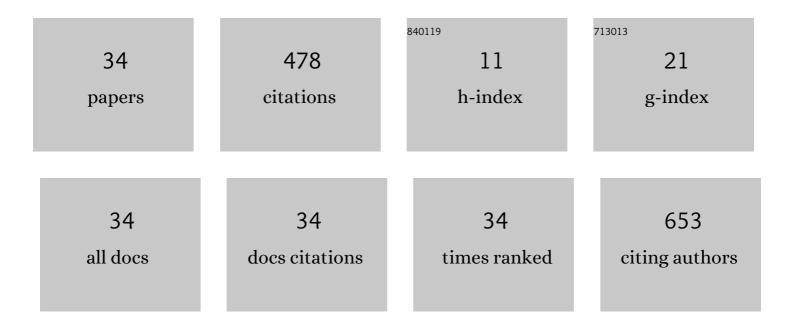
## Xiaoyan Liu

List of Publications by Year in descending order

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XIAOVANLUU

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

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#	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, , .		Ο
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 protein–protein interaction and gene–gene coâ€regulation information. FEBS Open Bio, 2015, 5, 251-256.	1.0	16
27	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
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