

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	Graph embedding on biomedical networks: methods, applications and evaluations. <i>Bioinformatics</i> , 2020, 36, 1241-1251.	4.1	253
2	Predicting potential drug-drug interactions by integrating chemical, biological, phenotypic and network data. <i>BMC Bioinformatics</i> , 2017, 18, 18.	2.6	231
3	Predicting drug-disease associations by using similarity constrained matrix factorization. <i>BMC Bioinformatics</i> , 2018, 19, 233.	2.6	206
4	A multimodal deep learning framework for predicting drug-drug interaction events. <i>Bioinformatics</i> , 2020, 36, 4316-4322.	4.1	202
5	Predicting drug-disease associations through layer attention graph convolutional network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	186
6	The linear neighborhood propagation method for predicting long non-coding RNA-protein interactions. <i>Neurocomputing</i> , 2018, 273, 526-534.	5.9	171
7	SFPEL-LPI: Sequence-based feature projection ensemble learning for predicting LncRNA-protein interactions. <i>PLoS Computational Biology</i> , 2018, 14, e1006616.	3.2	164
8	Predicting drug side effects by multi-label learning and ensemble learning. <i>BMC Bioinformatics</i> , 2015, 16, 365.	2.6	138
9	SFLLN: A sparse feature learning ensemble method with linear neighborhood regularization for predicting drug-drug interactions. <i>Information Sciences</i> , 2019, 497, 189-201.	6.9	129
10	Predicting potential side effects of drugs by recommender methods and ensemble learning. <i>Neurocomputing</i> , 2016, 173, 979-987.	5.9	109
11	Manifold regularized matrix factorization for drug-drug interaction prediction. <i>Journal of Biomedical Informatics</i> , 2018, 88, 90-97.	4.3	104
12	Predicting drug-disease associations and their therapeutic function based on the drug-disease association bipartite network. <i>Methods</i> , 2018, 145, 51-59.	3.8	104
13	Feature-derived graph regularized matrix factorization for predicting drug side effects. <i>Neurocomputing</i> , 2018, 287, 154-162.	5.9	96
14	Prediction of conformational B-cell epitopes from 3D structures by random forests with a distance-based feature. <i>BMC Bioinformatics</i> , 2011, 12, 341.	2.6	92
15	A Fast Linear Neighborhood Similarity-Based Network Link Inference Method to Predict MicroRNA-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 405-415.	3.0	89
16	IRWNRLPI: Integrating Random Walk and Neighborhood Regularized Logistic Matrix Factorization for lncRNA-Protein Interaction Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 239.	2.3	83
17	A genetic algorithm-based weighted ensemble method for predicting transposon-derived piRNAs. <i>BMC Bioinformatics</i> , 2016, 17, 329.	2.6	70
18	A unified frame of predicting side effects of drugs by using linear neighborhood similarity. <i>BMC Systems Biology</i> , 2017, 11, 101.	3.0	70

#	ARTICLE	IF	CITATIONS
19	Drug-Target Interaction Prediction through Label Propagation with Linear Neighborhood Information. <i>Molecules</i> , 2017, 22, 2056.	3.8	68
20	A network embedding-based multiple information integration method for the MiRNA-disease association prediction. <i>BMC Bioinformatics</i> , 2019, 20, 468.	2.6	62
21	ncRNA-eQTL: a database to systematically evaluate the effects of SNPs on non-coding RNA expression across cancer types. <i>Nucleic Acids Research</i> , 2020, 48, D956-D963.	14.5	56
22	Computational Prediction of Conformational B-Cell Epitopes from Antigen Primary Structures by Ensemble Learning. <i>PLoS ONE</i> , 2012, 7, e43575.	2.5	52
23	Accurate Prediction of Transposon-Derived piRNAs by Integrating Various Sequential and Physicochemical Features. <i>PLoS ONE</i> , 2016, 11, e0153268.	2.5	52
24	The Bi-Direction Similarity Integration Method for Predicting Microbe-Disease Associations. <i>IEEE Access</i> , 2018, 6, 38052-38061.	4.2	50
25	Tensor decomposition with relational constraints for predicting multiple types of microRNA-disease associations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	50
26	LncRNA-miRNA interaction prediction through sequence-derived linear neighborhood propagation method with information combination. <i>BMC Genomics</i> , 2019, 20, 946.	2.8	49
27	Predicting drug-drug interactions using multi-modal deep auto-encoders based network embedding and positive-unlabeled learning. <i>Methods</i> , 2020, 179, 37-46.	3.8	49
28	Predicting CircRNA-Disease Associations Through Linear Neighborhood Label Propagation Method. <i>IEEE Access</i> , 2019, 7, 83474-83483.	4.2	48
29	Recent Advances in the Machine Learning-Based Drug-Target Interaction Prediction. <i>Current Drug Metabolism</i> , 2019, 20, 194-202.	1.2	48
30	MVGCN: data integration through multi-view graph convolutional network for predicting links in biomedical bipartite networks. <i>Bioinformatics</i> , 2022, 38, 426-434.	4.1	40
31	Drug side effect prediction through linear neighborhoods and multiple data source integration. , 2016, , .		39
32	A Comprehensive Review of Computational Methods For Drug-Drug Interaction Detection. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1968-1985.	3.0	38
33	GraphCDR: a graph neural network method with contrastive learning for cancer drug response prediction. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	38
34	Credit risk prediction of SMEs in supply chain finance by fusing demographic and behavioral data. <i>Transportation Research, Part E: Logistics and Transportation Review</i> , 2022, 158, 102611.	7.4	37
35	Prediction of heme binding residues from protein sequences with integrative sequence profiles. <i>Proteome Science</i> , 2012, 10, S20.	1.7	36
36	LPI-NRLMF: lncRNA-protein interaction prediction by neighborhood regularized logistic matrix factorization. <i>Oncotarget</i> , 2017, 8, 103975-103984.	1.8	35

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37	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
38	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
39	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
40	FixerCache. , 2014, , .		29
41	META-DDIE: predicting drug-drug interaction events with few-shot learning. Briefings in Bioinformatics, 2022, 23, .	6.5	26
42	Predicting drug-disease associations based on the known association bipartite network. , 2017, , .		24
43	Predicting human splicing branchpoints by combining sequence-derived features and multi-label learning methods. BMC Bioinformatics, 2017, 18, 464.	2.6	24
44	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
45	ACP-DA: Improving the Prediction of Anticancer Peptides Using Data Augmentation. Frontiers in Genetics, 2021, 12, 698477.	2.3	22
46	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
47	Structural Network Embedding using Multi-modal Deep Auto-encoders for Predicting Drug-drug Interactions. , 2019, , .		21
48	Predicting gene-disease associations from the heterogeneous network using graph embedding. , 2019, , .		21
49	Quantitative prediction of drug side effects based on drug-related features. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 434-444.	3.6	20
50	DevNet: Exploring Developer Collaboration in Heterogeneous Networks of Bug Repositories. , 2013, , .		19
51	Heterogeneous Network Analysis of Developer Contribution in Bug Repositories. , 2013, , .		19
52	PHIAF: prediction of phage-host interactions with GAN-based data augmentation and sequence-based feature fusion. Briefings in Bioinformatics, 2022, 23, .	6.5	18
53	GRIM-19 inhibition induced autophagy through activation of ERK and HIF-1 α not STAT3 in Hela cells. Tumor Biology, 2016, 37, 9789-9796.	1.8	17
54	Graph embedding ensemble methods based on the heterogeneous network for lncRNA-miRNA interaction prediction. BMC Genomics, 2020, 21, 867.	2.8	17

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55	Gene Selection Using Rough Set Theory. Lecture Notes in Computer Science, 2006, , 778-785.	1.3	17
56	Quantitative prediction of MHC-II binding affinity using particle swarm optimization. Artificial Intelligence in Medicine, 2010, 50, 127-132.	6.5	16
57	Sequence-based bacterial small RNAs prediction using ensemble learning strategies. BMC Bioinformatics, 2018, 19, 503.	2.6	16
58	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
59	A heterogeneous network-based method with attentive meta-path extraction for predicting drug-target interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	15
60	SGNNMD: signed graph neural network for predicting deregulation types of miRNA-disease associations. Briefings in Bioinformatics, 2022, 23, .	6.5	14
61	A systematic review of computational methods for predicting long noncoding RNAs. Briefings in Functional Genomics, 2021, 20, 162-173.	2.7	13
62	LncRNA-miRNA interaction prediction from the heterogeneous network through graph embedding ensemble learning. , 2019, , .		12
63	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
64	A Multimodal Framework for Improving <i>in Silico</i> Drug Repositioning With the Prior Knowledge From Knowledge Graphs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2623-2631.	3.0	12
65	MicroRNA-126 accelerates IgE-mediated mast cell degranulation associated with the PI3K/Akt signaling pathway by promoting Ca ²⁺ influx. Experimental and Therapeutic Medicine, 2018, 16, 2763-2769.	1.8	11
66	CSGNN: Contrastive Self-Supervised Graph Neural Network for Molecular Interaction Prediction. , 2021, , .		11
67	Quantitative prediction of MHC-II peptide binding affinity using relevance vector machine. Applied Intelligence, 2009, 31, 180-187.	5.3	10
68	Predicting immunogenic T-cell epitopes by combining various sequence-derived features. , 2013, , .		10
69	MiRNA-Drug Resistance Association Prediction Through the Attentive Multimodal Graph Convolutional Network. Frontiers in Pharmacology, 2021, 12, 799108.	3.5	9
70	Sequence-derived linear neighborhood propagation method for predicting lncRNA-miRNA interactions. , 2018, , .		8
71	Prediction of Drug-Disease Associations and Their Effects by Signed Network-Based Nonnegative Matrix Factorization. , 2018, , .		8
72	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

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73	HNGRNMf: Heterogeneous Network-based Graph Regularized Nonnegative Matrix Factorization for predicting events of microbe-disease associations. , 2018, , .		6
74	ADEIP: an integrated platform of age-dependent expression and immune profiles across human tissues. Briefings in Bioinformatics, 2021, 22, .	6.5	6
75	Predicting flexible length linear B-cell epitopes using pairwise sequence similarity. , 2010, , .		5
76	An Ensemble Strategy to Predict Prognosis in Ovarian Cancer Based on Gene Modules. Frontiers in Genetics, 2019, 10, 366.	2.3	5
77	LncPred-IEL: A Long Non-coding RNA Prediction Method using Iterative Ensemble Learning. , 2019, , .		5
78	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
79	Prediction of Conformational B-Cell Epitopes. Methods in Molecular Biology, 2014, 1184, 185-196.	0.9	5
80	Databases for B-Cell Epitopes. Methods in Molecular Biology, 2014, 1184, 135-148.	0.9	5
81	BUTTER: An Approach to Bug Triage with Topic Modeling and Heterogeneous Network Analysis. , 2014, , .		4
82	Predicting small RNAs in bacteria via sequence learning ensemble method. , 2017, , .		4
83	Detection of Cell Types from Single-cell RNA-seq Data using Similarity via Kernel Preserving Learning Embedding. , 2019, , .		4
84	An improved cerebral vessel extraction method for MRA images. Bio-Medical Materials and Engineering, 2015, 26, S1231-S1240.	0.6	3
85	The prediction of human splicing branchpoints by multi-label learning. , 2016, , .		3
86	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
87	Multi-Domain Manifold Learning for Drug-Target Interaction Prediction. , 2016, , .		2
88	Predicting Long non-coding RNAs through feature ensemble learning. BMC Genomics, 2020, 21, 865.	2.8	2
89	Feature selection based on fuzzy joint mutual information maximization. Mathematical Biosciences and Engineering, 2021, 18, 305-327.	1.9	2
90	DSEATM: drug set enrichment analysis uncovering disease mechanisms by biomedical text mining. Briefings in Bioinformatics, 2022, 23, .	6.5	2

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91	Gene Selection for Cancer Classification Using Relevance Vector Machine. , 2007, , .		1
92	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
93	GPU-Based Medical Visualization for Large Datasets. Journal of Medical Imaging and Health Informatics, 2015, 5, 1467-1473.	0.3	1
94	A robust drug representation learning model for eliminating cell specificity in gene expression profile and its application. , 2021, , .		1
95	Predicting Drug-miRNA Resistance with Layer Attention Graph Convolution Network and Multi Channel Feature Extraction. , 2021, , .		1
96	Quantitative Prediction of MHC-II Peptide Binding Affinity Using Global Description of Peptide Sequences. , 2008, , .		0
97	The research and implement of tamper-proof in surveillance audio coding. , 2008, , .		0
98	Predicting cleavage sites in exogenous antigen using weighted SVM. , 2010, , .		0
99	Prediction of Heme Binding Sites in Heme Proteins Using an Integrative Sequence Profile Coupling Evolutionary Information with Physicochemical Properties. , 2011, , .		0
100	Graph embedding and ensemble learning for predicting gene-disease associations. International Journal of Data Mining and Bioinformatics, 2020, 23, 360.	0.1	0
101	LSG: A Unified Multi-dimensional Latent Semantic Graph for Personal Information Retrieval. Lecture Notes in Computer Science, 2014, , 540-552.	1.3	0
102	Graph embedding and ensemble learning for predicting gene-disease associations. International Journal of Data Mining and Bioinformatics, 2020, 23, 360.	0.1	0