Zheng-Wei Li

List of Publications by Year
in descending order

32 papers	1,083 citations	516710 16 h-index	454955 30 g-index
33 all docs	33 docs citations	33 times ranked	719 citing authors

#	Article	IF	Citations
1	Predicting miRNA–disease associations based on graph random propagation network and attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	25
2	Hierarchical graph attention network for miRNA-disease association prediction. Molecular Therapy, 2022, 30, 1775-1786.	8.2	31
3	iGRLCDA: identifying circRNA–disease association based on graph representation learning. Briefings in Bioinformatics, 2022, 23, .	6.5	17
4	A graph auto-encoder model for miRNA-disease associations prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	63
5	Delineating QSAR Descriptors to Explore the Inherent Properties of Naturally Occurring Polyphenols, Responsible for Alpha-Synuclein Amyloid Disaggregation Scheming Towards Effective Therapeutics Against Parkinson's Disorder. Lecture Notes in Computer Science, 2021, , 231-241.	1.3	0
6	Combined embedding model for MiRNA-disease association prediction. BMC Bioinformatics, 2021, 22, 161.	2.6	17
7	DF-MDA: An effective diffusion-based computational model for predicting miRNA-disease association. Molecular Therapy, 2021, 29, 1501-1511.	8.2	12
8	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. BMC Medical Informatics and Decision Making, 2021, 21, 254.	3.0	3
9	DANE-MDA: Predicting microRNA-disease associations via deep attributed network embedding. IScience, 2021, 24, 102455.	4.1	14
10	DBMDA: A Unified Embedding for Sequence-Based miRNA Similarity Measure with Applications to Predict and Validate miRNA-Disease Associations. Molecular Therapy - Nucleic Acids, 2020, 19, 602-611.	5.1	49
11	Predicting MiRNA-disease associations by multiple meta-paths fusion graph embedding model. BMC Bioinformatics, 2020, 21, 470.	2.6	19
12	FCGCNMDA: predicting miRNA-disease associations by applying fully connected graph convolutional networks. Molecular Genetics and Genomics, 2020, 295, 1197-1209.	2.1	23
13	A Network Embedding-Based Method for Predicting miRNA-Disease Associations by Integrating Multiple Information. Lecture Notes in Computer Science, 2020, , 367-377.	1.3	1
14	Expression and Gene Regulation Network of ELF3 in Breast Invasive Carcinoma Based on Data Mining. Lecture Notes in Computer Science, 2020, , 514-523.	1.3	0
15	GCNSP: A Novel Prediction Method of Self-Interacting Proteins Based on Graph Convolutional Networks. Lecture Notes in Computer Science, 2020, , 109-120.	1.3	1
16	MLMDA: a machine learning approach to predict and validate MicroRNA–disease associations by integrating of heterogenous information sources. Journal of Translational Medicine, 2019, 17, 260.	4.4	68
17	Precise Prediction of Pathogenic Microorganisms Using 16S rRNA Gene Sequences. Lecture Notes in Computer Science, 2019, , 138-150.	1.3	5
18	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. Knowledge-Based Systems, 2019, 186, 104963.	7.1	24

#	Article	IF	Citations
19	CMSENN: Computational Modification Sites with Ensemble Neural Network. Chemometrics and Intelligent Laboratory Systems, 2019, 185, 65-72.	3.5	20
20	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. International Journal of Molecular Sciences, 2019, 20, 113.	4.1	14
21	Using discriminative vector machine model with 2DPCA to predict interactions among proteins. BMC Bioinformatics, 2019, 20, 694.	2.6	7
22	An Efficient LightGBM Model to Predict Protein Self-interacting Using Chebyshev Moments and Bi-gram. Lecture Notes in Computer Science, 2019, , 453-459.	1.3	2
23	DRMDA: deep representationsâ€based miRNAâ€"disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485.	3.6	75
24	Efficient Framework for Predicting ncRNA-Protein Interactions Based on Sequence Information by Deep Learning. Lecture Notes in Computer Science, 2018, , 337-344.	1.3	3
25	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. Scientific Reports, 2017, 7, 11174.	3.3	62
26	PRMDA: personalized recommendation-based MiRNA-disease association prediction. Oncotarget, 2017, 8, 85568-85583.	1.8	32
27	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. PLoS Computational Biology, 2017, 13, e1005455.	3.2	387
28	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
29	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
30	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. International Journal of Molecular Sciences, 2016, 17, 1396.	4.1	35
31	A Self-Adaptive Mutation-Particle Swarm Optimization Algorithm. , 2008, , .		6
32	Research on the User Interest Modeling of personalized Search Engine. Wuhan University Journal of Natural Sciences, 2007, 12, 893-896.	0.4	6