

Xiao-Gen Zhou

List of Publications by Year in descending order

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516215

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docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	De novo Protein Structure Prediction by Coupling Contact With Distance Profile. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 395-406.	1.9	10
2	DeepUMQA: ultrafast shape recognition-based protein model quality assessment using deep learning. Bioinformatics, 2022, 38, 1895-1903.	1.8	25
3	RTL8 promotes nuclear localization of UBQLN2 to subnuclear compartments associated with protein quality control. Cellular and Molecular Life Sciences, 2022, 79, 176.	2.4	3
4	LOMETS3: integrating deep learning and profile alignment for advanced protein template recognition and function annotation. Nucleic Acids Research, 2022, 50, W454-W464.	6.5	17
5	DEMO2: Assemble multi-domain protein structures by coupling analogous template alignments with deep-learning inter-domain restraint prediction. Nucleic Acids Research, 2022, 50, W235-W245.	6.5	15
6	Progressive assembly of multi-domain protein structures from cryo-EM density maps. Nature Computational Science, 2022, 2, 265-275.	3.8	25
7	Protein Structure Prediction Using Population-Based Algorithm Guided by Information Entropy. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 697-707.	1.9	6
8	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks. PLoS Computational Biology, 2021, 17, e1008865.	1.5	70
9	MMpred: a distance-assisted multimodal conformation sampling for <i>de novo</i> protein structure prediction. Bioinformatics, 2021, 37, 4350-4356.	1.8	22
10	A sequential niche multimodal conformational sampling algorithm for protein structure prediction. Bioinformatics, 2021, 37, 4357-4365.	1.8	11
11	Protein structure prediction using deep learning distance and hydrogen bonding restraints in <i>CASP14</i> . Proteins: Structure, Function and Bioinformatics, 2021, 89, 1734-1751.	1.5	53
12	Protein inter-residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in <i>CASP14</i> . Proteins: Structure, Function and Bioinformatics, 2021, 89, 1911-1921.	1.5	23
13	Distance-guided protein folding based on generalized descent direction. Briefings in Bioinformatics, 2021, 22, .	3.2	3
14	A <i>de novo</i> protein structure prediction by iterative partition sampling, topology adjustment and residue-level distance deviation optimization. Bioinformatics, 2021, 38, 99-107.	1.8	8
15	Multi contact-based folding method for de novo protein structure prediction. Briefings in Bioinformatics, 2021, , .	3.2	0
16	Adaptive Differential Evolution With Information Entropy-Based Mutation Strategy. IEEE Access, 2021, 9, 146783-146796.	2.6	1
17	Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1068-1081.	1.9	29
18	Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 2119-2130.	1.9	3

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19	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.	1.8	36
20	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.	1.8	242
21	FUpred: detecting protein domains through deep-learning-based contact map prediction. <i>Bioinformatics</i> , 2020, 36, 3749-3757.	1.8	44
22	Multi-subpopulation Algorithm with Ensemble Mutation Strategies for Protein Structure Prediction. <i>Communications in Computer and Information Science</i> , 2020, , 255-268.	0.4	0
23	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.	3.3	104
24	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 567-577.	2.2	0
25	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.	7.5	22
26	TargetDBP: Accurate DNA-Binding Protein Prediction via Sequence-based Multi-View Feature Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	28
27	Differential Evolution With Underestimation-Based Multimutation Strategy. <i>IEEE Transactions on Cybernetics</i> , 2019, 49, 1353-1364.	6.2	46
28	Guiding exploration in conformational feature space with Lipschitz underestimation for ab-initio protein structure prediction. <i>Computational Biology and Chemistry</i> , 2018, 73, 105-119.	1.1	4
29	Enhancing Protein Conformational Space Sampling Using Distance Profile-Guided Differential Evolution. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1288-1301.	1.9	35
30	Abstract Convex Underestimation Assisted Multistage Differential Evolution. <i>IEEE Transactions on Cybernetics</i> , 2017, 47, 2730-2741.	6.2	41
31	Conformational Space Sampling Method Using Multi-Subpopulation Differential Evolution for De novo Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2017, 16, 618-633.	2.2	8
32	Differential evolution with multi-stage strategies for global optimization. , 2016, , .		10
33	A population-based conformational optimal algorithm using replica-exchange in ab-initio protein structure prediction. , 2016, , .		2
34	Enhanced differential evolution using local Lipschitz underestimate strategy for computationally expensive optimization problems. <i>Applied Soft Computing Journal</i> , 2016, 48, 169-181.	4.1	17
35	A novel differential evolution algorithm using local abstract convex underestimate strategy for global optimization. <i>Computers and Operations Research</i> , 2016, 75, 132-149.	2.4	27
36	A Novel Method Using Abstract Convex Underestimation in Ab-Initio Protein Structure Prediction for Guiding Search in Conformational Feature Space. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 887-900.	1.9	14

#	ARTICLE	IF	CITATIONS
37	Differential evolution with dynamic niche radius strategy for multimodal optimization. , 2015, , .		5