Tianjiao Zhang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2302303/publications.pdf

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21 papers	768 citations	1040056 9 h-index	996975 15 g-index
23 all docs	23 docs citations	23 times ranked	934 citing authors

#	ARTICLE	IF	CITATIONS
1	Effects of DNA Methylation on TFs in Human Embryonic Stem Cells. Frontiers in Genetics, 2021, 12, 639461.	2.3	15
2	Application of Multilayer Network Models in Bioinformatics. Frontiers in Genetics, 2021, 12, 664860.	2.3	14
3	iEnhancer-EBLSTM: Identifying Enhancers and Strengths by Ensembles of Bidirectional Long Short-Term Memory. Frontiers in Genetics, 2021, 12, 665498.	2.3	23
4	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
5	VTP-Identifier: Vesicular Transport Proteins Identification Based on PSSM Profiles and XGBoost. Frontiers in Genetics, 2021, 12, 808856.	2.3	4
6	AOPM: Application of Antioxidant Protein Classification Model in Predicting the Composition of Antioxidant Drugs. Frontiers in Pharmacology, 2021, 12, 818115.	3.5	1
7	SLDMS: A Tool for Calculating the Overlapping Regions of Sequences. Frontiers in Plant Science, 2021, 12, 813036.	3.6	0
8	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
9	An Information Gain-based Method for Evaluating the Classification Power of Features Towards Identifying Enhancers. Current Bioinformatics, 2020, 15, 574-580.	1.5	6
10	An Approach for Recognition of Enhancer-promoter Associations based on Random Forest. , 2019, , .		2
11	An Approach for Prediction of Enhancers Based on the Bayesian Model. , 2019, , .		0
12	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
13	Latent Semantic Analysis- and Hierarchical Clustering-Based Method for Detecting Remote Protein Homology. Current Proteomics, 2016, 13, 92-98.	0.3	0
14	Analyzing large-scale samples confirms the association between the rs1051730 polymorphism and lung cancer susceptibility. Scientific Reports, 2015, 5, 15642.	3.3	17
15	LncRNA2Function: a comprehensive resource for functional investigation of human lncRNAs based on RNA-seq data. BMC Genomics, 2015, 16, S2.	2.8	117
16	LncRNA2Target: a database for differentially expressed genes after lncRNA knockdown or overexpression. Nucleic Acids Research, 2015, 43, D193-D196.	14.5	124
17	The personal genome browser: visualizing functions of genetic variants. Nucleic Acids Research, 2014, 42, W192-W197.	14.5	7
18	SIDD: A Semantically Integrated Database towards a Global View of Human Disease. PLoS ONE, 2013, 8, e75504.	2.5	46

#	ARTICLE	IF	CITATIONS
19	Prioritization of disease microRNAs through a human phenome-microRNAome network. BMC Systems Biology, 2010, 4, S2.	3.0	335
20	Weighted Network-Based Inference of Human MicroRNA-Disease Associations. , 2010, , .		12
21	Predicting human microRNA-disease associations based on support vector machine. , 2010, , .		16