

# Xiaoyan Liu

## List of Publications by Year in descending order

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34  
papers

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citations

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713013

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times ranked

653  
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathogenic gene prediction based on network embedding. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
2	Predicting Sub-Golgi Apparatus Resident Protein With Primary Sequence Hybrid Features. <i>IEEE Access</i> , 2020, 8, 4442-4450.	2.6	3
3	FPSC-DTI: drug-target interaction prediction based on feature projection fuzzy classification and super cluster fusion. <i>Molecular Omics</i> , 2020, 16, 583-591.	1.4	4
4	PredAmyl-MLP: Prediction of Amyloid Proteins Using Multilayer Perceptron. <i>Computational and Mathematical Methods in Medicine</i> , 2020, 2020, 1-12.	0.7	17
5	Genetic Variants Detection Based on Weighted Sparse Group Lasso. <i>Frontiers in Genetics</i> , 2020, 11, 155.	1.1	4
6	Identification of Pan-Cancer Prognostic Biomarkers Through Integration of Multi-Omics Data. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 268.	2.0	21
7	Computational Detection of Breast Cancer Invasiveness with DNA Methylation Biomarkers. <i>Cells</i> , 2020, 9, 326.	1.8	5
8	Predicting MiRNA-Disease Association by Latent Feature Extraction with Positive Samples. <i>Genes</i> , 2019, 10, 80.	1.0	17
9	Combining Sparse Group Lasso and Linear Mixed Model Improves Power to Detect Genetic Variants Underlying Quantitative Traits. <i>Frontiers in Genetics</i> , 2019, 10, 271.	1.1	5
10	Density Peaks Clustering Based on Weighted Local Density Sequence and Nearest Neighbor Assignment. <i>IEEE Access</i> , 2019, 7, 34301-34317.	2.6	52
11	Drug-target interaction data cluster analysis based on improving the density peaks clustering algorithm. <i>Intelligent Data Analysis</i> , 2019, 23, 1335-1353.	0.4	8
12	Identification and prioritization of differentially expressed genes for time-series gene expression data. <i>Frontiers of Computer Science</i> , 2018, 12, 813-823.	1.6	1
13	An improved K-medoids algorithm based on step increasing and optimizing medoids. <i>Expert Systems With Applications</i> , 2018, 92, 464-473.	4.4	69
14	Gene-Based Nonparametric Testing of Interactions Using Distance Correlation Coefficient in Case-Control Association Studies. <i>Genes</i> , 2018, 9, 608.	1.0	4
15	Gene Regulatory Networks Reconstruction Using the Flooding-Pruning Hill-Climbing Algorithm. <i>Genes</i> , 2018, 9, 342.	1.0	7
16	Revealing protein functions based on relationships of interacting proteins and GO terms. <i>Journal of Biomedical Semantics</i> , 2017, 8, 27.	0.9	8
17	An improved Bayesian network method for reconstructing gene regulatory network based on candidate auto selection. <i>BMC Genomics</i> , 2017, 18, 844.	1.2	32
18	Refine gene functional similarity network based on interaction networks. <i>BMC Bioinformatics</i> , 2017, 18, 550.	1.2	8

#	ARTICLE	IF	CITATIONS
19	Epistasis detection using a permutation-based Gradient Boosting Machine. , 2016, , .		2
20	Revealing protein functions based on relationships of interacting proteins and GO terms. , 2016, , .		0
21	Inferring of miRNAs as Biomarker via Subspace Dimensionality Reduction and Clustering. , 2016, , .		0
22	Identify bilayer modules via pseudo-3D clustering: applications to miRNA-gene bilayer networks. Nucleic Acids Research, 2016, 44, gkw679.	6.5	20
23	eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform. Scientific Reports, 2016, 6, 30595.	1.6	9
24	SGFSC: speeding the gene functional similarity calculation based on hash tables. BMC Bioinformatics, 2016, 17, 445.	1.2	6
25	An improved method for functional similarity analysis of genes based on Gene Ontology. BMC Systems Biology, 2016, 10, 119.	3.0	23
26	Mining disease genes using integrated proteinâ€“protein interaction and geneâ€“gene coâ€“regulation information. FEBS Open Bio, 2015, 5, 251-256.	1.0	16
27	A gene-based information gain method for detecting geneâ€“gene interactions in caseâ€“control studies. European Journal of Human Genetics, 2015, 23, 1566-1572.	1.4	20
28	Computational Prediction of Protein Function Based on Weighted Mapping of Domains and GO Terms. BioMed Research International, 2014, 2014, 1-9.	0.9	3
29	Identification of functional miRNA regulatory modules and their associations via dynamic miRNA regulatory function. , 2014, , .		2
30	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
31	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
32	MLPA: Detecting overlapping communities by multi-label propagation approach. , 2013, , .		4
33	Measuring gene functional similarity based on group-wise comparison of GO terms. Bioinformatics, 2013, 29, 1424-1432.	1.8	83
34	Effective constructing training sets for object detection. , 2013, , .		0