Xing Chen

List of Publications by Citations

133 papers	9,498 citations	50 h-index	95 g-index
145 ext. papers	12,637 ext. citations	6.1 avg, IF	7.13 L-index

#	Paper	IF	Citations
133	LncRNADisease: a database for long-non-coding RNA-associated diseases. *Nucleic Acids Research*, **2013**, 41, D983-6	20.1	670
132	Novel human lncRNA-disease association inference based on lncRNA expression profiles. *Bioinformatics*, **2013**, 29, 2617-24	7.2	370
131	Drug-target interaction prediction by random walk on the heterogeneous network. *Molecular BioSystems*, **2012**, 8, 1970-8		331
130	Long non-coding RNAs and complex diseases: from experimental results to computational models. *Briefings in Bioinformatics*, **2017**, 18, 558-576	13.4	329
129	Drug-target interaction prediction: databases, web servers and computational models. *Briefings in Bioinformatics*, **2016**, 17, 696-712	13.4	319
128	MicroRNAs and complex diseases: from experimental results to computational models. *Briefings in Bioinformatics*, **2019**, 20, 515-539	13.4	296
127	RWRMDA: predicting novel human microRNA-disease associations. *Molecular BioSystems*, **2012**, 8, 2792-8		294
126	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. *PLoS Computational Biology*, **2017**, 13, e1005455	5	263
125	Semi-supervised learning for potential human microRNA-disease associations inference. *Scientific Reports*, **2014**, 4, 5501	4.9	255
124	WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. *Scientific Reports*, **2016**, 6, 21106	4.9	238
123	Predicting miRNA-disease association based on inductive matrix completion. *Bioinformatics*, **2018**, 34, 4256-4265	7.2	219
122	BNPMDA: Bipartite Network Projection for MiRNA-Disease Association prediction. *Bioinformatics*, **2018**, 34, 3178-3186	7.2	204
121	MDHGI: Matrix Decomposition and Heterogeneous Graph Inference for miRNA-disease association prediction. *PLoS Computational Biology*, **2018**, 14, e1006418	5	199
120	HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. *Oncotarget*, **2016**, 7, 65257-65269	3.3	178
119	LRSSLMDA: Laplacian Regularized Sparse Subspace Learning for MiRNA-Disease Association prediction. *PLoS Computational Biology*, **2017**, 13, e1005912	5	177
118	NLLSS: Predicting Synergistic Drug Combinations Based on Semi-supervised Learning. *PLoS Computational Biology*, **2016**, 12, e1004975	5	170
117	Predicting lncRNA-disease associations and constructing lncRNA functional similarity network based on the information of miRNA. *Scientific Reports*, **2015**, 5, 13186	4.9	157

116	EGBMMDA: Extreme Gradient Boosting Machine for MiRNA-Disease Association prediction. *Cell Death and Disease*, **2018**, 9, 3	9.8	156
115	MCMDA: Matrix completion for MiRNA-disease association prediction. *Oncotarget*, **2017**, 8, 21187-21199	3.3	144
114	KATZLDA: KATZ measure for the lncRNA-disease association prediction. *Scientific Reports*, **2015**, 5, 16840	4.9	144
113	IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. *Oncotarget*, **2016**, 7, 57919-57931	3.3	142
112	Constructing lncRNA functional similarity network based on lncRNA-disease associations and disease semantic similarity. *Scientific Reports*, **2015**, 5, 11338	4.9	134
111	RBMMMDA: predicting multiple types of disease-microRNA associations. *Scientific Reports*, **2015**, 5, 13877	4.9	122
110	RKNNMDA: Ranking-based KNN for MiRNA-Disease Association prediction. *RNA Biology*, **2017**, 14, 952-962	4.8	109
109	ILNCSIM: improved lncRNA functional similarity calculation model. *Oncotarget*, **2016**, 7, 25902-14	3.3	104
108	Feasibility and cardiac synchrony of permanent left bundle branch pacing through the interventricular septum. *Europace*, **2019**, 21, 1694-1702	3.9	97
107	Sequence-based prediction of protein-protein interactions using weighted sparse representation model combined with global encoding. *BMC Bioinformatics*, **2016**, 17, 184	3.6	94
106	DroidDet: Effective and robust detection of android malware using static analysis along with rotation forest model. *Neurocomputing*, **2018**, 272, 638-646	5.4	92
105	FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. *Oncotarget*, **2016**, 7, 45948-45958	3.3	90
104	Computational models for lncRNA function prediction and functional similarity calculation. *Briefings in Functional Genomics*, **2019**, 18, 58-82	4.9	88
103	A computational framework to infer human disease-associated long noncoding RNAs. *PLoS ONE*, **2014**, 9, e84408	3.7	87
102	Predicting protein-protein interactions from protein sequences by a stacked sparse autoencoder deep neural network. *Molecular BioSystems*, **2017**, 13, 1336-1344		86
101	A Computational-Based Method for Predicting Drug-Target Interactions by Using Stacked Autoencoder Deep Neural Network. *Journal of Computational Biology*, **2018**, 25, 361-373	1.7	85
100	Ensemble of decision tree reveals potential miRNA-disease associations. *PLoS Computational Biology*, **2019**, 15, e1007209	5	82
99	Smartphone-based sensing system using ZnO and graphene modified electrodes for VOCs detection. *Biosensors and Bioelectronics*, **2017**, 93, 94-101	11.8	79

98	A novel approach based on KATZ measure to predict associations of human microbiota with non-infectious diseases. *Bioinformatics*, **2017**, 33, 733-739	7.2	78
97	LMTRDA: Using logistic model tree to predict MiRNA-disease associations by fusing multi-source information of sequences and similarities. *PLoS Computational Biology*, **2019**, 15, e1006865	5	73
96	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. *Nucleic Acids Research*, **2018**, 46, D281-D287	20.1	73
95	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	2.8	71
94	Adaptive boosting-based computational model for predicting potential miRNA-disease associations. *Bioinformatics*, **2019**, 35, 4730-4738	7.2	66
93	Novel Human miRNA-Disease Association Inference Based on Random Forest. *Molecular Therapy - Nucleic Acids*, **2018**, 13, 568-579	10.7	63
92	MicroRNA-34a overcomes HGF-mediated gefitinib resistance in EGFR mutant lung cancer cells partly by targeting MET. *Cancer Letters*, **2014**, 351, 265-71	9.9	62
91	PBHMDA: Path-Based Human Microbe-Disease Association Prediction. *Frontiers in Microbiology*, **2017**, 8, 233	5.7	59
90	DRMDA: deep representations-based miRNA-disease association prediction. *Journal of Cellular and Molecular Medicine*, **2018**, 22, 472-485	5.6	58
89	MicroRNA-small molecule association identification: from experimental results to computational models. *Briefings in Bioinformatics*, **2018**,	13.4	54
88	Prediction of disease-related interactions between microRNAs and environmental factors based on a semi-supervised classifier. *PLoS ONE*, **2012**, 7, e43425	3.7	52
87	PCVMZM: Using the Probabilistic Classification Vector Machines Model Combined with a Zernike Moments Descriptor to Predict Protein-Protein Interactions from Protein Sequences. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	51
86	Prediction of microbe-disease association from the integration of neighbor and graph with collaborative recommendation model. *Journal of Translational Medicine*, **2017**, 15, 209	8.5	50
85	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. *Current Protein and Peptide Science*, **2018**, 19, 468-478	2.8	50
84	LRLSHMDA: Laplacian Regularized Least Squares for Human Microbe-Disease Association prediction. *Scientific Reports*, **2017**, 7, 7601	4.9	50
83	ASDCD: antifungal synergistic drug combination database. *PLoS ONE*, **2014**, 9, e86499	3.7	50
82	NCMCMDA: miRNA-disease association prediction through neighborhood constraint matrix completion. *Briefings in Bioinformatics*, **2021**, 22, 485-496	13.4	50
81	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	48

80	Inferring potential small molecule-miRNA association based on triple layer heterogeneous network. *Journal of Cheminformatics*, **2018**, 10, 30	8.6	48
79	Formulation and delivery mode affect disposition and activity of tyrphostin-loaded nanoparticles in the rat carotid model. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2001**, 21, 1434-9	9.4	47
78	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. *Scientific Reports*, **2017**, 7, 11174	4.9	46
77	miREFRWR: a novel disease-related microRNA-environmental factor interactions prediction method. *Molecular BioSystems*, **2016**, 12, 624-33		45
76	Prediction of Drug-Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. *Molecules*, **2017**, 22,	4.8	45
75	ELLPMDA: Ensemble learning and link prediction for miRNA-disease association prediction. *RNA Biology*, **2018**, 15, 807-818	4.8	44
74	VEGF stimulated the angiogenesis by promoting the mitochondrial functions. *Oncotarget*, **2017**, 8, 77020-77027	5.3	44
73	RNA methylation and diseases: experimental results, databases, Web servers and computational models. *Briefings in Bioinformatics*, **2019**, 20, 896-917	13.4	44
72	Prediction of subcellular location of apoptosis proteins by incorporating PsePSSM and DCCA coefficient based on LFDA dimensionality reduction. *BMC Genomics*, **2018**, 19, 478	4.5	42
71	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	2.3	41
70	FGF15 Activates Hippo Signaling to Suppress Bile Acid Metabolism and Liver Tumorigenesis. *Developmental Cell*, **2019**, 48, 460-474.e9	10.2	40
69	Detection of Interactions between Proteins through Rotation Forest and Local Phase Quantization Descriptors. *International Journal of Molecular Sciences*, **2015**, 17,	6.3	40
68	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	3.4	39
67	A novel computational model based on super-disease and miRNA for potential miRNA-disease association prediction. *Molecular BioSystems*, **2017**, 13, 1202-1212		37
66	Construction of reliable protein-protein interaction networks using weighted sparse representation based classifier with pseudo substitution matrix representation features. *Neurocomputing*, **2016**, 218, 131-138	5.4	36
65	HAMDA: Hybrid Approach for MiRNA-Disease Association prediction. *Journal of Biomedical Informatics*, **2017**, 76, 50-58	10.2	34
64	In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. *Molecular Therapy - Nucleic Acids*, **2019**, 14, 274-286	10.7	34
63	NRDTD: a database for clinically or experimentally supported non-coding RNAs and drug targets associations. *Database: the Journal of Biological Databases and Curation*, **2017**, 2017,	5	34

62	Anti-cancer Drug Response Prediction Using Neighbor-Based Collaborative Filtering with Global Effect Removal. *Molecular Therapy - Nucleic Acids*, **2018**, 13, 303-311	10.7	34
61	Accurate prediction of protein-protein interactions by integrating potential evolutionary information embedded in PSSM profile and discriminative vector machine classifier. *Oncotarget*, **2017**, 8, 23638-23649	3.3	33
60	An ensemble approach for large-scale identification of protein- protein interactions using the alignments of multiple sequences. *Oncotarget*, **2017**, 8, 5149-5159	3.3	32
59	MKRMDA: multiple kernel learning-based Kronecker regularized least squares for MiRNA-disease association prediction. *Journal of Translational Medicine*, **2017**, 15, 251	8.5	32
58	Modeling of signaling crosstalk-mediated drug resistance and its implications on drug combination. *Oncotarget*, **2016**, 7, 63995-64006	3.3	32
57	Anticancer Drug Response Prediction in Cell Lines Using Weighted Graph Regularized Matrix Factorization. *Molecular Therapy - Nucleic Acids*, **2019**, 17, 164-174	10.7	31
56	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. *International Journal of Molecular Sciences*, **2016**, 17,	6.3	30
55	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. *Journal of Translational Medicine*, **2018**, 16, 348	8.5	30
54	Circular RNAs and complex diseases: from experimental results to computational models. *Briefings in Bioinformatics*, **2021**, 22,	13.4	29
53	PRMDA: personalized recommendation-based MiRNA-disease association prediction. *Oncotarget*, **2017**, 8, 85568-85583	3.3	28
52	An improved efficient rotation forest algorithm to predict the interactions among proteins. *Soft Computing*, **2018**, 22, 3373-3381	3.5	27
51	SNMFSMMA: using symmetric nonnegative matrix factorization and Kronecker regularized least squares to predict potential small molecule-microRNA association. *RNA Biology*, **2020**, 17, 281-291	4.8	27
50	MDAD: A Special Resource for Microbe-Drug Associations. *Frontiers in Cellular and Infection Microbiology*, **2018**, 8, 424	5.9	26
49	Predicting microRNA-disease associations using bipartite local models and hubness-aware regression. *RNA Biology*, **2018**, 15, 1192-1205	4.8	26
48	RFSMMA: A New Computational Model to Identify and Prioritize Potential Small Molecule-MiRNA Associations. *Journal of Chemical Information and Modeling*, **2019**, 59, 1668-1679	6.1	25
47	NDAMDA: Network distance analysis for MiRNA-disease association prediction. *Journal of Cellular and Molecular Medicine*, **2018**, 22, 2884-2895	5.6	25
46	Improving protein-protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. *Protein Science*, **2016**, 25, 1825-33	6.3	25
45	A Novel Computational Method for the Identification of Potential miRNA-Disease Association Based on Symmetric Non-negative Matrix Factorization and Kronecker Regularized Least Square. *Frontiers in Genetics*, **2018**, 9, 324	4.5	24

44	GIMDA: Graphlet interaction-based MiRNA-disease association prediction. *Journal of Cellular and Molecular Medicine*, **2018**, 22, 1548-1561	5.6	23
43	Improved protein-protein interactions prediction via weighted sparse representation model combining continuous wavelet descriptor and PseAA composition. *BMC Systems Biology*, **2016**, 10, 120	3.5	23
42	Therapeutic Angiogenesis of Chinese Herbal Medicines in Ischemic Heart Disease: A Review. *Frontiers in Pharmacology*, **2018**, 9, 428	5.6	23
41	A Hybrid Interpolation Weighted Collaborative Filtering Method for Anti-cancer Drug Response Prediction. *Frontiers in Pharmacology*, **2018**, 9, 1017	5.6	23
40	A novel candidate disease genes prioritization method based on module partition and rank fusion. *OMICS A Journal of Integrative Biology*, **2010**, 14, 337-56	3.8	22
39	Integrating random walk and binary regression to identify novel miRNA-disease association. *BMC Bioinformatics*, **2019**, 20, 59	3.6	22
38	Deep-belief network for predicting potential miRNA-disease associations. *Briefings in Bioinformatics*, **2021**, 22,	13.4	21
37	Prediction of Potential miRNA-Disease Associations Through a Novel Unsupervised Deep Learning Framework with Variational Autoencoder. *Cells*, **2019**, 8,	7.9	20
36	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. *Oncotarget*, **2016**, 7, 82440-82449	3.3	20
35	An integrated framework for the identification of potential miRNA-disease association based on novel negative samples extraction strategy. *RNA Biology*, **2019**, 16, 257-269	4.8	20
34	TLHNMDA: Triple Layer Heterogeneous Network Based Inference for MiRNA-Disease Association Prediction. *Frontiers in Genetics*, **2018**, 9, 234	4.5	19
33	Prediction of Small Molecule-MicroRNA Associations by Sparse Learning and Heterogeneous Graph Inference. *Molecular Pharmaceutics*, **2019**, 16, 3157-3166	5.6	18
32	GRMDA: Graph Regression for MiRNA-Disease Association Prediction. *Frontiers in Physiology*, **2018**, 9, 92	4.6	18
31	Potential miRNA-disease association prediction based on kernelized Bayesian matrix factorization. *Genomics*, **2020**, 112, 809-819	4.3	18
30	Prediction of potential miRNA-disease associations using matrix decomposition and label propagation. *Knowledge-Based Systems*, **2019**, 186, 104963	7.3	17
29	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. *Molecular BioSystems*, **2016**, 12, 3702-3710		16
28	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	2.3	15
27	NARRMDA: negative-aware and rating-based recommendation algorithm for miRNA-disease association prediction. *Molecular BioSystems*, **2017**, 13, 2650-2659		15

26	A Computational Study of Potential miRNA-Disease Association Inference Based on Ensemble Learning and Kernel Ridge Regression. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 40	5.8	15
25	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*, **2021**, 1	8.8	15
24	Distributed image understanding with semantic dictionary and semantic expansion. *Neurocomputing*, **2016**, 174, 384-392	5.4	14
23	HNMDA: heterogeneous network-based miRNA-disease association prediction. *Molecular Genetics and Genomics*, **2018**, 293, 983-995	3.1	14
22	Prediction of Potential Small Molecule-Associated MicroRNAs Using Graphlet Interaction. *Frontiers in Pharmacology*, **2018**, 9, 1152	5.6	14
21	A Unified Framework for the Prediction of Small Molecule-MicroRNA Association Based on Cross-Layer Dependency Inference on Multilayered Networks. *Journal of Chemical Information and Modeling*, **2019**, 59, 5281-5293	6.1	13
20	Computational Model Development of Drug-Target Interaction Prediction: A Review. *Current Protein and Peptide Science*, **2019**, 20, 492-494	2.8	12
19	Computational Methods for the Prediction of Drug-Target Interactions from Drug Fingerprints and Protein Sequences by Stacked Auto-Encoder Deep Neural Network. *Lecture Notes in Computer Science*, **2017**, 46-58	0.9	11
18	Engineering On-Demand Magnetic Core–Shell Composite Wound Dressing Matrices via Electrohydrodynamic Micro-Scale Printing. *Advanced Engineering Materials*, **2019**, 21, 1900699	3.5	10
17	SSCMDA: spy and super cluster strategy for MiRNA-disease association prediction. *Oncotarget*, **2018**, 9, 1826-1842	3.3	9
16	DLREFD: a database providing associations of long non-coding RNAs, environmental factors and phenotypes. *Database: the Journal of Biological Databases and Curation*, **2017**, 2017,	5	8
15	Drug-pathway association prediction: from experimental results to computational models. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
14	Microbes and complex diseases: from experimental results to computational models. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
13	Predicting potential small molecule-miRNA associations based on bounded nuclear norm regularization. *Briefings in Bioinformatics*, **2021**, 22,	13.4	8
12	A potential target gene for the host-directed therapy of mycobacterial infection in murine macrophages. *International Journal of Molecular Medicine*, **2016**, 38, 823-33	4.4	7
11	Identification of miRNA-disease associations via multiple information integration with Bayesian ranking. *Briefings in Bioinformatics*, **2021**, 22,	13.4	5
10	Comparative evaluation of the wound-healing potency of recombinant bFGF and ski gene therapy in rats. *Growth Factors*, **2016**, 34, 119-27	1.6	4
9	Stochastic modeling suggests that noise reduces differentiation efficiency by inducing a heterogeneous drug response in glioma differentiation therapy. *BMC Systems Biology*, **2016**, 10, 73	3.5	4

List of Publications

8	Physiological Left Bundle Branch Pacing Validated by Ultra-High Density Ventricular Mapping in a Swine Model. *Circulation: Arrhythmia and Electrophysiology*, **2020**, 13, e007898	6.4	3
7	Large scale image understanding with non-convex multi-task learning **2014**,		3
6	Prediction of potential miRNA-disease associations based on stacked autoencoder.. *Briefings in Bioinformatics*, **2022**,	13.4	3
5	Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus Modulates Interferon-□ Expression Mainly Through Attenuating Interferon-Regulatory Factor 3 Phosphorylation. *DNA and Cell Biology*, **2016**, 35, 489-97	3.6	2
4	Enterovirus 71 infection impairs the reproductive capacity of female mice. *Experimental and Therapeutic Medicine*, **2017**, 14, 403-409	2.1	2
3	Ensemble of kernel ridge regression-based small molecule-miRNA association prediction in human disease. *Briefings in Bioinformatics*, **2021**,	13.4	2
2	Crosstalk between hypoxia-sensing ULK1/2 and YAP-driven glycolysis fuels pancreatic ductal adenocarcinoma development. *International Journal of Biological Sciences*, **2021**, 17, 2772-2794	11.2	2
1	Increased plasma prothrombin time is associated with poor prognosis in patients with paraquat poisoning. *Journal of Clinical Laboratory Analysis*, **2018**, 32, e22597	3	2