

Wenzheng Bao

List of Publications by Year in descending order

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45
papers

783
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687363
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26
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46
all docs

46
docs citations

46
times ranked

592
citing authors

#	ARTICLE	IF	CITATIONS
1	Recurrent Neural Network for Predicting Transcription Factor Binding Sites. Scientific Reports, 2018, 8, 15270.	3.3	147
2	Novel human microbe-disease association prediction using network consistency projection. BMC Bioinformatics, 2017, 18, 543.	2.6	67
3	A graph auto-encoder model for miRNA-disease associations prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	63
4	Mutli-Features Prediction of Protein Translational Modification Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1453-1460.	3.0	52
5	Pupylation sites prediction with ensemble classification model. International Journal of Data Mining and Bioinformatics, 2017, 18, 91.	0.1	46
6	Classification of Protein Structure Classes on Flexible Neutral Tree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1122-1133.	3.0	45
7	Prediction of protein structure classes with flexible neural tree. Bio-Medical Materials and Engineering, 2014, 24, 3797-3806.	0.6	43
8	Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	38
9	2-hydr_Ensemble: Lysine 2-hydroxyisobutyrylation identification with ensemble method. Chemometrics and Intelligent Laboratory Systems, 2021, 215, 104351.	3.5	34
10	Phage_UniR_LGBM: Phage Virion Proteins Classification with UniRep Features and LightGBM Model. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-8.	1.3	30
11	IMKPse: Identification of Protein Malonylation Sites by the Key Features Into General PseAAC. IEEE Access, 2019, 7, 54073-54083.	4.2	25
12	OUP accepted manuscript. Briefings in Bioinformatics, 2022, 23, .	6.5	22
13	CMSENN: Computational Modification Sites with Ensemble Neural Network. Chemometrics and Intelligent Laboratory Systems, 2019, 185, 65-72.	3.5	20
14	CIPPn: computational identification of protein pupylation sites by using neural network. Oncotarget, 2017, 8, 108867-108879.	1.8	16
15	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. International Journal of Molecular Sciences, 2019, 20, 113.	4.1	14
16	Inference of Large-scale Time-delayed Gene Regulatory Network with Parallel MapReduce Cloud Platform. Scientific Reports, 2018, 8, 17787.	3.3	13
17	Complex-Valued Ordinary Differential Equation Modeling for Time Series Identification. IEEE Access, 2019, 7, 41033-41042.	4.2	11
18	A survey on proteinâ€DNA-binding sites in computational biology. Briefings in Functional Genomics, 2022, 21, 357-375.	2.7	11

#	ARTICLE	IF	CITATIONS
19	LipoFNT: Lipoylation Sites Identification with Flexible Neural Tree. Complexity, 2019, 2019, 1-9.	1.6	10
20	ACT-SVM: Prediction of Protein-Protein Interactions Based on Support Vector Basis Model. Scientific Programming, 2020, 2020, 1-8.	0.7	10
21	HSCVFNT: Inference of Time-Delayed Gene Regulatory Network Based on Complex-Valued Flexible Neural Tree Model. International Journal of Molecular Sciences, 2018, 19, 3178.	4.1	9
22	RNDEtree: Regulatory Network With Differential Equation Based on Flexible Neural Tree With Novel Criterion Function. IEEE Access, 2019, 7, 58255-58263.	4.2	9
23	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
24	A Local Feature Descriptor Based on SIFT for 3D Pollen Image Recognition. IEEE Access, 2019, 7, 152658-152666.	4.2	7
25	Reverse engineering gene regulatory network based on complex-valued ordinary differential equation model. BMC Bioinformatics, 2021, 22, 448.	2.6	7
26	K_net: Lysine Malonylation Sites Identification With Neural Network. IEEE Access, 2020, 8, 47304-47311.	4.2	5
27	CSE: Complex-Valued System With Evolutionary Algorithm. IEEE Access, 2019, 7, 90268-90276.	4.2	3
28	Time Series Prediction Based on Complex-Valued S-System Model. Complexity, 2020, 2020, 1-13.	1.6	3
29	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. BMC Medical Informatics and Decision Making, 2021, 21, 254.	3.0	3
30	Multiple Feature Fusion Protein Tertiary Structure Prediction. , 2013, , .		2
31	Hypertension-Related Drug Activity Identification Based on Novel Ensemble Method. Frontiers in Genetics, 2021, 12, 768747.	2.3	2
32	Artificial Intelligence Techniques to Computational Proteomics, Genomics, and Biological Sequence Analysis. Current Protein and Peptide Science, 2020, 21, 1042-1043.	1.4	2
33	Single_cell_GRN: gene regulatory network identification based on supervised learning method and Single-cell RNA-seq data. BioData Mining, 2022, 15, .	4.0	2
34	A Novel Protein Structural Classes Prediction Method Based on Hierarchical Classification Model. , 2015, , .		1
35	An improved image registration and fusion algorithm. Wireless Networks, 2021, 27, 3597-3611.	3.0	1
36	SubRF_Seq: Identification of Sub-Golgi Protein Types with Random Forest with Partial Sequence Information. Scientific Programming, 2020, 2020, 1-7.	0.7	1

#	ARTICLE	IF	CITATIONS
37	Gene Regulatory Identification Based on the Novel Hybrid Time-Delayed Method. Frontiers in Genetics, 2022, 13, .	2.3	1
38	A new protein structure classification model. , 2014, , .		0
39	A novel protein structure classification model. , 2014, , .		0
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	ILSES: Identification lysine succinylation-sites with ensemble classification. , 2016, , .		0
43	Cross-validated smooth multi-instance learning. , 2017, , .		0
44	Prediction of Protein-Protein Interaction Based on Deep Learning Feature Representation and Random Forest. Lecture Notes in Computer Science, 2021, , 654-662.	1.3	0
45	Classification of Protein Modification Sites with Machine Learning. Lecture Notes in Computer Science, 2020, , 432-445.	1.3	0