

Zheng-Wei Li

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,083
citations

516215

16
h-index

454577

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. <i>PLoS Computational Biology</i> , 2017, 13, e1005455.	1.5	387
2	DRMDA: deep representations-based miRNA-disease association prediction. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 472-485.	1.6	75
3	MLMDA: a machine learning approach to predict and validate MicroRNA-disease associations by integrating of heterogenous information sources. <i>Journal of Translational Medicine</i> , 2019, 17, 260.	1.8	68
4	A graph auto-encoder model for miRNA-disease associations prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	63
5	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. <i>Scientific Reports</i> , 2017, 7, 11174.	1.6	62
6	DBMDA: A Unified Embedding for Sequence-Based miRNA Similarity Measure with Applications to Predict and Validate miRNA-Disease Associations. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 602-611.	2.3	49
7	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.	0.8	36
8	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1396.	1.8	35
9	PRMDA: personalized recommendation-based MiRNA-disease association prediction. <i>Oncotarget</i> , 2017, 8, 85568-85583.	0.8	32
10	Hierarchical graph attention network for miRNA-disease association prediction. <i>Molecular Therapy</i> , 2022, 30, 1775-1786.	3.7	31
11	Predicting miRNA-disease associations based on graph random propagation network and attention network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	25
12	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.	0.8	24
13	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. <i>Knowledge-Based Systems</i> , 2019, 186, 104963.	4.0	24
14	FCGCNMDA: predicting miRNA-disease associations by applying fully connected graph convolutional networks. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1197-1209.	1.0	23
15	CMSENN: Computational Modification Sites with Ensemble Neural Network. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 185, 65-72.	1.8	20
16	Predicting MiRNA-disease associations by multiple meta-paths fusion graph embedding model. <i>BMC Bioinformatics</i> , 2020, 21, 470.	1.2	19
17	Combined embedding model for MiRNA-disease association prediction. <i>BMC Bioinformatics</i> , 2021, 22, 161.	1.2	17
18	iGRLCDA: identifying circRNA-disease association based on graph representation learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	17

#	ARTICLE	IF	CITATIONS
19	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. International Journal of Molecular Sciences, 2019, 20, 113.	1.8	14
20	DANE-MDA: Predicting microRNA-disease associations via deep attributed network embedding. IScience, 2021, 24, 102455.	1.9	14
21	DF-MDA: An effective diffusion-based computational model for predicting miRNA-disease association. Molecular Therapy, 2021, 29, 1501-1511.	3.7	12
22	Using discriminative vector machine model with 2DPCA to predict interactions among proteins. BMC Bioinformatics, 2019, 20, 694.	1.2	7
23	Research on the User Interest Modeling of personalized Search Engine. Wuhan University Journal of Natural Sciences, 2007, 12, 893-896.	0.2	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.	1.0	5
26	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. BMC Medical Informatics and Decision Making, 2021, 21, 254.	1.5	3
27	Efficient Framework for Predicting ncRNA-Protein Interactions Based on Sequence Information by Deep Learning. Lecture Notes in Computer Science, 2018, , 337-344.	1.0	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.	1.0	2
29	A Network Embedding-Based Method for Predicting miRNA-Disease Associations by Integrating Multiple Information. Lecture Notes in Computer Science, 2020, , 367-377.	1.0	1
30	GCNSP: A Novel Prediction Method of Self-Interacting Proteins Based on Graph Convolutional Networks. Lecture Notes in Computer Science, 2020, , 109-120.	1.0	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 Parkinson's Disorder. Lecture Notes in Computer Science, 2021, , 231-241.	1.0	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.	1.0	0