

# Qinhu Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	RADIAL BASIS PROBABILISTIC NEURAL NETWORKS: MODEL AND APPLICATION. International Journal of Pattern Recognition and Artificial Intelligence, 1999, 13, 1083-1101.	1.2	392
2	A Constructive Hybrid Structure Optimization Methodology for Radial Basis Probabilistic Neural Networks. IEEE Transactions on Neural Networks, 2008, 19, 2099-2115.	4.2	374
3	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
4	Independent component analysis-based penalized discriminant method for tumor classification using gene expression data. Bioinformatics, 2006, 22, 1855-1862.	4.1	269
5	Tumor Clustering Using Nonnegative Matrix Factorization With Gene Selection. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 599-607.	3.2	186
6	iEnhancer-EL: identifying enhancers and their strength with ensemble learning approach. Bioinformatics, 2018, 34, 3835-3842.	4.1	172
7	Recurrent Neural Network for Predicting Transcription Factor Binding Sites. Scientific Reports, 2018, 8, 15270.	3.3	147
8	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
9	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
10	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
11	ILNCSIM: improved lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 25902-25914.	1.8	122
12	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
13	iRO-3wPseKNC: identify DNA replication origins by three-window-based PseKNC. Bioinformatics, 2018, 34, 3086-3093.	4.1	108
14	<b>An efficient approach based on multi-sources information to predict circRNA</b>â€“<b>disease associations using deep convolutional neural network</b>. Bioinformatics, 2020, 36, 4038-4046.	4.1	105
15	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
16	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
17	Identifying cancer-related microRNAs based on gene expression data. Bioinformatics, 2015, 31, 1226-1234.	4.1	92
18	t-LSE: A Novel Robust Geometric Approach for Modeling Protein-Protein Interaction Networks. PLoS ONE, 2013, 8, e58368.	2.5	81

#	ARTICLE	IF	CITATIONS
19	High-Order Convolutional Neural Network Architecture for Predicting DNA-Protein Binding Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1184-1192.	3.0	78
20	miRNA-Disease Association Prediction with Collaborative Matrix Factorization. <i>Complexity</i> , 2017, 2017, 1-9.	1.6	73
21	SFAPS: An R package for structure/function analysis of protein sequences based on informational spectrum method. <i>Methods</i> , 2014, 69, 207-212.	3.8	70
22	Novel human microbe-disease association prediction using network consistency projection. <i>BMC Bioinformatics</i> , 2017, 18, 543.	2.6	67
23	Robust dimensionality reduction via feature space to feature space distance metric learning. <i>Neural Networks</i> , 2019, 112, 1-14.	5.9	66
24	Graph representation learning in bioinformatics: trends, methods and applications. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	64
25	A Two-Stage Geometric Method for Pruning Unreliable Links in Protein-Protein Networks. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 528-534.	3.3	62
26	ChIP-PIT: Enhancing the Analysis of ChIP-Seq Data Using Convex-Relaxed Pair-Wise Interaction Tensor Decomposition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 55-63.	3.0	61
27	A survey on deep learning in DNA/RNA motif mining. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	59
28	Mutli-Features Prediction of Protein Translational Modification Sites. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1453-1460.	3.0	52
29	Increasing the reliability of protein-protein interaction networks via non-convex semantic embedding. <i>Neurocomputing</i> , 2013, 121, 99-107.	5.9	51
30	Classification of caesarean section and normal vaginal deliveries using foetal heart rate signals and advanced machine learning algorithms. <i>BioMedical Engineering OnLine</i> , 2017, 16, 89.	2.7	51
31	Attention Deep Model With Multi-Scale Deep Supervision for Person Re-Identification. <i>IEEE Transactions on Emerging Topics in Computational Intelligence</i> , 2021, 5, 70-78.	4.9	46
32	Predicting <i>in-vitro</i> Transcription Factor Binding Sites Using DNA Sequence + Shape. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 667-676.	3.0	44
33	FAACOSE: A Fast Adaptive Ant Colony Optimization Algorithm for Detecting SNP Epistasis. <i>Complexity</i> , 2017, 2017, 1-10.	1.6	42
34	Modeling in-vivo protein-DNA binding by combining multiple-instance learning with a hybrid deep neural network. <i>Scientific Reports</i> , 2019, 9, 8484.	3.3	42
35	Person Reidentification by Multiscale Feature Representation Learning With Random Batch Feature Mask. <i>IEEE Transactions on Cognitive and Developmental Systems</i> , 2021, 13, 865-874.	3.8	41
36	Weakly-Supervised Convolutional Neural Network Architecture for Predicting Protein-DNA Binding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	38

#	ARTICLE	IF	CITATIONS
37	Accurate prediction of protein-protein interactions by integrating potential evolutionary information embedded in PSSM profile and discriminative vector machine classifier. <i>Oncotarget</i> , 2017, 8, 23638-23649.	1.8	36
38	Predicting Interactions between Virus and Host Proteins Using Repeat Patterns and Composition of Amino Acids. <i>Journal of Healthcare Engineering</i> , 2018, 2018, 1-9.	1.9	35
39	Direct AUC optimization of regulatory motifs. <i>Bioinformatics</i> , 2017, 33, i243-i251.	4.1	30
40	Locating transcription factor binding sites by fully convolutional neural network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	30
41	Predicting transcription factor binding sites using DNA shape features based on shared hybrid deep learning architecture. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 24, 154-163.	5.1	27
42	IMKPse: Identification of Protein Malonylation Sites by the Key Features Into General PseAAC. <i>IEEE Access</i> , 2019, 7, 54073-54083.	4.2	25
43	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. <i>Oncotarget</i> , 2016, 7, 82440-82449.	1.8	24
44	DiscMLA: An Efficient Discriminative Motif Learning Algorithm over High-Throughput Datasets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1810-1820.	3.0	24
45	An improved method for predicting interactions between virus and human proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650024.	0.8	23
46	WSMD: weakly-supervised motif discovery in transcription factor ChIP-seq data. <i>Scientific Reports</i> , 2017, 7, 3217.	3.3	21
47	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. <i>International Journal of Biological Sciences</i> , 2018, 14, 983-991.	6.4	19
48	3-D Facial Landmarks Detection for Intelligent Video Systems. <i>IEEE Transactions on Industrial Informatics</i> , 2021, 17, 578-586.	11.3	18
49	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. <i>Molecular BioSystems</i> , 2016, 12, 3702-3710.	2.9	17
50	A Network-guided Association Mapping Approach from DNA Methylation to Disease. <i>Scientific Reports</i> , 2019, 9, 5601.	3.3	17
51	Learning Representations to Predict Intermolecular Interactions on Large-Scale Heterogeneous Molecular Association Network. <i>IScience</i> , 2020, 23, 101261.	4.1	16
52	CIPPN: computational identification of protein pupylation sites by using neural network. <i>Oncotarget</i> , 2017, 8, 108867-108879.	1.8	16
53	A Rayleigh-Ritz style method for large-scale discriminant analysis. <i>Pattern Recognition</i> , 2014, 47, 1698-1708.	8.1	15
54	Inference of Large-scale Time-delayed Gene Regulatory Network with Parallel MapReduce Cloud Platform. <i>Scientific Reports</i> , 2018, 8, 17787.	3.3	13

#	ARTICLE	IF	CITATIONS
55	Base-resolution prediction of transcription factor binding signals by a deep learning framework. PLoS Computational Biology, 2022, 18, e1009941.	3.2	13
56	Module Based Differential Coexpression Analysis Method for Type 2 Diabetes. BioMed Research International, 2015, 2015, 1-8.	1.9	12
57	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
58	Image segmentation fusion using weakly supervised trace-norm multi-task learning method. IET Image Processing, 2018, 12, 1079-1085.	2.5	12
59	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
60	Image Co-Segmentation via Locally Biased Discriminative Clustering. IEEE Transactions on Knowledge and Data Engineering, 2019, 31, 2228-2233.	5.7	11
61	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
62	Constructing cancer patient-specific and group-specific gene networks with multi-omics data. BMC Medical Genomics, 2020, 13, 81.	1.5	10
63	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
64	Learning regulatory motifs by direct optimization of Fisher Exact Test Score. , 2016, , .		8
65	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
66	Motif Discovery via Convolutional Networks with K-mer Embedding. Lecture Notes in Computer Science, 2019, , 374-382.	1.3	6
67	Hierarchical Graph Pooling With Self-Adaptive Cluster Aggregation. IEEE Transactions on Cognitive and Developmental Systems, 2022, 14, 1198-1207.	3.8	6
68	A novel diversity-guided ensemble of neural network based on attractive and repulsive particle swarm optimization. , 2015, , .		5
69	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
70	Editorial: Special Issue on Advanced Intelligent Computing: Theory and Applications. Neurocomputing, 2017, 228, 1-2.	5.9	2
71	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
72	A two-stage geometric method for detecting unreliable links in protein-protein networks. , 2014, , .		1

#	ARTICLE	IF	CITATIONS
73	Visual data completion via local sensitive low rank tensor learning. , 2016, , .		1
74	Convex local sensitive low rank matrix approximation. , 2017, , .		1
75	Soft-bag based motif discovery for ChIP-seq datasets. , 2017, , .		1
76	Improving Type 2 Diabetes Phenotypic Classification by Combining Genetics and Conventional Risk Factors. , 2018, , .		1
77	Fast sequence analysis based on diamond sampling. PLoS ONE, 2018, 13, e0198922.	2.5	1
78	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
79	A novel texture image segmentation model based on multi-scale structure. , 2014, , .		0
80	Imputation of ChIP-seq datasets via Low Rank Convex Co-Embedding. , 2015, , .		0
81	ILSES: Identification lysine succinylation-sites with ensemble classification. , 2016, , .		0
82	Representing logical relations automatically by Probabilistic Logical Dynamical Neural Network. , 2016, , .		0
83	Cross-validated smooth multi-instance learning. , 2017, , .		0
84	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
85	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
86	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
87	Guest Editorial for Special Section on the 15 <sup>th</sup> International Conference on Intelligent Computing (ICIC). IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1730-1732.	3.0	0
88	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