

Xing Chen

List of Publications by Year in descending order

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Version: 2024-02-01

143
papers

14,364
citations

23500

58
h-index

20307

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. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	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. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2022, 49, 732-742.	3.3	55
3	Dual-Network Collaborative Matrix Factorization for predicting small molecule-miRNA associations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	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. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2022, 49, 2199-2208.	3.3	1
5	Prediction of potential miRNA-disease associations based on stacked autoencoder. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	31
6	Drug-pathway association prediction: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	30
7	NCMCMDA: miRNA-disease association prediction through neighborhood constraint matrix completion. <i>Briefings in Bioinformatics</i> , 2021, 22, 485-496.	3.2	148
8	Microbes and complex diseases: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	29
9	Deep-belief network for predicting potential miRNA-disease associations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	101
10	Crosstalk between hypoxia-sensing ULK1/2 and YAP-driven glycolysis fuels pancreatic ductal adenocarcinoma development. <i>International Journal of Biological Sciences</i> , 2021, 17, 2772-2794.	2.6	9
11	Circular RNAs and complex diseases: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	116
12	Identification of miRNA-disease associations via multiple information integration with Bayesian ranking. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
13	Predicting potential small molecule-miRNA associations based on bounded nuclear norm regularization. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	44
14	Potential miRNA-disease association prediction based on kernelized Bayesian matrix factorization. <i>Genomics</i> , 2020, 112, 809-819.	1.3	32
15	SNMFSMMA: using symmetric nonnegative matrix factorization and Kronecker regularized least squares to predict potential small molecule-microRNA association. <i>RNA Biology</i> , 2020, 17, 281-291.	1.5	50
16	Current Computational Models for Prediction of the Varied Interactions Related to Protein - Part 2. <i>Protein and Peptide Letters</i> , 2020, 27, 347-347.	0.4	0
17	Editorial: Bioinformatics in Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 100.	1.5	5
18	Computational Models in Non-Coding RNA and Human Disease. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1557.	1.8	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.	2.0	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.	2.1	5
21	Feasibility and cardiac synchrony of permanent left bundle branch pacing through the interventricular septum. <i>Europace</i> , 2019, 21, 1694-1702.	0.7	173
22	Ensemble of decision tree reveals potential miRNA-disease associations. <i>PLoS Computational Biology</i> , 2019, 15, e1007209.	1.5	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.	2.3	62
24	Engineering On-Demand Magnetic Core-Shell Composite Wound Dressing Matrices via Electrohydrodynamic Micro-Scale Printing. <i>Advanced Engineering Materials</i> , 2019, 21, 1900699.	1.6	16
25	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. <i>Knowledge-Based Systems</i> , 2019, 186, 104963.	4.0	24
26	Prediction of Potential miRNA-Disease Associations Through a Novel Unsupervised Deep Learning Framework with Variational Autoencoder. <i>Cells</i> , 2019, 8, 1040.	1.8	47
27	Prediction of Small Molecule-MicroRNA Associations by Sparse Learning and Heterogeneous Graph Inference. <i>Molecular Pharmaceutics</i> , 2019, 16, 3157-3166.	2.3	38
28	Computational Model Development of Drug-Target Interaction Prediction: A Review. <i>Current Protein and Peptide Science</i> , 2019, 20, 492-494.	0.7	23
29	Adaptive boosting-based computational model for predicting potential miRNA-disease associations. <i>Bioinformatics</i> , 2019, 35, 4730-4738.	1.8	125
30	RFSMMA: A New Computational Model to Identify and Prioritize Potential Small Molecule-MiRNA Associations. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1668-1679.	2.5	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.	2.3	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.	1.5	111
33	FGF15 Activates Hippo Signaling to Suppress Bile Acid Metabolism and Liver Tumorigenesis. <i>Developmental Cell</i> , 2019, 48, 460-474.e9.	3.1	68
34	Integrating random walk and binary regression to identify novel miRNA-disease association. <i>BMC Bioinformatics</i> , 2019, 20, 59.	1.2	30
35	A Unified Framework for the Prediction of Small Molecule-MicroRNA Association Based on Cross-Layer Dependency Inference on Multilayered Networks. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 5281-5293.	2.5	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.	1.5	35

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37	Computational models for lncRNA function prediction and functional similarity calculation. Briefings in Functional Genomics, 2019, 18, 58-82.	1.3	141
38	MicroRNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2019, 20, 515-539.	3.2	507
39	RNA methylation and diseases: experimental results, databases, Web servers and computational models. Briefings in Bioinformatics, 2019, 20, 896-917.	3.2	74
40	HNMDA: heterogeneous network-based miRNA-disease association prediction. Molecular Genetics and Genomics, 2018, 293, 983-995.	1.0	19
41	ELLPMDA: Ensemble learning and link prediction for miRNA-disease association prediction. RNA Biology, 2018, 15, 1-12.	1.5	58
42	GIMDA: Graphlet interaction-based MiRNA-disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 1548-1561.	1.6	25
43	EGBMMDA: Extreme Gradient Boosting Machine for MiRNA-Disease Association prediction. Cell Death and Disease, 2018, 9, 3.	2.7	256
44	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. Nucleic Acids Research, 2018, 46, D281-D287.	6.5	115
45	BNPMDA: Bipartite Network Projection for MiRNA-disease Association prediction. Bioinformatics, 2018, 34, 3178-3186.	1.8	307
46	NDAMDA: Network distance analysis for MiRNA-disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 2884-2895.	1.6	34
47	An improved efficient rotation forest algorithm to predict the interactions among proteins. Soft Computing, 2018, 22, 3373-3381.	2.1	34
48	DroidDet: Effective and robust detection of android malware using static analysis along with rotation forest model. Neurocomputing, 2018, 272, 638-646.	3.5	146
49	DRMDA: deep representations-based miRNA-disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485.	1.6	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.	0.8	140
51	MDAD: A Special Resource for Microbe-Drug Associations. Frontiers in Cellular and Infection Microbiology, 2018, 8, 424.	1.8	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.	0.7	94
53	Current Computational Models for Prediction of the Varied Interactions Related to Protein - PART 1. Protein and Peptide Letters, 2018, 25, 806-806.	0.4	0
54	Novel Human miRNA-Disease Association Inference Based on Random Forest. Molecular Therapy - Nucleic Acids, 2018, 13, 568-579.	2.3	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.	1.8	41
56	Developing Novel Computational Techniques for Medicine and Pharmacy. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 947-948.	1.0	2
57	Predicting microRNA-disease associations using bipartite local models and hubness-aware regression. <i>RNA Biology</i> , 2018, 15, 1192-1205.	1.5	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.	2.3	56
59	MicroRNA-small molecule association identification: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	105
60	Prediction of Potential Small Molecule-Associated MicroRNAs Using Graphlet Interaction. <i>Frontiers in Pharmacology</i> , 2018, 9, 1152.	1.6	33
61	A Hybrid Interpolation Weighted Collaborative Filtering Method for Anti-cancer Drug Response Prediction. <i>Frontiers in Pharmacology</i> , 2018, 9, 1017.	1.6	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.	0.9	4
63	Predicting miRNA-disease association based on inductive matrix completion. <i>Bioinformatics</i> , 2018, 34, 4256-4265.	1.8	448
64	Therapeutic Angiogenesis of Chinese Herbal Medicines in Ischemic Heart Disease: A Review. <i>Frontiers in Pharmacology</i> , 2018, 9, 428.	1.6	37
65	GRMDA: Graph Regression for MiRNA-Disease Association Prediction. <i>Frontiers in Physiology</i> , 2018, 9, 92.	1.3	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.	0.7	0
67	Inferring potential small molecule-miRNA association based on triple layer heterogeneous network. <i>Journal of Cheminformatics</i> , 2018, 10, 30.	2.8	65
68	SSCMDA: spy and super cluster strategy for MiRNA-disease association prediction. <i>Oncotarget</i> , 2018, 9, 1826-1842.	0.8	10
69	MDHGI: Matrix Decomposition and Heterogeneous Graph Inference for miRNA-disease association prediction. <i>PLoS Computational Biology</i> , 2018, 14, e1006418.	1.5	323
70	TLHNMDA: Triple Layer Heterogeneous Network Based Inference for MiRNA-Disease Association Prediction. <i>Frontiers in Genetics</i> , 2018, 9, 234.	1.1	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.	1.2	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.	1.1	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.	0.7	1
74	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. Current Protein and Peptide Science, 2018, 19, 468-478.	0.7	69
75	A novel approach based on KATZ measure to predict associations of human microbiota with non-infectious diseases. Bioinformatics, 2017, 33, 733-739.	1.8	222
76	Long non-coding RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2017, 18, bbw060.	3.2	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.	1.9	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.	0.8	50
79	RKNNMDA: Ranking-based KNN for MiRNA-Disease Association prediction. RNA Biology, 2017, 14, 952-962.	1.5	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.	0.8	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.	2.5	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.	1.6	62
86	LRLSHMDA: Laplacian Regularized Least Squares for Human Microbeâ€“Disease Association prediction. Scientific Reports, 2017, 7, 7601.	1.6	112
87	Enterovirus 71 infection impairs the reproductive capacity of female mice. Experimental and Therapeutic Medicine, 2017, 14, 403-409.	0.8	2
88	Smartphone-based sensing system using ZnO and graphene modified electrodes for VOCs detection. Biosensors and Bioelectronics, 2017, 93, 94-101.	5.3	95
89	MKRMDA: multiple kernel learning-based Kronecker regularized least squares for MiRNAâ€“disease association prediction. Journal of Translational Medicine, 2017, 15, 251.	1.8	43
90	MCMDA: Matrix completion for MiRNA-disease association prediction. Oncotarget, 2017, 8, 21187-21199.	0.8	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.	1.7	61
92	PBHMDA: Path-Based Human Microbe-Disease Association Prediction. <i>Frontiers in Microbiology</i> , 2017, 8, 233.	1.5	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, .	1.4	60
94	LRSSLMDA: Laplacian Regularized Sparse Subspace Learning for MiRNA-Disease Association prediction. <i>PLoS Computational Biology</i> , 2017, 13, e1005912.	1.5	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.	1.8	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.	1.8	61
97	PRMDA: personalized recommendation-based MiRNA-disease association prediction. <i>Oncotarget</i> , 2017, 8, 85568-85583.	0.8	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.	0.8	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, .	1.4	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.	1.0	12
101	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
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.	0.8	36
103	VEGF stimulated the angiogenesis by promoting the mitochondrial functions. <i>Oncotarget</i> , 2017, 8, 77020-77027.	0.8	66
104	FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. <i>Oncotarget</i> , 2016, 7, 45948-45958.	0.8	103
105	HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. <i>Oncotarget</i> , 2016, 7, 65257-65269.	0.8	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.	0.8	24
107	Current Computational Models for Prediction of the Varied Interactions Related to Noncoding RNAs. <i>BioMed Research International</i> , 2016, 2016, 1-2.	0.9	3
108	IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. <i>Oncotarget</i> , 2016, 7, 57919-57931.	0.8	200

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109	Detection of Interactions between Proteins through Rotation Forest and Local Phase Quantization Descriptors. <i>International Journal of Molecular Sciences</i> , 2016, 17, 21.	1.8	51
110	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
111	Stochastic modeling suggests that noise reduces differentiation efficiency by inducing a heterogeneous drug response in glioma differentiation therapy. <i>BMC Systems Biology</i> , 2016, 10, 73.	3.0	8
112	WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. <i>Scientific Reports</i> , 2016, 6, 21106.	1.6	314
113	Quercetin ameliorates ischemia/reperfusion-induced cognitive deficits by inhibiting ASK1/JNK3/caspase-3 by enhancing the Akt signaling pathway. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 199-205.	1.0	57
114	A potential target gene for the host-directed therapy of mycobacterial infection in murine macrophages. <i>International Journal of Molecular Medicine</i> , 2016, 38, 823-833.	1.8	7
115	Construction of reliable protein-protein interaction networks using weighted sparse representation based classifier with pseudo substitution matrix representation features. <i>Neurocomputing</i> , 2016, 218, 131-138.	3.5	45
116	Improving protein-protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. <i>Protein Science</i> , 2016, 25, 1825-1833.	3.1	31
117	Comparative evaluation of the wound-healing potency of recombinant bFGF and ski gene therapy in rats. <i>Growth Factors</i> , 2016, 34, 119-127.	0.5	4
118	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. <i>Molecular BioSystems</i> , 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. <i>BMC Systems Biology</i> , 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. <i>DNA and Cell Biology</i> , 2016, 35, 489-497.	0.9	3
121	Sequence-based prediction of protein-protein interactions using weighted sparse representation model combined with global encoding. <i>BMC Bioinformatics</i> , 2016, 17, 184.	1.2	125
122	miREFRWR: a novel disease-related microRNA-environmental factor interactions prediction method. <i>Molecular BioSystems</i> , 2016, 12, 624-633.	2.9	55
123	Distributed image understanding with semantic dictionary and semantic expansion. <i>Neurocomputing</i> , 2016, 174, 384-392.	3.5	23
124	Drug-target interaction prediction: databases, web servers and computational models. <i>Briefings in Bioinformatics</i> , 2016, 17, 696-712.	3.2	496
125	NLLSS: Predicting Synergistic Drug Combinations Based on Semi-supervised Learning. <i>PLoS Computational Biology</i> , 2016, 12, e1004975.	1.5	250
126	Modeling of signaling crosstalk-mediated drug resistance and its implications on drug combination. <i>Oncotarget</i> , 2016, 7, 63995-64006.	0.8	43

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127	ILNCSIM: improved lncRNA functional similarity calculation model. <i>Oncotarget</i> , 2016, 7, 25902-25914.	0.8	122
128	Predicting lncRNA-disease associations and constructing lncRNA functional similarity network based on the information of miRNA. <i>Scientific Reports</i> , 2015, 5, 13186.	1.6	207
129	KATZLDA: KATZ measure for the lncRNA-disease association prediction. <i>Scientific Reports</i> , 2015, 5, 16840.	1.6	205
130	RBMMMDA: predicting multiple types of disease-microRNA associations. <i>Scientific Reports</i> , 2015, 5, 13877.	1.6	154
131	Constructing lncRNA functional similarity network based on lncRNA-disease associations and disease semantic similarity. <i>Scientific Reports</i> , 2015, 5, 11338.	1.6	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. <i>Cancer Letters</i> , 2014, 351, 265-271.	3.2	75
134	Semi-supervised learning for potential human microRNA-disease associations inference. <i>Scientific Reports</i> , 2014, 4, 5501.	1.6	324
135	A Computational Framework to Infer Human Disease-Associated Long Noncoding RNAs. <i>PLoS ONE</i> , 2014, 9, e84408.	1.1	130
136	ASDCD: Antifungal Synergistic Drug Combination Database. <i>PLoS ONE</i> , 2014, 9, e86499.	1.1	65
137	Novel human lncRNAâ€“disease association inference based on lncRNA expression profiles. <i>Bioinformatics</i> , 2013, 29, 2617-2624.	1.8	558
138	lncRNADisease: a database for long-non-coding RNA-associated diseases. <i>Nucleic Acids Research</i> , 2012, 41, D983-D986.	6.5	869
139	RWRMDA: predicting novel human microRNAâ€“disease associations. <i>Molecular BioSystems</i> , 2012, 8, 2792.	2.9	389
140	Drugâ€“target interaction prediction by random walk on the heterogeneous network. <i>Molecular BioSystems</i> , 2012, 8, 1970.	2.9	442
141	Prediction of Disease-Related Interactions between MicroRNAs and Environmental Factors Based on a Semi-Supervised Classifier. <i>PLoS ONE</i> , 2012, 7, e43425.	1.1	66
142	A Novel Candidate Disease Genes Prioritization Method Based on Module Partition and Rank Fusion. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 337-356.	1.0	25
143	Formulation and Delivery Mode Affect Disposition and Activity of Tyrphostin-Loaded Nanoparticles in the Rat Carotid Model. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2001, 21, 1434-1439.	1.1	53