

Qingfeng Chen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5032221/publications.pdf>

Version: 2024-02-01

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	Anomaly Detection in Dynamic Graphs via Transformer. IEEE Transactions on Knowledge and Data Engineering, 2023, 35, 12081-12094.	5.7	17
2	Enhancing drug-drug interaction prediction by three-way decision and knowledge graph embedding. Granular Computing, 2023, 8, 67-76.	8.0	6
3	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
4	GANLDA: Graph attention network for lncRNA-disease associations prediction. Neurocomputing, 2022, 469, 384-393.	5.9	43
5	KGANCD: predicting circRNA-disease associations based on knowledge graph attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	33
6	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
7	Prediction of phosphorylation sites based on granular support vector machine. Granular Computing, 2021, 6, 107-117.	8.0	3
8	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
9	Network-based methods for gene function prediction. Briefings in Functional Genomics, 2021, 20, 249-257.	2.7	13
10	GADTI: Graph Autoencoder Approach for DTI Prediction From Heterogeneous Network. Frontiers in Genetics, 2021, 12, 650821.	2.3	15
11	Survey of Network Embedding for Drug Analysis and Prediction. Current Protein and Peptide Science, 2021, 22, 237-250.	1.4	4
12	Prediction of circRNA-miRNA Associations Based on Network Embedding. Complexity, 2021, 2021, 1-10.	1.6	5
13	Editorial: Graph Embedding Methods for Multiple-Omics Data Analysis. Frontiers in Genetics, 2021, 12, 762274.	2.3	0
14	Classifying Conserved RNA Secondary Structures With Pseudoknots by Vector-Edit Distance. IEEE Access, 2021, 9, 32008-32018.	4.2	0
15	Community detection in complex network based on APT method. Pattern Recognition Letters, 2020, 138, 193-200.	4.2	9
16	CircR2Cancer: a manually curated database of associations between circRNAs and cancers. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	27
17	Inferring LncRNA-disease associations based on graph autoencoder matrix completion. Computational Biology and Chemistry, 2020, 87, 107282.	2.3	40
18	Identifying miRNA-disease association based on integrating miRNA topological similarity and functional similarity. Quantitative Biology, 2019, 7, 202-209.	0.5	7

#	ARTICLE	IF	CITATIONS
19	KSIMC: Predicting Kinase-Substrate Interactions Based on Matrix Completion. International Journal of Molecular Sciences, 2019, 20, 302.	4.1	3
20	Identifying Interactions Between Kinases and Substrates Based on Protein-Protein Interaction Network. Journal of Computational Biology, 2019, 26, 836-845.	1.6	5
21	Predicting miRNA-disease interaction based on recommend method. Information Discovery and Delivery, 2019, 48, 35-40.	2.1	0
22	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
23	Identifying Interactions Between Long Noncoding RNAs and Diseases Based on Computational Methods. Methods in Molecular Biology, 2018, 1754, 205-221.	0.9	19
24	Inferring microRNA-Environmental Factor Interactions Based on Multiple Biological Information Fusion. Molecules, 2018, 23, 2439.	3.8	14
25	Exploring Consensus RNA Substructural Patterns Using Subgraph Mining. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1134-1146.	3.0	10
26	Visual phrase recognition by modeling 3D spatial context of multiple objects. Neurocomputing, 2017, 253, 183-192.	5.9	6
27	Using propensity scores to predict the kinases of unannotated phosphopeptides. Knowledge-Based Systems, 2017, 135, 60-76.	7.1	7
28	Grouping miRNAs of similar functions via weighted information content of gene ontology. BMC Bioinformatics, 2016, 17, 507.	2.6	13
29	Interval-Based Similarity for Classifying Conserved RNA Secondary Structures. IEEE Intelligent Systems, 2016, 31, 78-85.	4.0	6
30	Bioinformatics in protein kinases regulatory network and drug discovery. Mathematical Biosciences, 2015, 262, 147-156.	1.9	17
31	Editorial (Thematic Issue: Protein Systems Biology: Method, Regulation, and Network). Current Protein and Peptide Science, 2014, 15, 519-521.	1.4	1
32	Identification of Important Positions within miRNAs by Integrating Sequential and Structural Features. Current Protein and Peptide Science, 2014, 15, 591-597.	1.4	12
33	Protein Systems Biology: Method, Regulation, and Networks. Current Protein and Peptide Science, 2014, , .	1.4	0
34	Effective Identification of Negative Regulation Patterns of Protein Kinases. IEEE Transactions on Nanobioscience, 2013, 12, 98-105.	3.3	1
35	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
36	Convergence of gradient method with penalty for Ridge Polynomial neural network. Neurocomputing, 2012, 97, 405-409.	5.9	17

#	ARTICLE	IF	CITATIONS
37	Discovering Inhibition Pathways for Protein Kinases. IEEE Intelligent Systems, 2012, 27, 19-26.	4.0	4
38	Function Annotation for Pseudoknot Using Structure Similarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1535-1544.	3.0	3
39	Mining Protein Kinases Regulation Using Graphical Models. IEEE Transactions on Nanobioscience, 2011, 10, 1-8.	3.3	3
40	Modeling Conserved Structure Patterns for Functional Noncoding RNA. IEEE Transactions on Biomedical Engineering, 2011, 58, 1528-1533.	4.2	5
41	Interval-based distance function for identifying RNA structure candidates. Journal of Theoretical Biology, 2011, 269, 280-286.	1.7	10
42	Discovery of MicroRNA conservative sites in drosophila melanogaster. , 2011, , .		0
43	Mining Characteristic Relations Bind to RNA Secondary Structures. IEEE Transactions on Information Technology in Biomedicine, 2010, 14, 10-15.	3.2	2
44	Discovery of Structural and Functional Features in RNA Pseudoknots. IEEE Transactions on Knowledge and Data Engineering, 2009, 21, 974-984.	5.7	14
45	Detecting inconsistency in biological molecular databases using ontologies. Data Mining and Knowledge Discovery, 2007, 15, 275-296.	3.7	15
46	Mining frequent patterns for AMP-activated protein kinase regulation on skeletal muscle. BMC Bioinformatics, 2006, 7, 394.	2.6	37