Lingtao Su

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6777309/publications.pdf

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		1478505	1372567
15	108	6	10
papers	citations	h-index	g-index
15	15	15	154
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	A Multi-Level Iterative Bi-Clustering Method for Discovering miRNA Co-regulation Network of Abiotic Stress Tolerance in Soybeans. Frontiers in Plant Science, 2022, 13, 860791.	3.6	2
2	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. Evolutionary Bioinformatics, 2021, 17, 117693432110646.	1.2	5
3	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. Frontiers in Bioengineering and Biotechnology, 2020, 8, 349.	4.1	2
4	SEE: a novel multi-objective evolutionary algorithm for identifying SNP epistasis in genome-wide association studies. Biotechnology and Biotechnological Equipment, 2019, 33, 529-547.	1.3	7
5	A rectified factor network based biclustering method for detecting cancer-related coding genes and miRNAs, and their interactions. Methods, 2019, 166, 22-30.	3.8	4
6	HS-MMGKG: A Fast Multi-objective Harmony Search Algorithm for Two-locus Model Detection in GWAS. Current Bioinformatics, 2019, 14, 749-761.	1.5	9
7	Functional clusters analysis and research based on differential coexpression networks. Biotechnology and Biotechnological Equipment, 2018, 32, 171-182.	1.3	4
8	LPRP: A Gene–Gene Interaction Network Construction Algorithm and Its Application in Breast Cancer Data Analysis. Interdisciplinary Sciences, Computational Life Sciences, 2018, 10, 131-142.	3.6	5
9	Predicting overlapping protein complexes based on core-attachment and a local modularity structure. BMC Bioinformatics, 2018, 19, 305.	2.6	26
10	MGOGP: a gene module-based heuristic algorithm for cancer-related gene prioritization. BMC Bioinformatics, 2018, 19, 215.	2.6	6
11	OMPcontact: An Outer Membrane Protein Inter-Barrel Residue Contact Prediction Method. Journal of Computational Biology, 2017, 24, 217-228.	1.6	6
12	A new approach to detect epistasis utilizing parallel implementation of ant colony optimization by MapReduce framework. International Journal of Computer Mathematics, 2016, 93, 511-523.	1.8	11
13	Research on Single Nucleotide Polymorphisms Interaction Detection from Network Perspective. PLoS ONE, 2015, 10, e0119146.	2.5	14
14	GECluster: a novel protein complex prediction method. Biotechnology and Biotechnological Equipment, 2014, 28, 753-761.	1.3	3
15	CChi: An efficient cloud epistasis test model in human genome wide association studies. , 2013, , .		4