

# Lingtao Su

## List of Publications by Year in descending order

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

Version: 2024-02-01

15  
papers

108  
citations

1478505

6  
h-index

1372567

10  
g-index

15  
all docs

15  
docs citations

15  
times ranked

154  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting overlapping protein complexes based on core-attachment and a local modularity structure. BMC Bioinformatics, 2018, 19, 305.	2.6	26
2	Research on Single Nucleotide Polymorphisms Interaction Detection from Network Perspective. PLoS ONE, 2015, 10, e0119146.	2.5	14
3	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
4	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
5	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
6	OMPcontact: An Outer Membrane Protein Inter-Barrel Residue Contact Prediction Method. Journal of Computational Biology, 2017, 24, 217-228.	1.6	6
7	MGOGP: a gene module-based heuristic algorithm for cancer-related gene prioritization. BMC Bioinformatics, 2018, 19, 215.	2.6	6
8	LPRP: A Gene-Genome 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	Evolutionary Dynamics of Indels in SARS-CoV-2 Spike Glycoprotein. Evolutionary Bioinformatics, 2021, 17, 117693432110646.	1.2	5
10	CChi: An efficient cloud epistasis test model in human genome wide association studies. , 2013, , .		4
11	Functional clusters analysis and research based on differential coexpression networks. Biotechnology and Biotechnological Equipment, 2018, 32, 171-182.	1.3	4
12	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
13	GECluster: a novel protein complex prediction method. Biotechnology and Biotechnological Equipment, 2014, 28, 753-761.	1.3	3
14	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. Frontiers in Bioengineering and Biotechnology, 2020, 8, 349.	4.1	2
15	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