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	EDIL3 deficiency ameliorates adverse cardiac remodelling by neutrophil extracellular traps (NET)-mediated macrophage polarization. Cardiovascular Research, 2022, 118, 2179-2195.	3.8	29
2	Unprecedented Processable Hypercrosslinked Polymers with Controlled Knitting. Macromolecular Rapid Communications, 2022, 43, e2100449.	3.9	4
3	GPU-I-TASSER: a GPU accelerated I-TASSER protein structure prediction tool. Bioinformatics, 2022, 38, 1754-1755.	4.1	6
4	CSSR: assignment of secondary structure to coarse-grained RNA tertiary structures. Acta Crystallographica Section D: Structural Biology, 2022, 78, 466-471.	2.3	7
5	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
6	AMIGOS III: pseudo-torsion angle visualization and motif-based structure comparison of nucleic acids. Bioinformatics, 2022, 38, 2937-2939.	4.1	1
7	Soluble CD13 induces inflammatory arthritis by activating the bradykinin receptor B1. Journal of Clinical Investigation, 2022, 132, .	8.2	6
8	TripletGO: Integrating Transcript Expression Profiles with Protein Homology Inferences for Gene Function Prediction. Genomics, Proteomics and Bioinformatics, 2022, 20, 1013-1027.	6.9	4
9	Progressive assembly of multi-domain protein structures from cryo-EM density maps. Nature Computational Science, 2022, 2, 265-275.	8.0	25
10	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. IScience, 2022, 25, 104425.	4.1	7
11	Generation of a live attenuated influenza A vaccine by proteolysis targeting. Nature Biotechnology, 2022, 40, 1370-1377.	17.5	26
12	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
13	Rational Design of Adenylate Kinase Thermostability through Coevolution and Sequence Divergence Analysis. International Journal of Molecular Sciences, 2021, 22, 2768.	4.1	5
14	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
15	ADDRESS: A Database of Disease-associated Human Variants Incorporating Protein Structure and Folding Stabilities. Journal of Molecular Biology, 2021, 433, 166840.	4.2	15
16	Integrating Multimeric Threading With High-throughput Experiments for Structural Interactome of Escherichia coli. Journal of Molecular Biology, 2021, 433, 166944.	4.2	9
17	Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. Cell Reports Methods, 2021, 1, 100014.	2.9	272
18	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

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19	Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. Nature Communications, 2021, 12, 5011.	12.8	44
20	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
21	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
22	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
23	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
24	Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons. Bioinformatics, 2020, 36, 4383-4388.	4.1	10
25	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
26	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
27	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
28	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
29	Deepâ€learning contactâ€map guided protein structure prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1149-1164.	2.6	180
30	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
31	Detecting distant-homology protein structures by aligning deep neural-network based contact maps. PLoS Computational Biology, 2019, 15, e1007411.	3.2	45
32	Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. Genome Biology, 2019, 20, 229.	8.8	28
33	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. Bioinformatics, 2019, 35, 4647-4655.	4.1	142
34	I-TASSER gateway: A protein structure and function prediction server powered by XSEDE. Future Generation Computer Systems, 2019, 99, 73-85.	7.5	80
35	RNA-align: quick and accurate alignment of RNA 3D structures based on size-independent TM-scoreRNA. Bioinformatics, 2019, 35, 4459-4461.	4.1	44
36	Synthesis of MWCNT-Based Hyper-Cross-Linked Polymers with Thickness-Tunable Organic Porous Layers. ACS Macro Letters, 2019, 8, 403-408.	4.8	14

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37	Controlling Monomer Feeding Rate to Achieve Highly Crystalline Covalent Triazine Frameworks. Advanced Materials, 2019, 31, e1807865.	21.0	158
38	Porous hypercrosslinked polymer-TiO2-graphene composite photocatalysts for visible-light-driven CO2 conversion. Nature Communications, 2019, 10, 676.	12.8	278
39	Function Prediction for G Protein-Coupled Receptors through Text Mining and Induction Matrix Completion. ACS Omega, 2019, 4, 3045-3054.	3.5	2
40	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
41	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
42	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
43	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
44	PyMod 2.0: improvements in protein sequence-structure analysis and homology modeling within PyMOL. Bioinformatics, 2017, 33, 444-446.	4.1	183
45	COFACTOR: improved protein function prediction by combining structure, sequence and proteinâ€“protein interaction information. Nucleic Acids Research, 2017, 45, W291-W299.	14.5	424
46	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
47	Layered microporous polymers by solvent knitting method. Science Advances, 2017, 3, e1602610.	10.3	135
48	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
49	Novel fullerene-based porous materials constructed by a solvent knitting strategy. Chemical Communications, 2017, 53, 12758-12761.	4.1	9
50	Approaches toab initiomolecular replacement of Î±-helical transmembrane proteins. Acta Crystallographica Section D: Structural Biology, 2017, 73, 985-996.	2.3	6
51	Novel POSS-based organicâ€“inorganic hybrid porous materials by low cost strategies. Journal of Materials Chemistry A, 2015, 3, 6542-6548.	10.3	81