

# Gui-Jun Zhang

## List of Publications by Year in descending order

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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	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
2	Differential Evolution With Underestimation-Based Multimutation Strategy. IEEE Transactions on Cybernetics, 2019, 49, 1353-1364.	6.2	46
3	Abstract Convex Underestimation Assisted Multistage Differential Evolution. IEEE Transactions on Cybernetics, 2017, 47, 2730-2741.	6.2	41
4	CGLFold: a contact-assisted <i>de novo</i> protein structure prediction using global exploration and loop perturbation sampling algorithm. Bioinformatics, 2020, 36, 2443-2450.	1.8	36
5	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
6	Efficient and Dynamic Clustering Scheme for Heterogeneous Multi-level Wireless Sensor Networks. Zidonghua Xuebao/Acta Automatica Sinica, 2013, 39, 454-460.	1.5	29
7	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
8	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
9	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
10	DeepUMQA: ultrafast shape recognition-based protein model quality assessment using deep learning. Bioinformatics, 2022, 38, 1895-1903.	1.8	25
11	Progressive assembly of multi-domain protein structures from cryo-EM density maps. Nature Computational Science, 2022, 2, 265-275.	3.8	25
12	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
13	MMpred: a distance-assisted multimodal conformation sampling for <i>de novo</i> protein structure prediction. Bioinformatics, 2021, 37, 4350-4356.	1.8	22
14	scTPA: a web tool for single-cell transcriptome analysis of pathway activation signatures. Bioinformatics, 2020, 36, 4217-4219.	1.8	21
15	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
16	A simultaneous approach for singular optimal control based on partial moving grid. AIChE Journal, 2019, 65, e16584.	1.8	18
17	Enhanced differential evolution using local Lipschitz underestimate strategy for computationally expensive optimization problems. Applied Soft Computing Journal, 2016, 48, 169-181.	4.1	17
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	A Clustering Based GA for Multimodal Optimization in Uneven Search Space. , 2006, , .		11
22	TargetDBP+: Enhancing the Performance of Identifying DNA-Binding Proteins via Weighted Convolutional Features. Journal of Chemical Information and Modeling, 2021, 61, 505-515.	2.5	11
23	A sequential niche multimodal conformational sampling algorithm for protein structure prediction. Bioinformatics, 2021, 37, 4357-4365.	1.8	11
24	Differential evolution with multi-stage strategies for global optimization. , 2016, , .		10
25	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
26	Compression algorithm of road traffic data in time series based on temporal correlation. IET Intelligent Transport Systems, 2018, 12, 177-185.	1.7	9
27	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
28	An urban commutersâ€™ OD hybrid prediction method based on big GPS data. Chaos, 2020, 30, 093128.	1.0	8
29	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
30	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
31	Accurate prediction of protein-ATP binding residues using position-specific frequency matrix. Analytical Biochemistry, 2021, 626, 114241.	1.1	6
32	Modeling and Implementing Research of Multimodal Transportation Network. , 2009, , .		5
33	Differential evolution with dynamic niche radius strategy for multimodal optimization. , 2015, , .		5
34	Analysis of Hospitalizing Behaviors Based on Big Trajectory Data. IEEE Transactions on Computational Social Systems, 2019, 6, 692-701.	3.2	5
35	ATPdock: a template-based method for ATP-specific proteinâ€™ligand docking. Bioinformatics, 2022, 38, 556-558.	1.8	5
36	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

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37	Identification of ligand-binding residues using protein sequence profile alignment and query-specific support vector machine model. <i>Analytical Biochemistry</i> , 2020, 604, 113799.	1.1	4
38	Construct a variable-length fragment library for de novo protein structure prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	4
39	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
40	Distance-guided protein folding based on generalized descent direction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
41	A population-based conformational optimal algorithm using replica-exchange in ab-initio protein structure prediction. , 2016, , .		2
42	RDAClone: Deciphering Tumor Heterozygosity through Single-Cell Genomics Data Analysis with Robust Deep Autoencoder. <i>Genes</i> , 2021, 12, 1847.	1.0	2
43	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
44	The acquisition approach of Reference sequences of road traffic running characteristics. , 2016, , .		1
45	Double estimation of distribution guided sampling algorithm for de-novo protein structure prediction. , 2017, , .		1
46	Improved protein relative solvent accessibility prediction using deep multi-view feature learning framework. <i>Analytical Biochemistry</i> , 2021, 631, 114358.	1.1	1
47	Adaptive Differential Evolution With Information Entropy-Based Mutation Strategy. <i>IEEE Access</i> , 2021, 9, 146783-146796.	2.6	1
48	A New Method for the Binocular Reconstruction of 3D Circle. , 2006, , .		0
49	A hybrid global optimization algorithm for polypeptide structure determination. , 2012, , .		0
50	Loop Enhanced Conformational Resampling Method for Protein Structure Prediction. <i>IEEE Transactions on Nanobioscience</i> , 2019, 18, 567-577.	2.2	0
51	Multi contact-based folding method for de novo protein structure prediction. <i>Briefings in Bioinformatics</i> , 2021, , .	3.2	0
52	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