiple raw coevolutionary features with deep residual neural networks for contactâ€map prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1082-1091.	2.6	96
17	Templateâ€based and free modeling of Iâ€TASSER and QUARK pipelines using predicted contact maps in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 136-151.	2.6	86
18	Novel POSS-based organicâ€“inorganic hybrid porous materials by low cost strategies. Journal of Materials Chemistry A, 2015, 3, 6542-6548.	10.3	81

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19	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. Future Generation Computer Systems, 2019, 99, 73-85.	7.5	80
20	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks. PLoS Computational Biology, 2021, 17, e1008865.	3.2	70
21	MetaGO: Predicting Gene Ontology of Non-homologous Proteins Through Low-Resolution Protein Structure Prediction and Proteinâ€“Protein Network Mapping. Journal of Molecular Biology, 2018, 430, 2256-2265.	4.2	58
22	Protein structure prediction using deep learning distance and hydrogenâ€bonding restraints in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1734-1751.	2.6	53
23	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. PLoS Computational Biology, 2019, 15, e1007411.	3.2	45
24	RNA-align: quick and accurate alignment of RNA 3D structures based on size-independent TM-scoreRNA. Bioinformatics, 2019, 35, 4459-4461.	4.1	44
25	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. Nature Communications, 2021, 12, 5011.	12.8	44
26	EDIL3 deficiency ameliorates adverse cardiac remodelling by neutrophil extracellular traps (NET)-mediated macrophage polarization. Cardiovascular Research, 2022, 118, 2179-2195.	3.8	29
27	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. Genome Biology, 2019, 20, 229.	8.8	28
28	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.	3.7	27
29	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.	3.7	27
30	Generation of a live attenuated influenza A vaccine by proteolysis targeting. Nature Biotechnology, 2022, 40, 1370-1377.	17.5	26
31	Progressive assembly of multi-domain protein structures from cryo-EM density maps. Nature Computational Science, 2022, 2, 265-275.	8.0	25
32	hiPSC Modeling of Lineage-Specific Smooth Muscle Cell Defects Caused by TGFBR1 ^{A230T} Variant, and Its Therapeutic Implications for Loeys-Dietz Syndrome. Circulation, 2021, 144, 1145-1159.	1.6	24
33	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.	3.7	23
34	Protein interâ€residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1911-1921.	2.6	23
35	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018â€“2019 Additions to neXtProt and the CAFA3 Challenge. Journal of Proteome Research, 2019, 18, 4154-4166.	3.7	20
36	ADDRESS: A Database of Disease-associated Human Variants Incorporating Protein Structure and Folding Stabilities. Journal of Molecular Biology, 2021, 433, 166840.	4.2	15

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37	Synthesis of MWCNT-Based Hyper-Cross-Linked Polymers with Thickness-Tunable Organic Porous Layers. ACS Macro Letters, 2019, 8, 403-408.	4.8	14
38	Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons. Bioinformatics, 2020, 36, 4383-4388.	4.1	10
39	Novel fullerene-based porous materials constructed by a solvent knitting strategy. Chemical Communications, 2017, 53, 12758-12761.	4.1	9
40	Integrating Multimeric Threading With High-throughput Experiments for Structural Interactome of Escherichia coli. Journal of Molecular Biology, 2021, 433, 166944.	4.2	9
41	CSSR: assignment of secondary structure to coarse-grained RNA tertiary structures. Acta Crystallographica Section D: Structural Biology, 2022, 78, 466-471.	2.3	7
42	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. IScience, 2022, 25, 104425.	4.1	7
43	Approaches toab initiomolecular replacement of Î±-helical transmembrane proteins. Acta Crystallographica Section D: Structural Biology, 2017, 73, 985-996.	2.3	6
44	GPU-I-TASSER: a GPU accelerated I-TASSER protein structure prediction tool. Bioinformatics, 2022, 38, 1754-1755.	4.1	6
45	Soluble CD13 induces inflammatory arthritis by activating the bradykinin receptor B1. Journal of Clinical Investigation, 2022, 132, .	8.2	6
46	Rational Design of Adenylate Kinase Thermostability through Coevolution and Sequence Divergence Analysis. International Journal of Molecular Sciences, 2021, 22, 2768.	4.1	5
47	Unprecedented Processable Hypercrosslinked Polymers with Controlled Knitting. Macromolecular Rapid Communications, 2022, 43, e2100449.	3.9	4
48	TripletGO: Integrating Transcript Expression Profiles with Protein Homology Inferences for Gene Function Prediction. Genomics, Proteomics and Bioinformatics, 2022, 20, 1013-1027.	6.9	4
49	RTL8 promotes nuclear localization of UBQLN2 to subnuclear compartments associated with protein quality control. Cellular and Molecular Life Sciences, 2022, 79, 176.	5.4	3
50	Function Prediction for G Protein-Coupled Receptors through Text Mining and Induction Matrix Completion. ACS Omega, 2019, 4, 3045-3054.	3.5	2
51	AMIGOS III: pseudo-torsion angle visualization and motif-based structure comparison of nucleic acids. Bioinformatics, 2022, 38, 2937-2939.	4.1	1