Qinhu Zhang

List of Publications by Year
in descending order

88 papers	4,603 citations	109321 35 h-index	102487 66 g-index
93 all docs	93 docs citations	93 times ranked	2586 citing authors

#	Article	IF	Citations
1	Hierarchical Graph Pooling With Self-Adaptive Cluster Aggregation. IEEE Transactions on Cognitive and Developmental Systems, 2022, 14, 1198-1207.	3.8	6
2	Graph representation learning in bioinformatics: trends, methods and applications. Briefings in Bioinformatics, 2022, 23, .	6.5	64
3	FCNGRU: Locating Transcription Factor Binding Sites by Combing Fully Convolutional Neural Network With Gated Recurrent Unit. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 1883-1890.	6.3	8
4	Base-resolution prediction of transcription factor binding signals by a deep learning framework. PLoS Computational Biology, 2022, 18, e1009941.	3.2	13
5	Multi-Scale Capsule Network for Predicting DNA-Protein Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1793-1800.	3.0	11
6	Predicting TF-DNA Binding Motifs from ChIP-seq Datasets Using the Bag-Based Classifier Combined With a Multi-Fold Learning Scheme. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1743-1751.	3.0	3
7	A survey on deep learning in DNA/RNA motif mining. Briefings in Bioinformatics, 2021, 22, .	6.5	59
8	Person Reidentification by Multiscale Feature Representation Learning With Random Batch Feature Mask. IEEE Transactions on Cognitive and Developmental Systems, 2021, 13, 865-874.	3.8	41
9	3-D Facial Landmarks Detection for Intelligent Video Systems. IEEE Transactions on Industrial Informatics, 2021, 17, 578-586.	11.3	18
10	Predicting *in-vitro* Transcription Factor Binding Sites Using DNA Sequence + Shape. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 667-676.	3.0	44
11	Locating transcription factor binding sites by fully convolutional neural network. Briefings in Bioinformatics, 2021, 22, .	6.5	30
12	Attention Deep Model With Multi-Scale Deep Supervision for Person Re-Identification. IEEE Transactions on Emerging Topics in Computational Intelligence, 2021, 5, 70-78.	4.9	46
13	Predicting transcription factor binding sites using DNA shape features based on shared hybrid deep learning architecture. Molecular Therapy - Nucleic Acids, 2021, 24, 154-163.	5.1	27
14	Predicting Interactions Between Pathogen and Human Proteins Based on the Relation Between Sequence Length and Amino Acid Composition. Current Bioinformatics, 2021, 16, 799-806.	1.5	1
15	Guest Editorial for Special Section on the 15th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1730-1732.	3.0	0
16	**An efficient approach based on multi-sources information to predict circRNA**–**disease associations using deep convolutional neural network**. Bioinformatics, 2020, 36, 4038-4046.	4.1	105
17	Learning Representations to Predict Intermolecular Interactions on Large-Scale Heterogeneous Molecular Association Network. IScience, 2020, 23, 101261.	4.1	16
18	Constructing cancer patient-specific and group-specific gene networks with multi-omics data. BMC Medical Genomics, 2020, 13, 81.	1.5	10

#	Article	IF	Citations
19	Guest Editorial for Special Section on the 14th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 1474-1475.	3.0	0
20	A New Method Combining DNA Shape Features to Improve the Prediction Accuracy of Transcription Factor Binding Sites. Lecture Notes in Computer Science, 2020, , 79-89.	1.3	2
21	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
22	Motif Discovery via Convolutional Networks with K-mer Embedding. Lecture Notes in Computer Science, 2019, , 374-382.	1.3	6
23	Guest Editorial for Special Section on the 13th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 749-750.	3.0	0
24	Robust dimensionality reduction via feature space to feature space distance metric learning. Neural Networks, 2019, 112, 1-14.	5.9	66
25	Modeling in-vivo protein-DNA binding by combining multiple-instance learning with a hybrid deep neural network. Scientific Reports, 2019, 9, 8484.	3.3	42
26	Image Co-Segmentation via Locally Biased Discriminative Clustering. IEEE Transactions on Knowledge and Data Engineering, 2019, 31, 2228-2233.	5.7	11
27	IMKPse: Identification of Protein Malonylation Sites by the Key Features Into General PseAAC. IEEE Access, 2019, 7, 54073-54083.	4.2	25
28	A Network-guided Association Mapping Approach from DNA Methylation to Disease. Scientific Reports, 2019, 9, 5601.	3.3	17
29	High-Order Convolutional Neural Network Architecture for Predicting DNA-Protein Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1184-1192.	3.0	78
30	Mutli-Features Prediction of Protein Translational Modification Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1453-1460.	3.0	52
31	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. Molecular Therapy - Nucleic Acids, 2018, 11, 337-344.	5.1	116
32	DiscMLA: An Efficient Discriminative Motif Learning Algorithm over High-Throughput Datasets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1810-1820.	3.0	24
33	iPromoter-2L: a two-layer predictor for identifying promoters and their types by multi-window-based PseKNC. Bioinformatics, 2018, 34, 33-40.	4.1	277
34	Guest Editorial for Special Section on the 12th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1433-1435.	3.0	0
35	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
36	Inference of Large-scale Time-delayed Gene Regulatory Network with Parallel MapReduce Cloud Platform. Scientific Reports, 2018, 8, 17787.	3.3	13

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37	Improving Type 2 Diabetes Phenotypic Classification by Combining Genetics and Conventional Risk Factors. , 2018, , .		1
38	Recurrent Neural Network for Predicting Transcription Factor Binding Sites. Scientific Reports, 2018, 8, 15270.	3.3	147
39	Fast sequence analysis based on diamond sampling. PLoS ONE, 2018, 13, e0198922.	2.5	1
40	iRO-3wPseKNC: identify DNA replication origins by three-window-based PseKNC. Bioinformatics, 2018, 34, 3086-3093.	4.1	108
41	Predicting Interactions between Virus and Host Proteins Using Repeat Patterns and Composition of Amino Acids. Journal of Healthcare Engineering, 2018, 2018, 1-9.	1.9	35
42	Image segmentation fusion using weakly supervised trace–norm multi–task learning method. IET Image Processing, 2018, 12, 1079-1085.	2.5	12
43	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. International Journal of Biological Sciences, 2018, 14, 983-991.	6.4	19
44	iEnhancer-EL: identifying enhancers and their strength with ensemble learning approach. Bioinformatics, 2018, 34, 3835-3842.	4.1	172
45	An improved method for predicting interactions between virus and human proteins. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650024.	0.8	23
46	Cross-validated smooth multi-instance learning. , 2017, , .		0
47	WSMD: weakly-supervised motif discovery in transcription factor ChIP-seq data. Scientific Reports, 2017, 7, 3217.	3.3	21
48	Convex local sensitive low rank matrix approximation. , 2017, , .		1
49	Editorial: Special Issue on Advanced Intelligent Computing: Theory and Applications. Neurocomputing, 2017, 228, 1-2.	5.9	2
50	Guest Editorial for Special Section on the 11th International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1104-1105.	3.0	0
51	Soft-bag based motif discovery for ChIP-seq datasets. , 2017, , .		1
52	Direct AUC optimization of regulatory motifs. Bioinformatics, 2017, 33, i243-i251.	4.1	30
53	miRNA-Disease Association Prediction with Collaborative Matrix Factorization. Complexity, 2017, 2017, 1-9.	1.6	73
54	FAACOSE: A Fast Adaptive Ant Colony Optimization Algorithm for Detecting SNP Epistasis. Complexity, 2017, 2017, 1-10.	1.6	42

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55	Classification of caesarean section and normal vaginal deliveries using foetal heart rate signals and advanced machine learning algorithms. BioMedical Engineering OnLine, 2017, 16, 89.	2.7	51
56	Novel human microbe-disease association prediction using network consistency projection. BMC Bioinformatics, 2017, 18, 543.	2.6	67
57	Accurate prediction of protein-protein interactions by integrating potential evolutionary information embedded in PSSM profile and discriminative vector machine classifier. Oncotarget, 2017, 8, 23638-23649.	1.8	36
58	CIPPN: computational identification of protein pupylation sites by using neural network. Oncotarget, 2017, 8, 108867-108879.	1.8	16
59	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. Oncotarget, 2016, 7, 82440-82449.	1.8	24
60	An Improved Ensemble of Random Vector Functional Link Networks Based on Particle Swarm Optimization with Double Optimization Strategy. PLoS ONE, 2016, 11, e0165803.	2.5	11
61	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
62	Visual data completion via local sensitive low rank tensor learning. , 2016, , .		1
63	ILSES: Identification lysine succinylation-sites with ensemble classification. , 2016, , .		0
64	A regression model for calculating the second dimension retention index in comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry. Journal of Chromatography A, 2016, 1451, 127-134.	3.7	12
65	Representing logical relations automatically by Probabilistic Logical Dynamical Neural Network. , 2016, , .		0
66	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. Molecular BioSystems, 2016, 12, 3702-3710.	2.9	17
67	ChIP-PIT: Enhancing the Analysis of ChIP-Seq Data Using Convex-Relaxed Pair-Wise Interaction Tensor Decomposition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 55-63.	3.0	61
68	Predicting Hub Genes Associated with Cervical Cancer through Gene Co-Expression Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 27-35.	3.0	133
69	ILNCSIM: improved lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 25902-25914.	1.8	122
70	Imputation of ChIP-seq datasets via Low Rank Convex Co-Embedding. , 2015, , .		0
71	Mining the bladder cancer-associated genes by an integrated strategy for the construction and analysis of differential co-expression networks. BMC Genomics, 2015, 16, S4.	2.8	100
72	Module Based Differential Coexpression Analysis Method for Type 2 Diabetes. BioMed Research International, 2015, 2015, 1-8.	1.9	12

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73	A novel diversity-guided ensemble of neural network based on attractive and repulsive particle swarm optimization. , 2015, , .		5
74	A Two-Stage Geometric Method for Pruning Unreliable Links in Protein-Protein Networks. IEEE Transactions on Nanobioscience, 2015, 14, 528-534.	3.3	62
75	Identifying cancer-related microRNAs based on gene expression data. Bioinformatics, 2015, 31, 1226-1234.	4.1	92
76	A novel texture image segmentation model based on multi-scale structure. , 2014, , .		0
77	A two-stage geometric method for detecting unreliable links in protein-protein networks. , 2014, , .		1
78	SFAPS: An R package for structure/function analysis of protein sequences based on informational spectrum method. Methods, 2014, 69, 207-212.	3.8	70
79	A Rayleighâ€"Ritz style method for large-scale discriminant analysis. Pattern Recognition, 2014, 47, 1698-1708.	8.1	15
80	Prediction of Protein-Protein Interactions Based on Protein-Protein Correlation Using Least Squares Regression. Current Protein and Peptide Science, 2014, 15, 553-560.	1.4	103
81	Increasing the reliability of proteinâ€"protein interaction networks via non-convex semantic embedding. Neurocomputing, 2013, 121, 99-107.	5.9	51
82	Normalized Feature Vectors: A Novel Alignment-Free Sequence Comparison Method Based on the Numbers of Adjacent Amino Acids. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 457-467.	3.0	135
83	t-LSE: A Novel Robust Geometric Approach for Modeling Protein-Protein Interaction Networks. PLoS ONE, 2013, 8, e58368.	2.5	81
84	A General CPL-AdS Methodology for Fixing Dynamic Parameters in Dual Environments. IEEE Transactions on Systems, Man, and Cybernetics, 2012, 42, 1489-1500.	5.0	127
85	Tumor Clustering Using Nonnegative Matrix Factorization With Gene Selection. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 599-607.	3.2	186
86	A Constructive Hybrid Structure Optimization Methodology for Radial Basis Probabilistic Neural Networks. IEEE Transactions on Neural Networks, 2008, 19, 2099-2115.	4.2	374
87	Independent component analysis-based penalized discriminant method for tumor classification using gene expression data. Bioinformatics, 2006, 22, 1855-1862.	4.1	269
88	RADIAL BASIS PROBABILISTIC NEURAL NETWORKS: MODEL AND APPLICATION. International Journal of Pattern Recognition and Artificial Intelligence, 1999, 13, 1083-1101.	1.2	392