

Yongqing Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8819451/publications.pdf>

Version: 2024-02-01

47
papers

525
citations

687363

13
h-index

752698

20
g-index

47
all docs

47
docs citations

47
times ranked

496
citing authors

#	ARTICLE	IF	CITATIONS
1	DeepSite: bidirectional LSTM and CNN models for predicting DNA-protein binding. <i>International Journal of Machine Learning and Cybernetics</i> , 2020, 11, 841-851.	3.6	63
2	Review of the Applications of Deep Learning in Bioinformatics. <i>Current Bioinformatics</i> , 2021, 15, 898-911.	1.5	40
3	Using ensemble methods to deal with imbalanced data in predicting protein-protein interactions. <i>Computational Biology and Chemistry</i> , 2012, 36, 36-41.	2.3	35
4	Identification of DNA-protein binding sites by bootstrap multiple convolutional neural networks on sequence information. <i>Engineering Applications of Artificial Intelligence</i> , 2019, 79, 58-66.	8.1	30
5	An extended fractional Kalman filter for inferring gene regulatory networks using time-series data. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2014, 138, 57-63.	3.5	26
6	Generative Adversarial Networks in Medical Image Processing. <i>Current Pharmaceutical Design</i> , 2021, 27, 1856-1868.	1.9	26
7	High-resolution transcription factor binding sites prediction improved performance and interpretability by deep learning method. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	24
8	Prediction of adverse drug reactions by a network based external link prediction method. <i>Analytical Methods</i> , 2013, 5, 6120.	2.7	21
9	A point-of-interest suggestion algorithm in Multi-source geo-social networks. <i>Engineering Applications of Artificial Intelligence</i> , 2020, 88, 103374.	8.1	19
10	Using gene expression programming to infer gene regulatory networks from time-series data. <i>Computational Biology and Chemistry</i> , 2013, 47, 198-206.	2.3	18
11	MFFNet: Multi-dimensional Feature Fusion Network based on attention mechanism for sEMG analysis to detect muscle fatigue. <i>Expert Systems With Applications</i> , 2021, 185, 115639.	7.6	17
12	A novel convolution attention model for predicting transcription factor binding sites by combination of sequence and shape. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	17
13	A Review About Transcription Factor Binding Sites Prediction Based on Deep Learning. <i>IEEE Access</i> , 2020, 8, 219256-219274.	4.2	16
14	A Novel Method to Predict Protein-Protein Interactions Based on the Information of Protein-Protein Interaction Networks and Protein Sequence. <i>Protein and Peptide Letters</i> , 2011, 18, 906-911.	0.9	14
15	ICANet: a simple cascade linear convolution network for face recognition. <i>Eurasip Journal on Image and Video Processing</i> , 2018, 2018, .	2.6	12
16	CAE-CNN: Predicting transcription factor binding site with convolutional autoencoder and convolutional neural network. <i>Expert Systems With Applications</i> , 2021, 183, 115404.	7.6	12
17	GeNemo: a search engine for web-based functional genomic data. <i>Nucleic Acids Research</i> , 2016, 44, W122-W127.	14.5	11
18	Prediction of flavin mono-nucleotide binding sites using modified PSSM profile and ensemble support vector machine. <i>Computers in Biology and Medicine</i> , 2012, 42, 1053-1059.	7.0	10

#	ARTICLE	IF	CITATIONS
19	Combining generative adversarial network and multi-output CNN for motor imagery classification. <i>Journal of Neural Engineering</i> , 2021, 18, 046026.	3.5	10
20	How to balance the bioinformatics data: pseudo-negative sampling. <i>BMC Bioinformatics</i> , 2019, 20, 695.	2.6	9
21	Automatic Sleep Staging Algorithm Based on Time Attention Mechanism. <i>Frontiers in Human Neuroscience</i> , 2021, 15, 692054.	2.0	9
22	Age-related changes in functional connectivity between young adulthood and late adulthood. <i>Analytical Methods</i> , 2015, 7, 4111-4122.	2.7	8
23	Applications of Machine Learning in Drug Target Discovery. <i>Current Drug Metabolism</i> , 2020, 21, 790-803.	1.2	8
24	A survey on the algorithm and development of multiple sequence alignment. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	8
25	Gene regulatory networks analysis of muscle-invasive bladder cancer subtypes using differential graphical model. <i>BMC Genomics</i> , 2021, 22, 863.	2.8	6
26	Efficient and Robust Supervised Learning Algorithm for Spiking Neural Networks. <i>Sensing and Imaging</i> , 2018, 19, 1.	1.5	5
27	SOTB: Semi-Supervised Oversampling Approach Based on Trigonal Barycenter Theory. <i>IEEE Access</i> , 2020, 8, 50180-50189.	4.2	5
28	Cervical Cancer Single Cell Image Data Augmentation Using Residual Condition Generative Adversarial Networks. , 2020, , .		4
29	Balancing large margin nearest neighbours for imbalanced data. <i>Journal of Engineering</i> , 2020, 2020, 316-321.	1.1	4
30	GRRFNet: Guided Regularized Random Forest-based Gene Regulatory Network Inference Using Data Integration. , 2020, , .		4
31	BindTransNet: A Transferable Transformer-Based Architecture for Cross-Cell Type DNA-Protein Binding Sites Prediction. <i>Lecture Notes in Computer Science</i> , 2021, , 203-214.	1.3	4
32	A Zero-Padding Frequency Domain Convolutional Neural Network for SSVEP Classification. <i>Frontiers in Human Neuroscience</i> , 2022, 16, 815163.	2.0	4
33	A hybrid ensemble and evolutionary algorithm for imbalanced classification and its application on bioinformatics. <i>Computational Biology and Chemistry</i> , 2022, 98, 107646.	2.3	4
34	By hybrid neural networks for prediction and interpretation of transcription factor binding sites based on multi-omics. , 2021, , .		4
35	Mining effective multi-segment sliding window for pathogen incidence rate prediction. <i>Data and Knowledge Engineering</i> , 2013, 87, 425-444.	3.4	3
36	ENSEMBLE-CNN: Predicting DNA Binding Sites in Protein Sequences by an Ensemble Deep Learning Method. <i>Lecture Notes in Computer Science</i> , 2018, , 301-306.	1.3	3

#	ARTICLE	IF	CITATIONS
37	Affective EEG-Based Person Identification Using Channel Attention Convolutional Neural Dense Connection Network. Security and Communication Networks, 2021, 2021, 1-10.	1.5	3
38	Prediction of Nicotinamide Adenine Dinucleotide Interacting Sites Based on Ensemble Support Vector Machine. Protein and Peptide Letters, 2012, 19, 559-566.	0.9	2
39	Handover detection approach based on trajectory data mining techniques. Journal of Engineering, 2018, 2018, 1534-1537.	1.1	2
40	Evolutionary-Based Ensemble Under-Sampling for Imbalanced Data. , 2019, , .		2
41	A novel network model based ICA filter for face recognition. , 2017, , .		1
42	Unsupervised Feature Learning with Single Layer ICANet for Face Recognition. Sensing and Imaging, 2018, 19, 1.	1.5	1
43	Densely Convolutional Neural Network for Transcription Factor Binding Sites Prediction Using DNA Sequence and Histone Modification. , 2022, , .		1
44	ERMPD: An efficient and robustness membrane potential driven supervised learning in spiking neural networks. , 2017, , .		0
45	Gene Regulatory Networks Analysis for Subtypes of Muscle-Invasive Bladder Cancer Based on Pathway. , 2019, , .		0
46	A Transcription Factor Binding Site Prediction Algorithm Based on Semi-Supervised Learning. , 2019, , .		0
47	Fusion prior gene network for high reliable single-cell gene regulatory network inference. Computers in Biology and Medicine, 2022, 143, 105279.	7.0	0