

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	Predicting miRNA-disease associations based on graph random propagation network and attention network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	25
2	Hierarchical graph attention network for miRNA-disease association prediction. <i>Molecular Therapy</i> , 2022, 30, 1775-1786.	3.7	31
3	iGRLCDA: identifying circRNA-disease association based on graph representation learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	17
4	A graph auto-encoder model for miRNA-disease associations prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	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. <i>Lecture Notes in Computer Science</i> , 2021, , 231-241.	1.0	0
6	Combined embedding model for MiRNA-disease association prediction. <i>BMC Bioinformatics</i> , 2021, 22, 161.	1.2	17
7	DF-MDA: An effective diffusion-based computational model for predicting miRNA-disease association. <i>Molecular Therapy</i> , 2021, 29, 1501-1511.	3.7	12
8	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 254.	1.5	3
9	DANE-MDA: Predicting microRNA-disease associations via deep attributed network embedding. <i>IScience</i> , 2021, 24, 102455.	1.9	14
10	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
11	Predicting MiRNA-disease associations by multiple meta-paths fusion graph embedding model. <i>BMC Bioinformatics</i> , 2020, 21, 470.	1.2	19
12	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
13	A Network Embedding-Based Method for Predicting miRNA-Disease Associations by Integrating Multiple Information. <i>Lecture Notes in Computer Science</i> , 2020, , 367-377.	1.0	1
14	Expression and Gene Regulation Network of ELF3 in Breast Invasive Carcinoma Based on Data Mining. <i>Lecture Notes in Computer Science</i> , 2020, , 514-523.	1.0	0
15	GCNSP: A Novel Prediction Method of Self-Interacting Proteins Based on Graph Convolutional Networks. <i>Lecture Notes in Computer Science</i> , 2020, , 109-120.	1.0	1
16	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
17	Precise Prediction of Pathogenic Microorganisms Using 16S rRNA Gene Sequences. <i>Lecture Notes in Computer Science</i> , 2019, , 138-150.	1.0	5
18	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. <i>Knowledge-Based Systems</i> , 2019, 186, 104963.	4.0	24

#	ARTICLE	IF	CITATIONS
19	CMSENN: Computational Modification Sites with Ensemble Neural Network. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019, 185, 65-72.	1.8	20
20	LAIPT: Lysine Acetylation Site Identification with Polynomial Tree. <i>International Journal of Molecular Sciences</i> , 2019, 20, 113.	1.8	14
21	Using discriminative vector machine model with 2DPCA to predict interactions among proteins. <i>BMC Bioinformatics</i> , 2019, 20, 694.	1.2	7
22	An Efficient LightGBM Model to Predict Protein Self-interacting Using Chebyshev Moments and Bi-gram. <i>Lecture Notes in Computer Science</i> , 2019, , 453-459.	1.0	2
23	DRMDA: deep representations-based miRNA disease association prediction. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 472-485.	1.6	75
24	Efficient Framework for Predicting ncRNA-Protein Interactions Based on Sequence Information by Deep Learning. <i>Lecture Notes in Computer Science</i> , 2018, , 337-344.	1.0	3
25	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
26	PRMDA: personalized recommendation-based MiRNA-disease association prediction. <i>Oncotarget</i> , 2017, 8, 85568-85583.	0.8	32
27	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
28	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
29	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
30	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
31	A Self-Adaptive Mutation-Particle Swarm Optimization Algorithm. , 2008, , .		6
32	Research on the User Interest Modeling of personalized Search Engine. <i>Wuhan University Journal of Natural Sciences</i> , 2007, 12, 893-896.	0.2	6