

# Gui-Jun Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

52  
papers

756  
citations

566801

15  
h-index

642321

23  
g-index

61  
all docs

61  
docs citations

61  
times ranked

480  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	ATPdock: a template-based method for ATP-specific protein-ligand docking. <i>Bioinformatics</i> , 2022, 38, 556-558.	1.8	5
3	DeepUMQA: ultrafast shape recognition-based protein model quality assessment using deep learning. <i>Bioinformatics</i> , 2022, 38, 1895-1903.	1.8	25
4	Accurate flexible refinement for atomic-level protein structure using cryo-EM density maps and deep learning. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	2
5	Construct a variable-length fragment library for de novo protein structure prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
6	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
7	Progressive assembly of multi-domain protein structures from cryo-EM density maps. <i>Nature Computational Science</i> , 2022, 2, 265-275.	3.8	25
8	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
9	TargetDBP+: Enhancing the Performance of Identifying DNA-Binding Proteins via Weighted Convolutional Features. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 505-515.	2.5	11
10	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
11	A sequential niche multimodal conformational sampling algorithm for protein structure prediction. <i>Bioinformatics</i> , 2021, 37, 4357-4365.	1.8	11
12	Accurate prediction of protein-ATP binding residues using position-specific frequency matrix. <i>Analytical Biochemistry</i> , 2021, 626, 114241.	1.1	6
13	Distance-guided protein folding based on generalized descent direction. <i>Briefings in Bioinformatics</i> , 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. <i>Bioinformatics</i> , 2021, 38, 99-107.	1.8	8
15	Improved protein relative solvent accessibility prediction using deep multi-view feature learning framework. <i>Analytical Biochemistry</i> , 2021, 631, 114358.	1.1	1
16	Multi contact-based folding method for de novo protein structure prediction. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	0
17	Adaptive Differential Evolution With Information Entropy-Based Mutation Strategy. <i>IEEE Access</i> , 2021, 9, 146783-146796.	2.6	1
18	RDAClone: Deciphering Tumor Heterozygosity through Single-Cell Genomics Data Analysis with Robust Deep Autoencoder. <i>Genes</i> , 2021, 12, 1847.	1.0	2

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	CGLFold: a contact-assisted de novo protein structure prediction using global exploration and loop perturbation sampling algorithm. Bioinformatics, 2020, 36, 2443-2450.	1.8	36
22	An urban commuters' OD hybrid prediction method based on big GPS data. Chaos, 2020, 30, 093128.	1.0	8
23	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. Bioinformatics, 2020, 36, 4217-4219.	1.8	21
24	Identification of ligand-binding residues using protein sequence profile alignment and query-specific support vector machine model. Analytical Biochemistry, 2020, 604, 113799.	1.1	4
25	Multi-subpopulation Algorithm with Ensemble Mutation Strategies for Protein Structure Prediction. Communications in Computer and Information Science, 2020, , 255-268.	0.4	0
26	Analysis of Hospitalizing Behaviors Based on Big Trajectory Data. IEEE Transactions on Computational Social Systems, 2019, 6, 692-701.	3.2	5
27	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.	3.3	104
28	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. IEEE Transactions on Nanobioscience, 2019, 18, 567-577.	2.2	0
29	Underestimation-Assisted Global-Local Cooperative Differential Evolution and the Application to Protein Structure Prediction. IEEE Transactions on Evolutionary Computation, 2019, 24, 1-1.	7.5	22
30	A simultaneous approach for singular optimal control based on partial moving grid. AIChE Journal, 2019, 65, e16584.	1.8	18
31	TargetDBP: Accurate DNA-Binding Protein Prediction via Sequence-based Multi-View Feature Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	28
32	Differential Evolution With Underestimation-Based Multimutation Strategy. IEEE Transactions on Cybernetics, 2019, 49, 1353-1364.	6.2	46
33	Guiding exploration in conformational feature space with Lipschitz underestimation for ab-initio protein structure prediction. Computational Biology and Chemistry, 2018, 73, 105-119.	1.1	4
34	Compression algorithm of road traffic data in time series based on temporal correlation. IET Intelligent Transport Systems, 2018, 12, 177-185.	1.7	9
35	Enhancing Protein Conformational Space Sampling Using Distance Profile-Guided Differential Evolution. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1288-1301.	1.9	35
36	Abstract Convex Underestimation Assisted Multistage Differential Evolution. IEEE Transactions on Cybernetics, 2017, 47, 2730-2741.	6.2	41

#	ARTICLE	IF	CITATIONS
37	Double estimation of distribution guided sampling algorithm for de-novo protein structure prediction. , 2017, , .		1
38	Conformational Space Sampling Method Using Multi-Subpopulation Differential Evolution for De novo Protein Structure Prediction. IEEE Transactions on Nanobioscience, 2017, 16, 618-633.	2.2	8
39	Differential evolution with multi-stage strategies for global optimization. , 2016, , .		10
40	The acquisition approach of Reference sequences of road traffic running characteristics. , 2016, , .		1
41	A population-based conformational optimal algorithm using replica-exchange in ab-initio protein structure prediction. , 2016, , .		2
42	Real-time road traffic states estimation based on kernel-KNN matching of road traffic spatial characteristics. Journal of Central South University, 2016, 23, 2453-2464.	1.2	12
43	Enhanced differential evolution using local Lipschitz underestimate strategy for computationally expensive optimization problems. Applied Soft Computing Journal, 2016, 48, 169-181.	4.1	17
44	A novel differential evolution algorithm using local abstract convex underestimate strategy for global optimization. Computers and Operations Research, 2016, 75, 132-149.	2.4	27
45	A Novel Method Using Abstract Convex Underestimation in Ab-Initio Protein Structure Prediction for Guiding Search in Conformational Feature Space. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 887-900.	1.9	14
46	Differential evolution with dynamic niche radius strategy for multimodal optimization. , 2015, , .		5
47	Delay-dependent $H^{\infty}$ Control for Uncertain 2-D Discrete Systems with State Delay in the Roesser Model. Circuits, Systems, and Signal Processing, 2013, 32, 1097-1112.	1.2	20
48	Efficient and Dynamic Clustering Scheme for Heterogeneous Multi-level Wireless Sensor Networks. Zidonghua Xuebao/Acta Automatica Sinica, 2013, 39, 454-460.	1.5	29
49	A hybrid global optimization algorithm for polypeptide structure determination. , 2012, , .		0
50	Modeling and Implementing Research of Multimodal Transportation Network. , 2009, , .		5
51	A Clustering Based GA for Multimodal Optimization in Uneven Search Space. , 2006, , .		11
52	A New Method for the Binocular Reconstruction of 3D Circle. , 2006, , .		0