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	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. PLoS Computational Biology, 2017, 13, e1005455.	3.2	387
2	DRMDA: deep representations–based miRNA–disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485.	3.6	75
3	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
4	A graph auto-encoder model for miRNA-disease associations prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	63
5	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. Scientific Reports, 2017, 7, 11174.	3.3	62
6	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
7	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
8	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
9	PRMDA: personalized recommendation-based MiRNA-disease association prediction. Oncotarget, 2017, 8, 85568-85583.	1.8	32
10	Hierarchical graph attention network for miRNA-disease association prediction. Molecular Therapy, 2022, 30, 1775-1786.	8.2	31
11	Predicting miRNA–disease associations based on graph random propagation network and attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	25
12	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
13	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. Knowledge-Based Systems, 2019, 186, 104963.	7.1	24
14	FCGCNMDA: predicting miRNA-disease associations by applying fully connected graph convolutional networks. Molecular Genetics and Genomics, 2020, 295, 1197-1209.	2.1	23
15	CMSENN: Computational Modification Sites with Ensemble Neural Network. Chemometrics and Intelligent Laboratory Systems, 2019, 185, 65-72.	3.5	20
16	Predicting MiRNA-disease associations by multiple meta-paths fusion graph embedding model. BMC Bioinformatics, 2020, 21, 470.	2.6	19
17	Combined embedding model for MiRNA-disease association prediction. BMC Bioinformatics, 2021, 22, 161.	2.6	17
18	iGRLCDA: identifying circRNA–disease association based on graph representation learning. Briefings in Bioinformatics, 2022, 23, .	6.5	17

#	Article	IF	Citations
19	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. International Journal of Molecular Sciences, 2019, 20, 113.	4.1	14
20	DANE-MDA: Predicting microRNA-disease associations via deep attributed network embedding. IScience, 2021, 24, 102455.	4.1	14
21	DF-MDA: An effective diffusion-based computational model for predicting miRNA-disease association. Molecular Therapy, 2021, 29, 1501-1511.	8.2	12
22	Using discriminative vector machine model with 2DPCA to predict interactions among proteins. BMC Bioinformatics, 2019, 20, 694.	2.6	7
23	Research on the User Interest Modeling of personalized Search Engine. Wuhan University Journal of Natural Sciences, 2007, 12, 893-896.	0.4	6
24	A Self-Adaptive Mutation-Particle Swarm Optimization Algorithm. , 2008, , .		6
25	Precise Prediction of Pathogenic Microorganisms Using 16S rRNA Gene Sequences. Lecture Notes in Computer Science, 2019, , 138-150.	1.3	5
26	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
27	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
28	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
29	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
30	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
31	Delineating QSAR Descriptors to Explore the Inherent Properties of Naturally Occurring Polyphenols, Responsible for Alpha-Synuclein Amyloid Disaggregation Scheming Towards Effective Therapeutics Against Parkinsonâ€™s Disorder. Lecture Notes in Computer Science, 2021, , 231-241.	1.3	0
32	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