Wen Zhang

List of Publications by Year
in descending order

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102 papers	4,061 citations	126907 33 h-index	133252 59 g-index
104 all docs	104 docs citations	104 times ranked	2091 citing authors

#	Article	IF	Citations
1	Predicting Coding Potential of RNA Sequences by Solving Local Data Imbalance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1075-1083.	3.0	12
2	A Comprehensive Review of Computational Methods For Drug-Drug Interaction Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1968-1985.	3.0	38
3	A Multimodal Framework for Improvingin SilicoDrug Repositioning With the Prior Knowledge From Knowledge Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2623-2631.	3.0	12
4	PHIAF: prediction of phage-host interactions with GAN-based data augmentation and sequence-based feature fusion. Briefings in Bioinformatics, 2022, 23, .	6.5	18
5	MVGCN: data integration through multi-view graph convolutional network for predicting links in biomedical bipartite networks. Bioinformatics, 2022, 38, 426-434.	4.1	40
6	SGNNMD: signed graph neural network for predicting deregulation types of miRNA-disease associations. Briefings in Bioinformatics, 2022, 23, .	6.5	14
7	GraphCDR: a graph neural network method with contrastive learning for cancer drug response prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	38
8	Credit risk prediction of SMEs in supply chain finance by fusing demographic and behavioral data. Transportation Research, Part E: Logistics and Transportation Review, 2022, 158, 102611.	7.4	37
9	META-DDIE: predicting drugâ€“drug interaction events with few-shot learning. Briefings in Bioinformatics, 2022, 23, .	6.5	26
10	A heterogeneous network-based method with attentive meta-path extraction for predicting drugâ€“target interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	15
11	DSEATM: drug set enrichment analysis uncovering disease mechanisms by biomedical text mining. Briefings in Bioinformatics, 2022, 23, .	6.5	2
12	Predicting drugâ€“disease associations through layer attention graph convolutional network. Briefings in Bioinformatics, 2021, 22, .	6.5	186
13	Tensor decomposition with relational constraints for predicting multiple types of microRNA-disease associations. Briefings in Bioinformatics, 2021, 22, .	6.5	50
14	A Fast Linear Neighborhood Similarity-Based Network Link Inference Method to Predict MicroRNA-Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 405-415.	3.0	89
15	EPIHC: Improving Enhancer-Promoter Interaction Prediction by using Hybrid features and Communicative learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	3
16	Feature selection based on fuzzy joint mutual information maximization. Mathematical Biosciences and Engineering, 2021, 18, 305-327.	1.9	2
17	A systematic review of computational methods for predicting long noncoding RNAs. Briefings in Functional Genomics, 2021, 20, 162-173.	2.7	13
18	ACP-DA: Improving the Prediction of Anticancer Peptides Using Data Augmentation. Frontiers in Genetics, 2021, 12, 698477.	2.3	22

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19	ADEIP: an integrated platform of age-dependent expression and immune profiles across human tissues. Briefings in Bioinformatics, 2021, 22, .	6.5	6
20	CSGNN: Contrastive Self-Supervised Graph Neural Network for Molecular Interaction Prediction. , 2021, , .		11
21	A spatiotemporal estimation method for hourly rainfall based on F-SVD in the recommender system. Environmental Modelling and Software, 2021, 144, 105148.	4.5	8
22	A robust drug representation learning model for eliminating cell specificity in gene expression profile and its application. , 2021, , .		1
23	Predicting Drug-miRNA Resistance with Layer Attention Graph Convolution Network and Multi Channel Feature Extraction. , 2021, , .		1
24	MiRNA-Drug Resistance Association Prediction Through the Attentive Multimodal Graph Convolutional Network. Frontiers in Pharmacology, 2021, 12, 799108.	3.5	9
25	Graph embedding on biomedical networks: methods, applications and evaluations. Bioinformatics, 2020, 36, 1241-1251.	4.1	253
26	ncRNA-eQTL: a database to systematically evaluate the effects of SNPs on non-coding RNA expression across cancer types. Nucleic Acids Research, 2020, 48, D956-D963.	14.5	56
27	Graph embedding and ensemble learning for predicting gene-disease associations. International Journal of Data Mining and Bioinformatics, 2020, 23, 360.	0.1	0
28	Predicting Long non-coding RNAs through feature ensemble learning. BMC Genomics, 2020, 21, 865.	2.8	2
29	Graph embedding ensemble methods based on the heterogeneous network for lncRNA-miRNA interaction prediction. BMC Genomics, 2020, 21, 867.	2.8	17
30	A multimodal deep learning framework for predicting drugâ€“drug interaction events. Bioinformatics, 2020, 36, 4316-4322.	4.1	202
31	Predicting drug-drug interactions using multi-modal deep auto-encoders based network embedding and positive-unlabeled learning. Methods, 2020, 179, 37-46.	3.8	49
32	ItLnc-BXE: A Bagging-XGBoost-Ensemble Method With Comprehensive Sequence Features for Identification of Plant lncRNAs. IEEE Access, 2020, 8, 68811-68819.	4.2	5
33	Graph embedding and ensemble learning for predicting gene-disease associations. International Journal of Data Mining and Bioinformatics, 2020, 23, 360.	0.1	0
34	Predicting CircRNA-Disease Associations Through Linear Neighborhood Label Propagation Method. IEEE Access, 2019, 7, 83474-83483.	4.2	48
35	Recent Advances in the Machine Learning-Based Drug-Target Interaction Prediction. Current Drug Metabolism, 2019, 20, 194-202.	1.2	48
36	PredLnc-GFStack: A Global Sequence Feature Based on a Stacked Ensemble Learning Method for Predicting lncRNAs from Transcripts. Genes, 2019, 10, 672.	2.4	21

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37	A network embedding-based multiple information integration method for the MiRNA-disease association prediction. BMC Bioinformatics, 2019, 20, 468.	2.6	62
38	SFLLN: A sparse feature learning ensemble method with linear neighborhood regularization for predicting drugâ€“drug interactions. Information Sciences, 2019, 497, 189-201.	6.9	129
39	An Ensemble Strategy to Predict Prognosis in Ovarian Cancer Based on Gene Modules. Frontiers in Genetics, 2019, 10, 366.	2.3	5
40	Structural Network Embedding using Multi-modal Deep Auto-encoders for Predicting Drug-drug Interactions. , 2019, , .		21
41	LncRNA-miRNA interaction prediction from the heterogeneous network through graph embedding ensemble learning. , 2019, , .		12
42	LncPred-IEL: A Long Non-coding RNA Prediction Method using Iterative Ensemble Learning. , 2019, , .		5
43	Detection of Cell Types from Single-cell RNA-seq Data using Similarity via Kernel Preserving Learning Embedding. , 2019, , .		4
44	Predicting gene-disease associations from the heterogeneous network using graph embedding. , 2019, , .		21
45	LncRNA-miRNA interaction prediction through sequence-derived linear neighborhood propagation method with information combination. BMC Genomics, 2019, 20, 946.	2.8	49
46	Feature-derived graph regularized matrix factorization for predicting drug side effects. Neurocomputing, 2018, 287, 154-162.	5.9	96
47	The linear neighborhood propagation method for predicting long non-coding RNAâ€“protein interactions. Neurocomputing, 2018, 273, 526-534.	5.9	171
48	Sequence-derived linear neighborhood propagation method for predicting lncRNA-miRNA interactions. , 2018, , .		8
49	Prediction of Drug-Disease Associations and Their Effects by Signed Network-Based Nonnegative Matrix Factorization. , 2018, , .		8
50	HNGRNMF: Heterogeneous Network-based Graph Regularized Nonnegative Matrix Factorization for predicting events of microbe-disease associations. , 2018, , .		6
51	Manifold regularized matrix factorization for drug-drug interaction prediction. Journal of Biomedical Informatics, 2018, 88, 90-97.	4.3	104
52	Sequence-based bacterial small RNAs prediction using ensemble learning strategies. BMC Bioinformatics, 2018, 19, 503.	2.6	16
53	SFPEL-LPI: Sequence-based feature projection ensemble learning for predicting LncRNA-protein interactions. PLoS Computational Biology, 2018, 14, e1006616.	3.2	164
54	The Bi-Direction Similarity Integration Method for Predicting Microbe-Disease Associations. IEEE Access, 2018, 6, 38052-38061.	4.2	50

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55	MicroRNAâ€'126 accelerates IgEâ€'mediated mast cell degranulation associated with the PI3K/Akt signaling pathway by promoting Ca2+ influx. Experimental and Therapeutic Medicine, 2018, 16, 2763-2769.	1.8	11
56	IRWNRLPI: Integrating Random Walk and Neighborhood Regularized Logistic Matrix Factorization for lncRNA-Protein Interaction Prediction. Frontiers in Genetics, 2018, 9, 239.	2.3	83
57	Predicting drug-disease associations by using similarity constrained matrix factorization. BMC Bioinformatics, 2018, 19, 233.	2.6	206
58	Predicting drug-disease associations and their therapeutic function based on the drug-disease association bipartite network. Methods, 2018, 145, 51-59.	3.8	104
59	Quantitative prediction of drug side effects based on drug-related features. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 434-444.	3.6	20
60	Predicting drug-disease associations based on the known association bipartite network. , 2017, , .		24
61	Predicting small RNAs in bacteria via sequence learning ensemble method. , 2017, , .		4
62	Drug-Target Interaction Prediction through Label Propagation with Linear Neighborhood Information. Molecules, 2017, 22, 2056.	3.8	68
63	A unified frame of predicting side effects of drugs by using linear neighborhood similarity. BMC Systems Biology, 2017, 11, 101.	3.0	70
64	Predicting potential drug-drug interactions by integrating chemical, biological, phenotypic and network data. BMC Bioinformatics, 2017, 18, 18.	2.6	231
65	Predicting human splicing branchpoints by combining sequence-derived features and multi-label learning methods. BMC Bioinformatics, 2017, 18, 464.	2.6	24
66	LPI-NRLMF: lncRNA-protein interaction prediction by neighborhood regularized logistic matrix factorization. Oncotarget, 2017, 8, 103975-103984.	1.8	35
67	Multi-Domain Manifold Learning for Drug-Target Interaction Prediction. , 2016, , .		2
68	Drug side effect prediction through linear neighborhoods and multiple data source integration. , 2016, , .		39
69	A genetic algorithm-based weighted ensemble method for predicting transposon-derived piRNAs. BMC Bioinformatics, 2016, 17, 329.	2.6	70
70	The prediction of human splicing branchpoints by multi-label learning. , 2016, , .		3
71	GRIM-19 inhibition induced autophagy through activation of ERK and HIF-1Î± not STAT3 in Hela cells. Tumor Biology, 2016, 37, 9789-9796.	1.8	17
72	Predicting potential side effects of drugs by recommender methods and ensemble learning. Neurocomputing, 2016, 173, 979-987.	5.9	109

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73	Accurate Prediction of Transposon-Derived piRNAs by Integrating Various Sequential and Physicochemical Features. PLoS ONE, 2016, 11, e0153268.	2.5	52
74	GPU-Based Medical Visualization for Large Datasets. Journal of Medical Imaging and Health Informatics, 2015, 5, 1467-1473.	0.3	1
75	Predicting drug side effects by multi-label learning and ensemble learning. BMC Bioinformatics, 2015, 16, 365.	2.6	138
76	An improved cerebral vessel extraction method for MRA images. Bio-Medical Materials and Engineering, 2015, 26, S1231-S1240.	0.6	3
77	Accurate Prediction of Immunogenic T-Cell Epitopes from Epitope Sequences Using the Genetic Algorithm-Based Ensemble Learning. PLoS ONE, 2015, 10, e0128194.	2.5	35
78	BUTTER: An Approach to Bug Triage with Topic Modeling and Heterogeneous Network Analysis. , 2014, , .		4
79	FixerCache. , 2014, , .		29
80	Prediction of Conformational B-Cell Epitopes. Methods in Molecular Biology, 2014, 1184, 185-196.	0.9	5
81	Databases for B-Cell Epitopes. Methods in Molecular Biology, 2014, 1184, 135-148.	0.9	5
82	LSG: A Unified Multi-dimensional Latent Semantic Graph for Personal Information Retrieval. Lecture Notes in Computer Science, 2014, , 540-552.	1.3	0
83	DevNet: Exploring Developer Collaboration in Heterogeneous Networks of Bug Repositories. , 2013, , .		19
84	Heterogeneous Network Analysis of Developer Contribution in Bug Repositories. , 2013, , .		19
85	Predicting immunogenic T-cell epitopes by combining various sequence-derived features. , 2013, , .		10
86	Predicting linear B-cell epitopes by using sequence-derived structural and physicochemical features. International Journal of Data Mining and Bioinformatics, 2012, 6, 557.	0.1	22
87	Computational Prediction of Conformational B-Cell Epitopes from Antigen Primary Structures by Ensemble Learning. PLoS ONE, 2012, 7, e43575.	2.5	52
88	Prediction of heme binding residues from protein sequences with integrative sequence profiles. Proteome Science, 2012, 10, S20.	1.7	36
89	Prediction of Heme Binding Sites in Heme Proteins Using an Integrative Sequence Profile Coupling Evolutionary Information with Physicochemical Properties. , 2011, , .		0
90	Exploiting a Reduced Set of Weighted Average Features to Improve Prediction of DNA-Binding Residues from 3D Structures. PLoS ONE, 2011, 6, e28440.	2.5	30

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91	Prediction of conformational B-cell epitopes from 3D structures by random forests with a distance-based feature. BMC Bioinformatics, 2011, 12, 341.	2.6	92
92	Predicting cleavage sites in exogenous antigen using weighted SVM. , 2010, , .		0
93	A novel locally linear embedding and wavelet transform based encoding method for prediction of MHC-II binding affinity. Interdisciplinary Sciences, Computational Life Sciences, 2010, 2, 145-150.	3.6	1
94	Quantitative prediction of MHC-II binding affinity using particle swarm optimization. Artificial Intelligence in Medicine, 2010, 50, 127-132.	6.5	16
95	Predicting flexible length linear B-cell epitopes using pairwise sequence similarity. , 2010, , .		5
96	Quantitative prediction of MHC-II peptide binding affinity using relevance vector machine. Applied Intelligence, 2009, 31, 180-187.	5.3	10
97	Detecting the community structure in complex networks based on quantum mechanics. Physica A: Statistical Mechanics and Its Applications, 2008, 387, 6215-6224.	2.6	15
98	A Bayesian regression approach to the prediction of MHC-II binding affinity. Computer Methods and Programs in Biomedicine, 2008, 92, 1-7.	4.7	33
99	Quantitative Prediction of MHC-II Peptide Binding Affinity Using Global Description of Peptide Sequences. , 2008, , .		0
100	The research and implement of tamper-proof in surveillance audio coding. , 2008, , .		0
101	Gene Selection for Cancer Classification Using Relevance Vector Machine. , 2007, , .		1
102	Gene Selection Using Rough Set Theory. Lecture Notes in Computer Science, 2006, , 778-785.	1.3	17