

Wenzheng Bao

List of Publications by Year in descending order

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papers

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687220

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552653

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46
all docs

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times ranked

592
citing authors

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. Briefings in Bioinformatics, 2022, 23, .	3.2	22
2	Phage_UniR_LGBM: Phage Virion Proteins Classification with UniRep Features and LightGBM Model. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-8.	0.7	30
3	Gene Regulatory Identification Based on the Novel Hybrid Time-Delayed Method. Frontiers in Genetics, 2022, 13, .	1.1	1
4	A survey on proteinâ€“DNA-binding sites in computational biology. Briefings in Functional Genomics, 2022, 21, 357-375.	1.3	11
5	Single_cell_GRN: gene regulatory network identification based on supervised learning method and Single-cell RNA-seq data. BioData Mining, 2022, 15, .	2.2	2
6	An improved image registration and fusion algorithm. Wireless Networks, 2021, 27, 3597-3611.	2.0	1
7	A graph auto-encoder model for miRNA-disease associations prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	63
8	Prediction of Protein-Protein Interaction Based on Deep Learning Feature Representation and Random Forest. Lecture Notes in Computer Science, 2021, , 654-662.	1.0	0
9	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. BMC Medical Informatics and Decision Making, 2021, 21, 254.	1.5	3
10	Reverse engineering gene regulatory network based on complex-valued ordinary differential equation model. BMC Bioinformatics, 2021, 22, 448.	1.2	7
11	2-hydr_Ensemble: Lysine 2-hydroxyisobutyrylation identification with ensemble method. Chemometrics and Intelligent Laboratory Systems, 2021, 215, 104351.	1.8	34
12	Hypertension-Related Drug Activity Identification Based on Novel Ensemble Method. Frontiers in Genetics, 2021, 12, 768747.	1.1	2
13	SubRF_Seq: Identification of Sub-Golgi Protein Types with Random Forest with Partial Sequence Information. Scientific Programming, 2020, 2020, 1-7.	0.5	1
14	ACT-SVM: Prediction of Protein-Protein Interactions Based on Support Vector Basis Model. Scientific Programming, 2020, 2020, 1-8.	0.5	10
15	Time Series Prediction Based on Complex-Valued S-System Model. Complexity, 2020, 2020, 1-13.	0.9	3
16	K_net: Lysine Malonylation Sites Identification With Neural Network. IEEE Access, 2020, 8, 47304-47311.	2.6	5
17	Artificial Intelligence Techniques to Computational Proteomics, Genomics, and Biological Sequence Analysis. Current Protein and Peptide Science, 2020, 21, 1042-1043.	0.7	2
18	Classification of Protein Modification Sites with Machine Learning. Lecture Notes in Computer Science, 2020, , 432-445.	1.0	0

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19	Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	38
20	RNDEtree: Regulatory Network With Differential Equation Based on Flexible Neural Tree With Novel Criterion Function. IEEE Access, 2019, 7, 58255-58263.	2.6	9
21	LipoFNT: Lipoylation Sites Identification with Flexible Neural Tree. Complexity, 2019, 2019, 1-9.	0.9	10
22	A Local Feature Descriptor Based on SIFT for 3D Pollen Image Recognition. IEEE Access, 2019, 7, 152658-152666.	2.6	7
23	CSE: Complex-Valued System With Evolutionary Algorithm. IEEE Access, 2019, 7, 90268-90276.	2.6	3
24	CMSENN: Computational Modification Sites with Ensemble Neural Network. Chemometrics and Intelligent Laboratory Systems, 2019, 185, 65-72.	1.8	20
25	Complex-Valued Ordinary Differential Equation Modeling for Time Series Identification. IEEE Access, 2019, 7, 41033-41042.	2.6	11
26	IMKPse: Identification of Protein Malonylation Sites by the Key Features Into General PseAAC. IEEE Access, 2019, 7, 54073-54083.	2.6	25
27	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. International Journal of Molecular Sciences, 2019, 20, 113.	1.8	14
28	Mutli-Features Prediction of Protein Translational Modification Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1453-1460.	1.9	52
29	HSCVFNT: Inference of Time-Delayed Gene Regulatory Network Based on Complex-Valued Flexible Neural Tree Model. International Journal of Molecular Sciences, 2018, 19, 3178.	1.8	9
30	Inference of Large-scale Time-delayed Gene Regulatory Network with Parallel MapReduce Cloud Platform. Scientific Reports, 2018, 8, 17787.	1.6	13
31	Recurrent Neural Network for Predicting Transcription Factor Binding Sites. Scientific Reports, 2018, 8, 15270.	1.6	147
32	Cross-validated smooth multi-instance learning. , 2017, . .		0
33	Classification of Protein Structure Classes on Flexible Neutral Tree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1122-1133.	1.9	45
34	Novel human microbe-disease association prediction using network consistency projection. BMC Bioinformatics, 2017, 18, 543.	1.2	67
35	Pupylation sites prediction with ensemble classification model. International Journal of Data Mining and Bioinformatics, 2017, 18, 91.	0.1	46
36	CIPPN: computational identification of protein pupylation sites by using neural network. Oncotarget, 2017, 8, 108867-108879.	0.8	16

#	ARTICLE	IF	CITATIONS
37	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
38	ILSES: Identification lysine succinylation-sites with ensemble classification. , 2016, , .		0
39	A Novel Protein Structural Classes Prediction Method Based on Hierarchical Classification Model. , 2015, , .		1
40	A novel feature fusion method for predicting protein subcellular localization with multiple sites. , 2015, , .		0
41	Prediction of protein structure classes. , 2015, , .		0
42	A new protein structure classification model. , 2014, , .		0
43	A novel protein structure classification model. , 2014, , .		0
44	Prediction of protein structure classes with flexible neural tree. Bio-Medical Materials and Engineering, 2014, 24, 3797-3806.	0.4	43
45	Multiple Feature Fusion Protein Tertiary Structure Prediction. , 2013, , .		2