

Xiao-Gen Zhou

List of Publications by Year in descending order

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37
papers

1,049
citations

516215

16
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476904

29
g-index

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docs citations

49
times ranked

998
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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.	1.5	70
4	Protein structure prediction using deep learning distance and hydrogen bonding restraints in <scp>CASP14</scp>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1734-1751.	1.5	53
5	Differential Evolution With Underestimation-Based Multimutation Strategy. <i>IEEE Transactions on Cybernetics</i> , 2019, 49, 1353-1364.	6.2	46
6	FUpred: detecting protein domains through deep-learning-based contact map prediction. <i>Bioinformatics</i> , 2020, 36, 3749-3757.	1.8	44
7	Abstract Convex Underestimation Assisted Multistage Differential Evolution. <i>IEEE Transactions on Cybernetics</i> , 2017, 47, 2730-2741.	6.2	41
8	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
9	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
10	Secondary Structure and Contact Guided Differential Evolution for Protein Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1068-1081.	1.9	29
11	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
12	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
13	DeepUMQA: ultrafast shape recognition-based protein model quality assessment using deep learning. <i>Bioinformatics</i> , 2022, 38, 1895-1903.	1.8	25
14	Progressive assembly of multi-domain protein structures from cryo-EM density maps. <i>Nature Computational Science</i> , 2022, 2, 265-275.	3.8	25
15	Protein inter-residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in <scp>CASP14</scp>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1911-1921.	1.5	23
16	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
17	MMpred: a distance-assisted multimodal conformation sampling for <i>de novo</i> protein structure prediction. <i>Bioinformatics</i> , 2021, 37, 4350-4356.	1.8	22
18	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

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19	LOMETS3: integrating deep learning and profile alignment for advanced protein template recognition and function annotation. <i>Nucleic Acids Research</i> , 2022, 50, W454-W464.	6.5	17
20	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.	6.5	15
21	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
22	A sequential niche multimodal conformational sampling algorithm for protein structure prediction. <i>Bioinformatics</i> , 2021, 37, 4357-4365.	1.8	11
23	Differential evolution with multi-stage strategies for global optimization. , 2016, , .		10
24	De novo Protein Structure Prediction by Coupling Contact With Distance Profile. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 395-406.	1.9	10
25	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
26	A <i>de novo</i> protein structure prediction by iterative partition sampling, topology adjustment and residue-level distance deviation optimization. <i>Bioinformatics</i> , 2021, 38, 99-107.	1.8	8
27	Protein Structure Prediction Using Population-Based Algorithm Guided by Information Entropy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 697-707.	1.9	6
28	Differential evolution with dynamic niche radius strategy for multimodal optimization. , 2015, , .		5
29	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
30	Two-Stage Distance Feature-based Optimization Algorithm for De novo Protein Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 2119-2130.	1.9	3
31	Distance-guided protein folding based on generalized descent direction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
32	RTL8 promotes nuclear localization of UBQLN2 to subnuclear compartments associated with protein quality control. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, 176.	2.4	3
33	A population-based conformational optimal algorithm using replica-exchange in ab-initio protein structure prediction. , 2016, , .		2
34	Adaptive Differential Evolution With Information Entropy-Based Mutation Strategy. <i>IEEE Access</i> , 2021, 9, 146783-146796.	2.6	1
35	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 567-577.	2.2	0
36	Multi contact-based folding method for de novo protein structure prediction. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	0

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37	Multi-subpopulation Algorithm with Ensemble Mutation Strategies for Protein Structure Prediction. Communications in Computer and Information Science, 2020, , 255-268.	0.4	0