

Yongqing Zhang

List of Publications by Year in descending order

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47
papers

525
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687363

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47
all docs

47
docs citations

47
times ranked

496
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel convolution attention model for predicting transcription factor binding sites by combination of sequence and shape. Briefings in Bioinformatics, 2022, 23, .	6.5	17
2	Fusion prior gene network for high reliable single-cell gene regulatory network inference. Computers in Biology and Medicine, 2022, 143, 105279.	7.0	0
3	A survey on the algorithm and development of multiple sequence alignment. Briefings in Bioinformatics, 2022, 23, .	6.5	8
4	A Zero-Padding Frequency Domain Convolutional Neural Network for SSVEP Classification. Frontiers in Human Neuroscience, 2022, 16, 815163.	2.0	4
5	A hybrid ensemble and evolutionary algorithm for imbalanced classification and its application on bioinformatics. Computational Biology and Chemistry, 2022, 98, 107646.	2.3	4
6	Densely Convolutional Neural Network for Transcription Factor Binding Sites Prediction Using DNA Sequence and Histone Modification. , 2022, , .		1
7	Review of the Applications of Deep Learning in Bioinformatics. Current Bioinformatics, 2021, 15, 898-911.	1.5	40
8	Combining generative adversarial network and multi-output CNN for motor imagery classification. Journal of Neural Engineering, 2021, 18, 046026.	3.5	10
9	Generative Adversarial Networks in Medical Image Processing. Current Pharmaceutical Design, 2021, 27, 1856-1868.	1.9	26
10	High-resolution transcription factor binding sites prediction improved performance and interpretability by deep learning method. Briefings in Bioinformatics, 2021, 22, .	6.5	24
11	Automatic Sleep Staging Algorithm Based on Time Attention Mechanism. Frontiers in Human Neuroscience, 2021, 15, 692054.	2.0	9
12	CAE-CNN: Predicting transcription factor binding site with convolutional autoencoder and convolutional neural network. Expert Systems With Applications, 2021, 183, 115404.	7.6	12
13	MFFNet: Multi-dimensional Feature Fusion Network based on attention mechanism for sEMG analysis to detect muscle fatigue. Expert Systems With Applications, 2021, 185, 115639.	7.6	17
14	BindTransNet: A Transferable Transformer-Based Architecture for Cross-Cell Type DNA-Protein Binding Sites Prediction. Lecture Notes in Computer Science, 2021, , 203-214.	1.3	4
15	Affective EEG-Based Person Identification Using Channel Attention Convolutional Neural Dense Connection Network. Security and Communication Networks, 2021, 2021, 1-10.	1.5	3
16	Gene regulatory networks analysis of muscle-invasive bladder cancer subtypes using differential graphical model. BMC Genomics, 2021, 22, 863.	2.8	6
17	By hybrid neural networks for prediction and interpretation of transcription factor binding sites based on multi-omics. , 2021, , .		4
18	DeepSite: bidirectional LSTM and CNN models for predicting DNA-protein binding. International Journal of Machine Learning and Cybernetics, 2020, 11, 841-851.	3.6	63

#	ARTICLE	IF	CITATIONS
19	A point-of-interest suggestion algorithm in Multi-source geo-social networks. Engineering Applications of Artificial Intelligence, 2020, 88, 103374.	8.1	19
20	Cervical Cancer Single Cell Image Data Augmentation Using Residual Condition Generative Adversarial Networks. , 2020, , .		4
21	A Review About Transcription Factor Binding Sites Prediction Based on Deep Learning. IEEE Access, 2020, 8, 219256-219274.	4.2	16
22	SOTB: Semi-Supervised Oversampling Approach Based on Trigonal Barycenter Theory. IEEE Access, 2020, 8, 50180-50189.	4.2	5
23	Balancing large margin nearest neighbours for imbalanced data. Journal of Engineering, 2020, 2020, 316-321.	1.1	4
24	Applications of Machine Learning in Drug Target Discovery. Current Drug Metabolism, 2020, 21, 790-803.	1.2	8
25	GRRFNet: Guided Regularized Random Forest-based Gene Regulatory Network Inference Using Data Integration. , 2020, , .		4
26	Gene Regulatory Networks Analysis for Subtypes of Muscle-Invasive Bladder Cancer Based on Pathway. , 2019, , .		0
27	A Transcription Factor Binding Site Prediction Algorithm Based on Semi-Supervised Learning. , 2019, , .		0
28	Evolutionary-Based Ensemble Under-Sampling for Imbalanced Data. , 2019, , .		2
29	How to balance the bioinformatics data: pseudo-negative sampling. BMC Bioinformatics, 2019, 20, 695.	2.6	9
30	Identification of DNAâ€œprotein binding sites by bootstrap multiple convolutional neural networks on sequence information. Engineering Applications of Artificial Intelligence, 2019, 79, 58-66.	8.1	30
31	Unsupervised Feature Learning with Single Layer ICANet for Face Recognition. Sensing and Imaging, 2018, 19, 1.	1.5	1
32	Efficient and Robust Supervised Learning Algorithm for Spiking Neural Networks. Sensing and Imaging, 2018, 19, 1.	1.5	5
33	Handover detection approach based on trajectory data mining techniques. Journal of Engineering, 2018, 2018, 1534-1537.	1.1	2
34	ICANet: a simple cascade linear convolution network for face recognition. Eurasip Journal on Image and Video Processing, 2018, 2018, .	2.6	12
35	ENSEMBLE-CNN: Predicting DNA Binding Sites in Protein Sequences by an Ensemble Deep Learning Method. Lecture Notes in Computer Science, 2018, , 301-306.	1.3	3
36	ERMPD: An efficient and robustness membrane potential driven supervised learning in spiking neural networks. , 2017, , .		0

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37	A novel network model based ICA filter for face recognition. , 2017, , .		1
38	GeNemo: a search engine for web-based functional genomic data. Nucleic Acids Research, 2016, 44, W122-W127.	14.5	11
39	Age-related changes in functional connectivity between young adulthood and late adulthood. Analytical Methods, 2015, 7, 4111-4122.	2.7	8
40	An extended fractional Kalman filter for inferring gene regulatory networks using time-series data. Chemometrics and Intelligent Laboratory Systems, 2014, 138, 57-63.	3.5	26
41	Mining effective multi-segment sliding window for pathogen incidence rate prediction. Data and Knowledge Engineering, 2013, 87, 425-444.	3.4	3
42	Using gene expression programming to infer gene regulatory networks from time-series data. Computational Biology and Chemistry, 2013, 47, 198-206.	2.3	18
43	Prediction of adverse drug reactions by a network based external link prediction method. Analytical Methods, 2013, 5, 6120.	2.7	21
44	Prediction of Nicotinamide Adenine Dinucleotide Interacting Sites Based on Ensemble Support Vector Machine. Protein and Peptide Letters, 2012, 19, 559-566.	0.9	2
45	Prediction of flavin mono-nucleotide binding sites using modified PSSM profile and ensemble support vector machine. Computers in Biology and Medicine, 2012, 42, 1053-1059.	7.0	10
46	Using ensemble methods to deal with imbalanced data in predicting protein-protein interactions. Computational Biology and Chemistry, 2012, 36, 36-41.	2.3	35
47	A Novel Method to Predict Protein-Protein Interactions Based on the Information of Protein-Protein Interaction Networks and Protein Sequence. Protein and Peptide Letters, 2011, 18, 906-911.	0.9	14