

Pingjian Ding

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

942
citations

567144

15
h-index

454834

30
g-index

34
all docs

34
docs citations

34
times ranked

527
citing authors

#	ARTICLE	IF	CITATIONS
1	A graph regularized non-negative matrix factorization method for identifying microRNA-disease associations. <i>Bioinformatics</i> , 2018, 34, 239-248.	1.8	219
2	Collective Prediction of Disease-Associated miRNAs Based on Transduction Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 1468-1475.	1.9	63
3	Predicting microRNA-disease associations using label propagation based on linear neighborhood similarity. <i>Journal of Biomedical Informatics</i> , 2018, 82, 169-177.	2.5	63
4	Predicting MicroRNA-Disease Associations Using Kronecker Regularized Least Squares Based on Heterogeneous Omics Data. <i>IEEE Access</i> , 2017, 5, 2503-2513.	2.6	59
5	Predicting MicroRNA-Disease Associations Using Network Topological Similarity Based on DeepWalk. <i>IEEE Access</i> , 2017, 5, 24032-24039.	2.6	49
6	Prediction of LncRNA-Disease Associations Based on Network Consistency Projection. <i>IEEE Access</i> , 2019, 7, 58849-58856.	2.6	42
7	Ensemble Prediction of Synergistic Drug Combinations Incorporating Biological, Chemical, Pharmacological, and Network Knowledge. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 1336-1345.	3.9	39
8	NCPCDA: network consistency projection for circRNA-disease association prediction. <i>RSC Advances</i> , 2019, 9, 33222-33228.	1.7	39
9	Potential circRNA-disease association prediction using DeepWalk and network consistency projection. <i>Journal of Biomedical Informatics</i> , 2020, 112, 103624.	2.5	32
10	Semi-supervised prediction of human miRNA-disease association based on graph regularization framework in heterogeneous networks. <i>Neurocomputing</i> , 2018, 294, 29-38.	3.5	30
11	A path-based measurement for human miRNA functional similarities using miRNA-disease associations. <i>Scientific Reports</i> , 2016, 6, 32533.	1.6	29
12	KG-Predict: A knowledge graph computational framework for drug repurposing. <i>Journal of Biomedical Informatics</i> , 2022, 132, 104133.	2.5	28
13	Inferring MicroRNA Targets Based on Restricted Boltzmann Machines. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 427-436.	3.9	26
14	Human disease MiRNA inference by combining target information based on heterogeneous manifolds. <i>Journal of Biomedical Informatics</i> , 2018, 80, 26-36.	2.5	23
15	Heterogeneous information network and its application to human health and disease. <i>Briefings in Bioinformatics</i> , 2020, 21, 1327-1346.	3.2	17
16	Prediction of microRNA-disease associations with a Kronecker kernel matrix dimension reduction model. <i>RSC Advances</i> , 2018, 8, 4377-4385.	1.7	16
17	PCE-FR: A Novel Method for Identifying Overlapping Protein Complexes in Weighted Protein-Protein Interaction Networks Using Pseudo-Clique Extension Based on Fuzzy Relation. <i>IEEE Transactions on Nanobioscience</i> , 2016, 15, 728-738.	2.2	14
18	Incorporating Multisource Knowledge To Predict Drug Synergy Based on Graph Co-regularization. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 37-46.	2.5	14

#	ARTICLE	IF	CITATIONS
19	An in-silico method with graph-based multi-label learning for large-scale prediction of circRNA-disease associations. <i>Genomics</i> , 2020, 112, 3407-3415.	1.3	14
20	Multiview Joint Learning-Based Method for Identifying Small-Molecule-Associated MiRNAs by Integrating Pharmacological, Genomics, and Network Knowledge. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4085-4097.	2.5	13
21	Incorporating Clinical, Chemical and Biological Information for Predicting Small Molecule-microRNA Associations Based on Non-Negative Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2535-2545.	1.9	13
22	IDDkin: network-based influence deep diffusion model for enhancing prediction of kinase inhibitors. <i>Bioinformatics</i> , 2021, 36, 5481-5491.	1.8	13
23	Multiview Consensus Graph Learning for lncRNA-Disease Association Prediction. <i>Frontiers in Genetics</i> , 2020, 11, 89.	1.1	12
24	Detection of Protein Complexes Based on Penalized Matrix Decomposition in a Sparse Protein-Protein Interaction Network. <i>Molecules</i> , 2018, 23, 1460.	1.7	11
25	Self-Weighted Multi-Kernel Multi-Label Learning for Potential miRNA-Disease Association Prediction. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 414-423.	2.3	11
26	Identification of Small Molecule-miRNA Associations with Graph Regularization Techniques in Heterogeneous Networks. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 6709-6721.	2.5	11
27	A Meta-Path-Based Prediction Method for Human miRNA-Target Association. <i>BioMed Research International</i> , 2016, 2016, 1-9.	0.9	10
28	Discovering Synergistic Drug Combination from a Computational Perspective. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 965-974.	1.0	10
29	A Novel Group Wise-Based Method for Calculating Human miRNA Functional Similarity. <i>IEEE Access</i> , 2017, 5, 2364-2372.	2.6	8
30	GRTR: Drug-Disease Association Prediction Based on Graph Regularized Transductive Regression on Heterogeneous Network. <i>Lecture Notes in Computer Science</i> , 2018, , 13-25.	1.0	6
31	An In Silico Method for Predicting Drug Synergy Based on Multitask Learning. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 299-311.	2.2	4
32	Identification of overlapping protein complexes by fuzzy K-medoids clustering algorithm in yeast protein-protein interaction networks. <i>Journal of Intelligent and Fuzzy Systems</i> , 2018, 34, 93-103.	0.8	3
33	Inferring Synergistic Drug Combinations based on Symmetric Meta-Path in a Novel Heterogeneous Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	1
34	Meta-Path Based Inductive Classification in Heterogeneous Information Networks. <i>Journal of Computational and Theoretical Nanoscience</i> , 2016, 13, 6747-6753.	0.4	0