Qingfeng Chen

List of Publications by Year
in descending order

46 papers	585 citations	623734 14 h-index	677142 22 g-index
46 all docs	46 docs citations	46 times ranked	328 citing authors

#	Article	IF	Citations
1	ILDMSF: Inferring Associations Between Long Non-Coding RNA and Disease Based on Multi-Similarity Fusion. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1106-1112.	3.0	57
2	LDICDL: LncRNA-Disease Association Identification Based on Collaborative Deep Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1715-1723.	3.0	47
3	GANLDA: Graph attention network for lncRNA-disease associations prediction. Neurocomputing, 2022, 469, 384-393.	5.9	43
4	Inferring LncRNA-disease associations based on graph autoencoder matrix completion. Computational Biology and Chemistry, 2020, 87, 107282.	2.3	40
5	Mining frequent patterns for AMP-activated protein kinase regulation on skeletal muscle. BMC Bioinformatics, 2006, 7, 394.	2.6	37
6	KGANCDA: predicting circRNA-disease associations based on knowledge graph attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	33
7	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	27
8	Identifying Interactions Between Long Noncoding RNAs and Diseases Based on Computational Methods. Methods in Molecular Biology, 2018, 1754, 205-221.	0.9	19
9	Mining Featured Patterns of MiRNA Interaction Based on Sequence and Structure Similarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 415-422.	3.0	18
10	Convergence of gradient method with penalty for Ridge Polynomial neural network. Neurocomputing, 2012, 97, 405-409.	5.9	17
11	Bioinformatics in protein kinases regulatory network and drug discovery. Mathematical Biosciences, 2015, 262, 147-156.	1.9	17
12	Anomaly Detection in Dynamic Graphs via Transformer. IEEE Transactions on Knowledge and Data Engineering, 2023, 35, 12081-12094.	5.7	17
13	Detecting inconsistency in biological molecular databases using ontologies. Data Mining and Knowledge Discovery, 2007, 15, 275-296.	3.7	15
14	GADTI: Graph Autoencoder Approach for DTI Prediction From Heterogeneous Network. Frontiers in Genetics, 2021, 12, 650821.	2.3	15
15	Discovery of Structural and Functional Features in RNA Pseudoknots. IEEE Transactions on Knowledge and Data Engineering, 2009, 21, 974-984.	5.7	14
16	Inferring microRNA-Environmental Factor Interactions Based on Multiple Biological Information Fusion. Molecules, 2018, 23, 2439.	3.8	14
17	Grouping miRNAs of similar functions via weighted information content of gene ontology. BMC Bioinformatics, 2016, 17, 507.	2.6	13
18	IGNSCDA: Predicting CircRNA-Disease Associations Based on Improved Graph Convolutional Network and Negative Sampling. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	13

#	Article	IF	Citations
19	Network-based methods for gene function prediction. Briefings in Functional Genomics, 2021, 20, 249-257.	2.7	13
20	Identification of Important Positions within miRNAs by Integrating Sequential and Structural Features. Current Protein and Peptide Science, 2014, 15, 591-597.	1.4	12
21	Interval-based distance function for identifying RNA structure candidates. Journal of Theoretical Biology, 2011, 269, 280-286.	1.7	10
22	Exploring Consensus RNA Substructural Patterns Using Subgraph Mining. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1134-1146.	3.0	10
23	Community detection in complex network based on APT method. Pattern Recognition Letters, 2020, 138, 193-200.	4.2	9
24	Using propensity scores to predict the kinases of unannotated phosphopeptides. Knowledge-Based Systems, 2017, 135, 60-76.	7.1	7
25	Identifying miRNA–disease association based on integrating miRNA topological similarity and functional similarity. Quantitative Biology, 2019, 7, 202-209.	0.5	7
26	Interval-Based Similarity for Classifying Conserved RNA Secondary Structures. IEEE Intelligent Systems, 2016, 31, 78-85.	4.0	6
27	Visual phrase recognition by modeling 3D spatial context of multiple objects. Neurocomputing, 2017, 253, 183-192.	5.9	6
28	Enhancing drug–drug interaction prediction by three-way decision and knowledge graph embedding. Granular Computing, 2023, 8, 67-76.	8.0	6
29	Modeling Conserved Structure Patterns for Functional Noncoding RNA. IEEE Transactions on Biomedical Engineering, 2011, 58, 1528-1533.	4.2	5
30	Identifying Interactions Between Kinases and Substrates Based on Protein–Protein Interaction Network. Journal of Computational Biology, 2019, 26, 836-845.	1.6	5
31	Prediction of circRNA-miRNA Associations Based on Network Embedding. Complexity, 2021, 2021, 1-10.	1.6	5
32	Discovering Inhibition Pathways for Protein Kinases. IEEE Intelligent Systems, 2012, 27, 19-26.	4.0	4
33	ProBAPred: Inferring protein–protein binding affinity by incorporating protein sequence and structural features. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850011.	0.8	4
34	Survey of Network Embedding for Drug Analysis and Prediction. Current Protein and Peptide Science, 2021, 22, 237-250.	1.4	4
35	Function Annotation for Pseudoknot Using Structure Similarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1535-1544.	3.0	3
36	Mining Protein Kinases Regulation Using Graphical Models. IEEE Transactions on Nanobioscience, 2011, 10, 1-8.	3.3	3

#	ARTICLE	IF	CITATIONS
37	KSIMC: Predicting Kinaseâ€"Substrate Interactions Based on Matrix Completion. International Journal of Molecular Sciences, 2019, 20, 302.	4.1	3
38	Prediction of phosphorylation sites based on granular support vector machine. Granular Computing, 2021, 6, 107-117.	8.0	3
39	Mining Characteristic Relations Bind to RNA Secondary Structures. IEEE Transactions on Information Technology in Biomedicine, 2010, 14, 10-15.	3.2	2
40	Effective Identification of Negative Regulation Patterns of Protein Kinases. IEEE Transactions on Nanobioscience, 2013, 12, 98-105.	3.3	1
41	Editorial (Thematic Issue: Protein Systems Biology: Method, Regulation, and Network). Current Protein and Peptide Science, 2014, 15, 519-521.	1.4	1
42	Discovery of MicroRNA conservative sites in drosophila melanogaster. , 2011, , .		0
43	Predicting miRNA-disease interaction based on recommend method. Information Discovery and Delivery, 2019, 48, 35-40.	2.1	0
44	Editorial: Graph Embedding Methods for Multiple-Omics Data Analysis. Frontiers in Genetics, 2021, 12, 762274.	2.3	0
45	Classifying Conserved RNA Secondary Structures With Pseudoknots by Vector-Edit Distance. IEEE Access, 2021, 9, 32008-32018.	4.2	0
46	Protein Systems Biology: Method, Regulation, and Networks. Current Protein and Peptide Science, 2014, , .	1.4	0