Tianjiao Zhang

List of Publications by Year
in descending order

21	768	9	15
papers	citations	h-index	g-index
23	23	23	934
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prioritization of disease microRNAs through a human phenome-microRNAome network. BMC Systems Biology, 2010, 4, S2.	3.0	335
2	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	14.5	124
3	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	2.8	117
4	SIDD: A Semantically Integrated Database towards a Global View of Human Disease. PLoS ONE, 2013, 8, e75504.	2.5	46
5	iEnhancer-EBLSTM: Identifying Enhancers and Strengths by Ensembles of Bidirectional Long Short-Term Memory. Frontiers in Genetics, 2021, 12, 665498.	2.3	23
6	Analyzing large-scale samples confirms the association between the rs1051730 polymorphism and lung cancer susceptibility. Scientific Reports, 2015, 5, 15642.	3.3	17
7	Identifying Liver Cancer-Related Enhancer SNPs by Integrating GWAS and Histone Modification ChIP-seq Data. BioMed Research International, 2016, 2016, 1-6.	1.9	17
8	Predicting human microRNA-disease associations based on support vector machine. , 2010, , .		16
9	Effects of DNA Methylation on TFs in Human Embryonic Stem Cells. Frontiers in Genetics, 2021, 12, 639461.	2.3	15
10	Application of Multilayer Network Models in Bioinformatics. Frontiers in Genetics, 2021, 12, 664860.	2.3	14
11	Weighted Network-Based Inference of Human MicroRNA-Disease Associations. , 2010, , .		12
12	The personal genome browser: visualizing functions of genetic variants. Nucleic Acids Research, 2014, 42, W192-W197.	14.5	7
13	KK-DBP: A Multi-Feature Fusion Method for DNA-Binding Protein Identification Based on Random Forest. Frontiers in Genetics, 2021, 12, 811158.	2.3	7
14	An Information Gain-based Method for Evaluating the Classification Power of Features Towards Identifying Enhancers. Current Bioinformatics, 2020, 15, 574-580.	1.5	6
15	ERDS-Exome: A Hybrid Approach for Copy Number Variant Detection from Whole-Exome Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 796-803.	3.0	5
16	VTP-Identifier: Vesicular Transport Proteins Identification Based on PSSM Profiles and XGBoost. Frontiers in Genetics, 2021, 12, 808856.	2.3	4
17	An Approach for Recognition of Enhancer-promoter Associations based on Random Forest. , 2019, , .		2
18	AOPM: Application of Antioxidant Protein Classification Model in Predicting the Composition of Antioxidant Drugs. Frontiers in Pharmacology, 2021, 12, 818115.	3.5	1

#	Article	IF	Citations
19	An Approach for Prediction of Enhancers Based on the Bayesian Model. , 2019, , .		0
20	Latent Semantic Analysis- and Hierarchical Clustering-Based Method for Detecting Remote Protein Homology. Current Proteomics, 2016, 13, 92-98.	0.3	0
21	SLDMS: A Tool for Calculating the Overlapping Regions of Sequences. Frontiers in Plant Science, 2021, 12, 813036.	3.6	0