

Xing Chen

List of Publications by Year in descending order

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Version: 2024-02-01

143
papers

14,364
citations

23567

58
h-index

20358

116
g-index

145
all docs

145
docs citations

145
times ranked

6501
citing authors

#	ARTICLE	IF	CITATIONS
1	Ensemble of kernel ridge regression-based small molecule-miRNA association prediction in human disease. Briefings in Bioinformatics, 2022, 23, .	6.5	24
2	Comparison of [68Ga]Ga-FAPI-04 and [18F]-FDG for the detection of primary and metastatic lesions in patients with gastric cancer: a bicentric retrospective study. European Journal of Nuclear Medicine and Molecular Imaging, 2022, 49, 732-742.	6.4	55
3	Dual-Network Collaborative Matrix Factorization for predicting small molecule-miRNA associations. Briefings in Bioinformatics, 2022, 23, .	6.5	15
4	A two-stage cardiac PET and late gadolinium enhancement MRI co-registration method for improved assessment of non-ischemic cardiomyopathies using integrated PET/MR. European Journal of Nuclear Medicine and Molecular Imaging, 2022, 49, 2199-2208.	6.4	1
5	Prediction of potential miRNA-disease associations based on stacked autoencoder. Briefings in Bioinformatics, 2022, 23, .	6.5	31
6	Drug-pathway association prediction: from experimental results to computational models. Briefings in Bioinformatics, 2021, 22, .	6.5	30
7	NCMCMDA: miRNA-disease association prediction through neighborhood constraint matrix completion. Briefings in Bioinformatics, 2021, 22, 485-496.	6.5	148
8	Microbes and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2021, 22, .	6.5	29
9	Deep-belief network for predicting potential miRNA-disease associations. Briefings in Bioinformatics, 2021, 22, .	6.5	101
10	Crosstalk between hypoxia-sensing ULK1/2 and YAP-driven glycolysis fuels pancreatic ductal adenocarcinoma development. International Journal of Biological Sciences, 2021, 17, 2772-2794.	6.4	9
11	Circular RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2021, 22, .	6.5	116
12	Identification of miRNA-disease associations via multiple information integration with Bayesian ranking. Briefings in Bioinformatics, 2021, 22, .	6.5	17
13	Predicting potential small molecule-miRNA associations based on bounded nuclear norm regularization. Briefings in Bioinformatics, 2021, 22, .	6.5	44
14	Potential miRNA-disease association prediction based on kernelized Bayesian matrix factorization. Genomics, 2020, 112, 809-819.	2.9	32
15	SNMFSMMA: using symmetric nonnegative matrix factorization and Kronecker regularized least squares to predict potential small molecule-microRNA association. RNA Biology, 2020, 17, 281-291.	3.1	50
16	Current Computational Models for Prediction of the Varied Interactions Related to Protein - Part 2. Protein and Peptide Letters, 2020, 27, 347-347.	0.9	0
17	Editorial: Bioinformatics in Microbiota. Frontiers in Microbiology, 2020, 11, 100.	3.5	5
18	Computational Models in Non-Coding RNA and Human Disease. International Journal of Molecular Sciences, 2020, 21, 1557.	4.1	9

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19	A Computational Study of Potential miRNA-Disease Association Inference Based on Ensemble Learning and Kernel Ridge Regression. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 40.	4.1	37
20	Physiological Left Bundle Branch Pacing Validated by Ultra-High Density Ventricular Mapping in a Swine Model. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020, 13, e007898.	4.8	5
21	Feasibility and cardiac synchrony of permanent left bundle branch pacing through the interventricular septum. <i>Europace</i> , 2019, 21, 1694-1702.	1.7	173
22	Ensemble of decision tree reveals potential miRNA-disease associations. <i>PLoS Computational Biology</i> , 2019, 15, e1007209.	3.2	166
23	Anticancer Drug Response Prediction in Cell Lines Using Weighted Graph Regularized Matrix Factorization. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 164-174.	5.1	62
24	Engineering Onâ€Demand Magnetic Coreâ€Shell Composite Wound Dressing Matrices via Electrohydrodynamic Microâ€Scale Printing. <i>Advanced Engineering Materials</i> , 2019, 21, 1900699.	3.5	16
25	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. <i>Knowledge-Based Systems</i> , 2019, 186, 104963.	7.1	24
26	Prediction of Potential miRNAâ€Disease Associations Through a Novel Unsupervised Deep Learning Framework with Variational Autoencoder. <i>Cells</i> , 2019, 8, 1040.	4.1	47
27	Prediction of Small Moleculeâ€MicroRNA Associations by Sparse Learning and Heterogeneous Graph Inference. <i>Molecular Pharmaceutics</i> , 2019, 16, 3157-3166.	4.6	38
28	Computational Model Development of Drug-Target Interaction Prediction: A Review. <i>Current Protein and Peptide Science</i> , 2019, 20, 492-494.	1.4	23
29	Adaptive boosting-based computational model for predicting potential miRNA-disease associations. <i>Bioinformatics</i> , 2019, 35, 4730-4738.	4.1	125
30	RFSMMA: A New Computational Model to Identify and Prioritize Potential Small Moleculeâ€MiRNA Associations. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1668-1679.	5.4	45
31	In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 14, 274-286.	5.1	54
32	LMTRDA: Using logistic model tree to predict MiRNA-disease associations by fusing multi-source information of sequences and similarities. <i>PLoS Computational Biology</i> , 2019, 15, e1006865.	3.2	111
33	FGF15 Activates Hippo Signaling to Suppress Bile Acid Metabolism and Liver Tumorigenesis. <i>Developmental Cell</i> , 2019, 48, 460-474.e9.	7.0	68
34	Integrating random walk and binary regression to identify novel miRNA-disease association. <i>BMC Bioinformatics</i> , 2019, 20, 59.	2.6	30
35	A Unified Framework for the Prediction of Small Moleculeâ€MicroRNA Association Based on Cross-Layer Dependency Inference on Multilayered Networks. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 5281-5293.	5.4	22
36	An integrated framework for the identification of potential miRNA-disease association based on novel negative samples extraction strategy. <i>RNA Biology</i> , 2019, 16, 257-269.	3.1	35

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37	Computational models for lncRNA function prediction and functional similarity calculation. Briefings in Functional Genomics, 2019, 18, 58-82.	2.7	141
38	MicroRNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2019, 20, 515-539.	6.5	507
39	RNA methylation and diseases: experimental results, databases, Web servers and computational models. Briefings in Bioinformatics, 2019, 20, 896-917.	6.5	74
40	HNMDA: heterogeneous network-based miRNA-disease association prediction. Molecular Genetics and Genomics, 2018, 293, 983-995.	2.1	19
41	ELLPMDA: Ensemble learning and link prediction for miRNA-disease association prediction. RNA Biology, 2018, 15, 1-12.	3.1	58
42	GIMDA: Graphlet interaction-based MiRNA-disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 1548-1561.	3.6	25
43	EGBMMDA: Extreme Gradient Boosting Machine for MiRNA-Disease Association prediction. Cell Death and Disease, 2018, 9, 3.	6.3	256
44	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. Nucleic Acids Research, 2018, 46, D281-D287.	14.5	115
45	BNPMDA: Bipartite Network Projection for MiRNA-disease Association prediction. Bioinformatics, 2018, 34, 3178-3186.	4.1	307
46	NDAMDA: Network distance analysis for MiRNA-disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 2884-2895.	3.6	34
47	An improved efficient rotation forest algorithm to predict the interactions among proteins. Soft Computing, 2018, 22, 3373-3381.	3.6	34
48	DroidDet: Effective and robust detection of android malware using static analysis along with rotation forest model. Neurocomputing, 2018, 272, 638-646.	5.9	146
49	DRMDA: deep representations-based miRNA-disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485.	3.6	75
50	A Computational-Based Method for Predicting Drug-Target Interactions by Using Stacked Autoencoder Deep Neural Network. Journal of Computational Biology, 2018, 25, 361-373.	1.6	140
51	MDAD: A Special Resource for Microbe-Drug Associations. Frontiers in Cellular and Infection Microbiology, 2018, 8, 424.	3.9	57
52	RFDT: A Rotation Forest-based Predictor for Predicting Drug-Target Interactions Using Drug Structure and Protein Sequence Information. Current Protein and Peptide Science, 2018, 19, 445-454.	1.4	94
53	Current Computational Models for Prediction of the Varied Interactions Related to Protein - PART 1. Protein and Peptide Letters, 2018, 25, 806-806.	0.9	0
54	Novel Human miRNA-Disease Association Inference Based on Random Forest. Molecular Therapy - Nucleic Acids, 2018, 13, 568-579.	5.1	97

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55	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. <i>Journal of Translational Medicine</i> , 2018, 16, 348.	4.4	41
56	Developing Novel Computational Techniques for Medicine and Pharmacy. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 947-948.	2.1	2
57	Predicting microRNA-disease associations using bipartite local models and hubness-aware regression. <i>RNA Biology</i> , 2018, 15, 1192-1205.	3.1	32
58	Anti-cancer Drug Response Prediction Using Neighbor-Based Collaborative Filtering with Global Effect Removal. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 13, 303-311.	5.1	56
59	MicroRNA-small molecule association identification: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2018, , .	6.5	105
60	Prediction of Potential Small Molecule-Associated MicroRNAs Using Graphlet Interaction. <i>Frontiers in Pharmacology</i> , 2018, 9, 1152.	3.5	33
61	A Hybrid Interpolation Weighted Collaborative Filtering Method for Anti-cancer Drug Response Prediction. <i>Frontiers in Pharmacology</i> , 2018, 9, 1017.	3.5	38
62	Increased plasma prothrombin time is associated with poor prognosis in patients with paraquat poisoning. <i>Journal of Clinical Laboratory Analysis</i> , 2018, 32, e22597.	2.1	4
63	Predicting miRNA-disease association based on inductive matrix completion. <i>Bioinformatics</i> , 2018, 34, 4256-4265.	4.1	448
64	Therapeutic Angiogenesis of Chinese Herbal Medicines in Ischemic Heart Disease: A Review. <i>Frontiers in Pharmacology</i> , 2018, 9, 428.	3.5	37
65	GRMDA: Graph Regression for MiRNA-Disease Association Prediction. <i>Frontiers in Physiology</i> , 2018, 9, 92.	2.8	30
66	Editorial: Identifying Drug-target Interactions Based on Heterogeneous Biological Data - PART 2. <i>Current Protein and Peptide Science</i> , 2018, 19, 524-524.	1.4	0
67	Inferring potential small molecule-miRNA association based on triple layer heterogeneous network. <i>Journal of Cheminformatics</i> , 2018, 10, 30.	6.1	65
68	SSCMDA: spy and super cluster strategy for MiRNA-disease association prediction. <i>Oncotarget</i> , 2018, 9, 1826-1842.	1.8	10
69	MDHGI: Matrix Decomposition and Heterogeneous Graph Inference for miRNA-disease association prediction. <i>PLoS Computational Biology</i> , 2018, 14, e1006418.	3.2	323
70	TLHNMDA: Triple Layer Heterogeneous Network Based Inference for MiRNA-Disease Association Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 234.	2.3	27
71	Prediction of subcellular location of apoptosis proteins by incorporating PsePSSM and DCCA coefficient based on LFDA dimensionality reduction. <i>BMC Genomics</i> , 2018, 19, 478.	2.8	55
72	A Novel Computational Method for the Identification of Potential miRNA-Disease Association Based on Symmetric Non-negative Matrix Factorization and Kronecker Regularized Least Square. <i>Frontiers in Genetics</i> , 2018, 9, 324.	2.3	35

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73	Editorial: Identifying Drug-target Interactions Based on Heterogeneous Biological Data - PART 1. Current Protein and Peptide Science, 2018, 19, 428-429.	1.4	1
74	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. Current Protein and Peptide Science, 2018, 19, 468-478.	1.4	69
75	A novel approach based on KATZ measure to predict associations of human microbiota with non-infectious diseases. Bioinformatics, 2017, 33, 733-739.	4.1	222
76	Long non-coding RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2017, 18, bbw060.	6.5	477
77	PSPEL: In Silico Prediction of Self-Interacting Proteins from Amino Acids Sequences Using Ensemble Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1165-1172.	3.0	56
78	Advancing the prediction accuracy of protein-protein interactions by utilizing evolutionary information from position-specific scoring matrix and ensemble classifier. Journal of Theoretical Biology, 2017, 418, 105-110.	1.7	50
79	RKNNMDA: Ranking-based KNN for MiRNA-Disease Association prediction. RNA Biology, 2017, 14, 952-962.	3.1	152
80	A novel computational model based on super-disease and miRNA for potential miRNAâ€“disease association prediction. Molecular BioSystems, 2017, 13, 1202-1212.	2.9	47
81	Prediction of protein-protein interactions by label propagation with protein evolutionary and chemical information derived from heterogeneous network. Journal of Theoretical Biology, 2017, 430, 9-20.	1.7	17
82	Predicting proteinâ€“protein interactions from protein sequences by a stacked sparse autoencoder deep neural network. Molecular BioSystems, 2017, 13, 1336-1344.	2.9	114
83	HAMDA: Hybrid Approach for MiRNA-Disease Association prediction. Journal of Biomedical Informatics, 2017, 76, 50-58.	4.3	47
84	NARRMDA: negative-aware and rating-based recommendation algorithm for miRNAâ€“disease association prediction. Molecular BioSystems, 2017, 13, 2650-2659.	2.9	23
85	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. Scientific Reports, 2017, 7, 11174.	3.3	62
86	LRLSHMDA: Laplacian Regularized Least Squares for Human Microbeâ€“Disease Association prediction. Scientific Reports, 2017, 7, 7601.	3.3	112
87	Enterovirus 71 infection impairs the reproductive capacity of female mice. Experimental and Therapeutic Medicine, 2017, 14, 403-409.	1.8	2
88	Smartphone-based sensing system using ZnO and graphene modified electrodes for VOCs detection. Biosensors and Bioelectronics, 2017, 93, 94-101.	10.1	95
89	MKRMDA: multiple kernel learning-based Kronecker regularized least squares for MiRNAâ€“disease association prediction. Journal of Translational Medicine, 2017, 15, 251.	4.4	43
90	MCMDA: Matrix completion for MiRNA-disease association prediction. Oncotarget, 2017, 8, 21187-21199.	1.8	189

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91	Prediction of Drug-Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. <i>Molecules</i> , 2017, 22, 1119.	3.8	61
92	PBHMDA: Path-Based Human Microbe-Disease Association Prediction. <i>Frontiers in Microbiology</i> , 2017, 8, 233.	3.5	97
93	NRDTD: a database for clinically or experimentally supported non-coding RNAs and drug targets associations. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	60
94	LRSSLMDA: Laplacian Regularized Sparse Subspace Learning for MiRNA-Disease Association prediction. <i>PLoS Computational Biology</i> , 2017, 13, e1005912.	3.2	254
95	Prediction of microbe-disease association from the integration of neighbor and graph with collaborative recommendation model. <i>Journal of Translational Medicine</i> , 2017, 15, 209.	4.4	105
96	PCVMZM: Using the Probabilistic Classification Vector Machines Model Combined with a Zernike Moments Descriptor to Predict Protein-Protein Interactions from Protein Sequences. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1029.	4.1	61
97	PRMDA: personalized recommendation-based MiRNA-disease association prediction. <i>Oncotarget</i> , 2017, 8, 85568-85583.	1.8	32
98	An ensemble approach for large-scale identification of protein-protein interactions using the alignments of multiple sequences. <i>Oncotarget</i> , 2017, 8, 5149-5159.	1.8	40
99	DLREFD: a database providing associations of long non-coding RNAs, environmental factors and phenotypes. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	12
100	Computational Methods for the Prediction of Drug-Target Interactions from Drug Fingerprints and Protein Sequences by Stacked Auto-Encoder Deep Neural Network. <i>Lecture Notes in Computer Science</i> , 2017, , 46-58.	1.3	12
101	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. <i>PLoS Computational Biology</i> , 2017, 13, e1005455.	3.2	387
102	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.	1.8	36
103	VEGF stimulated the angiogenesis by promoting the mitochondrial functions. <i>Oncotarget</i> , 2017, 8, 77020-77027.	1.8	66
104	FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. <i>Oncotarget</i> , 2016, 7, 45948-45958.	1.8	103
105	HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. <i>Oncotarget</i> , 2016, 7, 65257-65269.	1.8	219
106	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.	1.8	24
107	Current Computational Models for Prediction of the Varied Interactions Related to Noncoding RNAs. <i>BioMed Research International</i> , 2016, 2016, 1-2.	1.9	3
108	IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. <i>Oncotarget</i> , 2016, 7, 57919-57931.	1.8	200

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109	Detection of Interactions between Proteins through Rotation Forest and Local Phase Quantization Descriptors. International Journal of Molecular Sciences, 2016, 17, 21.	4.1	51
110	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
111	Stochastic modeling suggests that noise reduces differentiation efficiency by inducing a heterogeneous drug response in glioma differentiation therapy. BMC Systems Biology, 2016, 10, 73.	3.0	8
112	WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. Scientific Reports, 2016, 6, 21106.	3.3	314
113	Quercetin ameliorates ischemia/reperfusion-induced cognitive deficits by inhibiting ASK1/JNK3/caspase-3 by enhancing the Akt signaling pathway. Biochemical and Biophysical Research Communications, 2016, 478, 199-205.	2.1	57
114	A potential target gene for the host-directed therapy of mycobacterial infection in murine macrophages. International Journal of Molecular Medicine, 2016, 38, 823-833.	4.0	7
115	Construction of reliable protein-protein interaction networks using weighted sparse representation based classifier with pseudo substitution matrix representation features. Neurocomputing, 2016, 218, 131-138.	5.9	45
116	Improving protein-protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. Protein Science, 2016, 25, 1825-1833.	7.6	31
117	Comparative evaluation of the wound-healing potency of recombinant bFGF and ski gene therapy in rats. Growth Factors, 2016, 34, 119-127.	1.7	4
118	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. Molecular BioSystems, 2016, 12, 3702-3710.	2.9	17
119	Improved protein-protein interactions prediction via weighted sparse representation model combining continuous wavelet descriptor and PseAA composition. BMC Systems Biology, 2016, 10, 120.	3.0	25
120	Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus Modulates Interferon- β Expression Mainly Through Attenuating Interferon-Regulatory Factor 3 Phosphorylation. DNA and Cell Biology, 2016, 35, 489-497.	1.9	3
121	Sequence-based prediction of protein-protein interactions using weighted sparse representation model combined with global encoding. BMC Bioinformatics, 2016, 17, 184.	2.6	125
122	miREFRWR: a novel disease-related microRNA-environmental factor interactions prediction method. Molecular BioSystems, 2016, 12, 624-633.	2.9	55
123	Distributed image understanding with semantic dictionary and semantic expansion. Neurocomputing, 2016, 174, 384-392.	5.9	23
124	Drug-target interaction prediction: databases, web servers and computational models. Briefings in Bioinformatics, 2016, 17, 696-712.	6.5	496
125	NLLSS: Predicting Synergistic Drug Combinations Based on Semi-supervised Learning. PLoS Computational Biology, 2016, 12, e1004975.	3.2	250
126	Modeling of signaling crosstalk-mediated drug resistance and its implications on drug combination. Oncotarget, 2016, 7, 63995-64006.	1.8	43

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127	ILNCSIM: improved lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 25902-25914.	1.8	122
128	Predicting lncRNA-disease associations and constructing lncRNA functional similarity network based on the information of miRNA. Scientific Reports, 2015, 5, 13186.	3.3	207
129	KATZLDA: KATZ measure for the lncRNA-disease association prediction. Scientific Reports, 2015, 5, 16840.	3.3	205
130	RBMMMDA: predicting multiple types of disease-microRNA associations. Scientific Reports, 2015, 5, 13877.	3.3	154
131	Constructing lncRNA functional similarity network based on lncRNA-disease associations and disease semantic similarity. Scientific Reports, 2015, 5, 11338.	3.3	195
132	Large scale image understanding with non-convex multi-task learning. , 2014, , .		3
133	MicroRNA-34a overcomes HGF-mediated gefitinib resistance in EGFR mutant lung cancer cells partly by targeting MET. Cancer Letters, 2014, 351, 265-271.	7.2	75
134	Semi-supervised learning for potential human microRNA-disease associations inference. Scientific Reports, 2014, 4, 5501.	3.3	324
135	A Computational Framework to Infer Human Disease-Associated Long Noncoding RNAs. PLoS ONE, 2014, 9, e84408.	2.5	130
136	ASDCD: Antifungal Synergistic Drug Combination Database. PLoS ONE, 2014, 9, e86499.	2.5	65
137	Novel human lncRNAâ€“disease association inference based on lncRNA expression profiles. Bioinformatics, 2013, 29, 2617-2624.	4.1	558
138	LncRNADisease: a database for long-non-coding RNA-associated diseases. Nucleic Acids Research, 2012, 41, D983-D986.	14.5	869
139	RWRMDA: predicting novel human microRNAâ€“disease associations. Molecular BioSystems, 2012, 8, 2792.	2.9	389
140	Drugâ€“target interaction prediction by random walk on the heterogeneous network. Molecular BioSystems, 2012, 8, 1970.	2.9	442
141	Prediction of Disease-Related Interactions between MicroRNAs and Environmental Factors Based on a Semi-Supervised Classifier. PLoS ONE, 2012, 7, e43425.	2.5	66
142	A Novel Candidate Disease Genes Prioritization Method Based on Module Partition and Rank Fusion. OMICS A Journal of Integrative Biology, 2010, 14, 337-356.	2.0	25
143	Formulation and Delivery Mode Affect Disposition and Activity of Tyrphostin-Loaded Nanoparticles in the Rat Carotid Model. Arteriosclerosis, Thrombosis, and Vascular Biology, 2001, 21, 1434-1439.	2.4	53