

# Le Li

## List of Publications by Year in descending order

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16  
papers

714  
citations

687363

13  
h-index

996975

15  
g-index

18  
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18  
docs citations

18  
times ranked

837  
citing authors

#	ARTICLE	IF	CITATIONS
1	OMMA enables population-scale analysis of complex genomic features and phylogenomic relationships from nanochannel-based optical maps. <i>GigaScience</i> , 2019, 8, .	6.4	5
2	Genome maps across 26 human populations reveal population-specific patterns of structural variation. <i>Nature Communications</i> , 2019, 10, 1025.	12.8	123
3	New guidelines for DNA methylome studies regarding 5-hydroxymethylcytosine for understanding transcriptional regulation. <i>Genome Research</i> , 2019, 29, 543-553.	5.5	21
4	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. <i>Genome Biology</i> , 2017, 18, 230.	8.8	28
5	ICN: a normalization method for gene expression data considering the over-expression of informative genes. <i>Molecular BioSystems</i> , 2016, 12, 3057-3066.	2.9	28
6	Integrating Information in Biological Ontologies and Molecular Networks to Infer Novel Terms. <i>Scientific Reports</i> , 2016, 6, 39237.	3.3	5
7	Adaptive Noise Immune Cluster Ensemble Using Affinity Propagation. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2015, 27, 3176-3189.	5.7	80
8	Hybrid Adaptive Classifier Ensemble. <i>IEEE Transactions on Cybernetics</i> , 2015, 45, 177-190.	9.5	82
9	Adaptive Fuzzy Consensus Clustering Framework for Clustering Analysis of Cancer Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 887-901.	3.0	55
10	Multi-view Based AdaBoost Classifier Ensemble for Class Prediction from Gene Expression Profiles. , 2014, , .		2
11	Hybrid clustering solution selection strategy. <i>Pattern Recognition</i> , 2014, 47, 3362-3375.	8.1	61
12	Probabilistic cluster structure ensemble. <i>Information Sciences</i> , 2014, 267, 16-34.	6.9	32
13	Double Selection Based Semi-Supervised Clustering Ensemble for Tumor Clustering from Gene Expression Profiles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 727-740.	3.0	60
14	Hybrid Fuzzy Cluster Ensemble Framework for Tumor Clustering from Biomolecular Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 657-670.	3.0	57
15	SC <sup>3</sup> : Triple Spectral Clustering-Based Consensus Clustering Framework for Class Discovery from Cancer Gene Expression Profiles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1751-1765.	3.0	60
16	Representative Distance: A New Similarity Measure for Class Discovery From Gene Expression Data. <i>IEEE Transactions on Nanobioscience</i> , 2012, 11, 341-351.	3.3	14