Pingjian Ding

List of Publications by Year
in descending order

34 papers	942 citations	567144 15 h-index
34 all docs	34 docs citations	34 times ranked

454834 30 g-index	527 citing authors

#	Article	IF	Citations
1	KG-Predict: A knowledge graph computational framework for drug repurposing. Journal of Biomedical Informatics, 2022, 132, 104133.	2.5	28
2	Incorporating Clinical, Chemical and Biological Information for Predicting Small Molecule-microRNA Associations Based on Non-Negative Matrix Factorization. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2535-2545.	1.9	13
3	An In Silico Method for Predicting Drug Synergy Based on Multitask Learning. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 299-311.	2.2	4
4	IDDkin: network-based influence deep diffusion model for enhancing prediction of kinase inhibitors. Bioinformatics, 2021, 36, 5481-5491.	1.8	13
5	Heterogeneous information network and its application to human health and disease. Briefings in Bioinformatics, 2020, 21, 1327-1346.	3.2	17
6	Incorporating Multisource Knowledge To Predict Drug Synergy Based on Graph Co-regularization. Journal of Chemical Information and Modeling, 2020, 60, 37-46.	2.5	14
7	Identification of Small Molecule–miRNA Associations with Graph Regularization Techniques in Heterogeneous Networks. Journal of Chemical Information and Modeling, 2020, 60, 6709-6721.	2.5	11
8	Potential circRNA-disease association prediction using DeepWalk and network consistency projection. Journal of Biomedical Informatics, 2020, 112, 103624.	2.5	32
9	Multiview Joint Learning-Based Method for Identifying Small-Molecule-Associated MiRNAs by Integrating Pharmacological, Genomics, and Network Knowledge. Journal of Chemical Information and Modeling, 2020, 60, 4085-4097.	2.5	13
10	An in-silico method with graph-based multi-label learning for large-scale prediction of circRNA-disease associations. Genomics, 2020, 112, 3407-3415.	1.3	14
11	Multiview Consensus Graph Learning for lncRNA–Disease Association Prediction. Frontiers in Genetics, 2020, 11, 89.	1.1	12
12	Ensemble Prediction of Synergistic Drug Combinations Incorporating Biological, Chemical, Pharmacological, and Network Knowledge. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1336-1345.	3.9	39
13	Self-Weighted Multi-Kernel Multi-Label Learning for Potential miRNA-Disease Association Prediction. Molecular Therapy - Nucleic Acids, 2019, 17, 414-423.	2.3	11
14	Prediction of LncRNA-Disease Associations Based on Network Consistency Projection. IEEE Access, 2019, 7, 58849-58856.	2.6	42
15	Inferring Synergistic Drug Combinations based on Symmetric Meta-Path in a Novel Heterogeneous Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	1
16	NCPCDA: network consistency projection for circRNA–disease association prediction. RSC Advances, 2019, 9, 33222-33228.	1.7	39
17	Inferring MicroRNA Targets Based on Restricted Boltzmann Machines. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 427-436.	3.9	26
18	Human disease MiRNA inference by combining target information based on heterogeneous manifolds. Journal of Biomedical Informatics, 2018, 80, 26-36.	2.5	23

#	Article	IF	Citations
19	Prediction of microRNA–disease associations with a Kronecker kernel matrix dimension reduction model. RSC Advances, 2018, 8, 4377-4385.	1.7	16
20	Identification of overlapping protein complexes by fuzzy K-medoids clustering algorithm in yeast protein-protein interaction networks. Journal of Intelligent and Fuzzy Systems, 2018, 34, 93-103.	0.8	3
21	Semi-supervised prediction of human miRNA-disease association based on graph regularization framework in heterogeneous networks. Neurocomputing, 2018, 294, 29-38.	3.5	30
22	A graph regularized non-negative matrix factorization method for identifying microRNA-disease associations. Bioinformatics, 2018, 34, 239-248.	1.8	219
23	Predicting microRNA-disease associations using label propagation based on linear neighborhood similarity. Journal of Biomedical Informatics, 2018, 82, 169-177.	2.5	63
24	GRTR: Drug-Disease Association Prediction Based on Graph Regularized Transductive Regression on Heterogeneous Network. Lecture Notes in Computer Science, 2018, , 13-25.	1.0	6
25	Detection of Protein Complexes Based on Penalized Matrix Decomposition in a Sparse Protein–Protein Interaction Network. Molecules, 2018, 23, 1460.	1.7	11
26	Discovering Synergistic Drug Combination from a Computational Perspective. Current Topics in Medicinal Chemistry, 2018, 18, 965-974.	1.0	10
27	A Novel Group Wise-Based Method for Calculating Human miRNA Functional Similarity. IEEE Access, 2017, 5, 2364-2372.	2.6	8
28	Predicting MicroRNA-Disease Associations Using Kronecker Regularized Least Squares Based on Heterogeneous Omics Data. IEEE Access, 2017, 5, 2503-2513.	2.6	59
29	Collective Prediction of Disease-Associated miRNAs Based on Transduction Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1468-1475.	1.9	63
30	Predicting MicroRNA-Disease Associations Using Network Topological Similarity Based on DeepWalk. IEEE Access, 2017, 5, 24032-24039.	2.6	49
31	A Meta-Path-Based Prediction Method for Human miRNA-Target Association. BioMed Research International, 2016, 2016, 1-9.	0.9	10
32	PCE-FR: A Novel Method for Identifying Overlapping Protein Complexes in Weighted Protein-Protein Interaction Networks Using Pseudo-Clique Extension Based on Fuzzy Relation. IEEE Transactions on Nanobioscience, 2016, 15, 728-738.	2.2	14
33	A path-based measurement for human miRNA functional similarities using miRNA-disease associations. Scientific Reports, 2016, 6, 32533.	1.6	29
34	Meta-Path Based Inductive Classification in Heterogeneous Information Networks. Journal of Computational and Theoretical Nanoscience, 2016, 13, 6747-6753.	0.4	0