Xiaoyan Liu

List of Publications by Year
in descending order

34 papers	478 citations	840119 11 h-index	713013 21 g-index
34 all docs	34 docs citations	34 times ranked	653 citing authors

#	Article	IF	Citations
1	Measuring gene functional similarity based on group-wise comparison of GO terms. Bioinformatics, 2013, 29, 1424-1432.	1.8	83
2	An improved K-medoids algorithm based on step increasing and optimizing medoids. Expert Systems With Applications, 2018, 92, 464-473.	4.4	69
3	Density Peaks Clustering Based on Weighted Local Density Sequence and Nearest Neighbor Assignment. IEEE Access, 2019, 7, 34301-34317.	2.6	52
4	An improved Bayesian network method for reconstructing gene regulatory network based on candidate auto selection. BMC Genomics, 2017, 18, 844.	1.2	32
5	An improved method for functional similarity analysis of genes based on Gene Ontology. BMC Systems Biology, 2016, 10, 119.	3.0	23
6	Identification of Pan-Cancer Prognostic Biomarkers Through Integration of Multi-Omics Data. Frontiers in Bioengineering and Biotechnology, 2020, 8, 268.	2.0	21
7	A gene-based information gain method for detecting gene–gene interactions in case–control studies. European Journal of Human Genetics, 2015, 23, 1566-1572.	1.4	20
8	Identify bilayer modules via pseudo-3D clustering: applications to miRNA-gene bilayer networks. Nucleic Acids Research, 2016, 44, gkw679.	6.5	20
9	Predicting MiRNA-Disease Association by Latent Feature Extraction with Positive Samples. Genes, 2019, 10, 80.	1.0	17
10	PredAmyl-MLP: Prediction of Amyloid Proteins Using Multilayer Perceptron. Computational and Mathematical Methods in Medicine, 2020, 2020, 1-12.	0.7	17
11	Mining disease genes using integrated protein–protein interaction and gene–gene co–regulation information. FEBS Open Bio, 2015, 5, 251-256.	1.0	16
12	Pathogenic gene prediction based on network embedding. Briefings in Bioinformatics, 2021, 22, .	3.2	12
13	eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform. Scientific Reports, 2016, 6, 30595.	1.6	9
14	System-Level Insights into the Cellular Interactome of a Non-Model Organism: Inferring, Modelling and Analysing Functional Gene Network of Soybean (Glycine max). PLoS ONE, 2014, 9, e113907.	1.1	9
15	Revealing protein functions based on relationships of interacting proteins and GO terms. Journal of Biomedical Semantics, 2017, 8, 27.	0.9	8
16	Refine gene functional similarity network based on interaction networks. BMC Bioinformatics, 2017, 18, 550.	1.2	8
17	Drug-target interaction data cluster analysis based on improving the density peaks clustering algorithm. Intelligent Data Analysis, 2019, 23, 1335-1353.	0.4	8
18	Gene Regulatory Networks Reconstruction Using the Flooding-Pruning Hill-Climbing Algorithm. Genes, 2018, 9, 342.	1.0	7

#	Article	IF	Citations
19	SGFSC: speeding the gene functional similarity calculation based on hash tables. BMC Bioinformatics, 2016, 17, 445.	1.2	6
20	Combining Sparse Group Lasso and Linear Mixed Model Improves Power to Detect Genetic Variants Underlying Quantitative Traits. Frontiers in Genetics, 2019, 10, 271.	1.1	5
21	Computational Detection of Breast Cancer Invasiveness with DNA Methylation Biomarkers. Cells, 2020, 9, 326.	1.8	5
22	MLPA: Detecting overlapping communities by multi-label propagation approach. , 2013, , .		4
23	A Least Square Method Based Model for Identifying Protein Complexes in Protein-Protein Interaction Network. BioMed Research International, 2014, 2014, 1-9.	0.9	4
24	Gene-Based Nonparametric Testing of Interactions Using Distance Correlation Coefficient in Case-Control Association Studies. Genes, 2018, 9, 608.	1.0	4
25	FPSC-DTI: drug–target interaction prediction based on feature projection fuzzy classification and super cluster fusion. Molecular Omics, 2020, 16, 583-591.	1.4	4
26	Genetic Variants Detection Based on Weighted Sparse Group Lasso. Frontiers in Genetics, 2020, 11, 155.	1.1	4
27	Computational Prediction of Protein Function Based on Weighted Mapping of Domains and GO Terms. BioMed Research International, 2014, 2014, 1-9.	0.9	3
28	Predicting Sub-Golgi Apparatus Resident Protein With Primary Sequence Hybrid Features. IEEE Access, 2020, 8, 4442-4450.	2.6	3
29	Identification of functional miRNA regulatory modules and their associations via dynamic miRNA regulatory function. , 2014, , .		2
30	Epistasis detection using a permutation-based Gradient Boosting Machine. , 2016, , .		2
31	Identification and prioritization of differentially expressed genes for time-series gene expression data. Frontiers of Computer Science, 2018, 12, 813-823.	1.6	1
32	Effective constructing training sets for object detection. , 2013, , .		0
33	Revealing protein functions based on relationships of interacting proteins and GO terms. , 2016, , .		0
34	Inferring of miRNAs as Biomarker via Subspace Dimensionality Reduction and Clustering. , 2016, , .		0