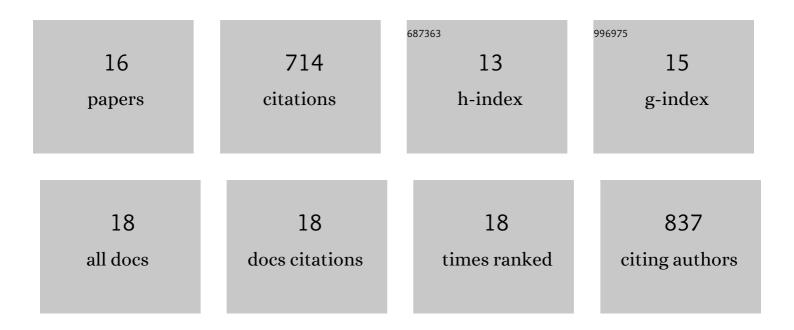


List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1778117/publications.pdf Version: 2024-02-01



IF # ARTICLE CITATIONS OMMA enables population-scale analysis of complex genomic features and phylogenomic relationships 6.4 from nanochannel-based optical maps. GigaScience, 2019, 8, . Genome maps across 26 human populations reveal population-specific patterns of structural 9 12.8 123 variation. Nature Communications, 2019, 10, 1025. New guidelines for DNA methylome studies regarding 5-hydroxymethylcytosine for understanding transcriptional regulation. Genome Research, 2019, 29, 543-553. 5.5 OMSV enables accurate and comprehensive identification of large structural variations from 4 8.8 28 nanochannel-based single-molecule optical maps. Genome Biology, 2017, 18, 230. ICN: a normalization method for gene expression data considering the over-expression of informative genes. Molecular BioSystems, 2016, 12, 3057-3066. 28 Integrating Information in Biological Ontologies and Molecular Networks to Infer Novel Terms. 3.3 5 6 Scientific Reports, 2016, 6, 39237. Adaptive Noise Immune Cluster Ensemble Using Affinity Propagation. IEEE Transactions on Knowledge and Data Engineering, 2015, 27, 3176-3189. 80 Hybrid Adaptive Classifier Ensemble. IEEE Transactions on Cybernetics, 2015, 45, 177-190. 8 9.5 82 Adaptive Fuzzy Consensus Clustering Framework for Clustering Analysis of Cancer Data. IEEE/ACM 3.0 Transactions on Computational Biology and Bioinformatics, 2015, 12, 887-901. Multi-view Based AdaBoost Classifier Ensemble for Class Prediction from Gene Expression Profiles. 10 9 2014, , . Hybrid clustering solution selection strategy. Pattern Recognition, 2014, 47, 3362-3375. 8.1 12 Probabilistic cluster structure ensemble. Information Sciences, 2014, 267, 16-34. 6.9 32 Double Selection Based Semi-Supervised Clustering Ensemble for Tumor Clustering from Gene Expression Profiles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 727-740. Hybrid Fuzzy Cluster Ensemble Framework for Tumor Clustering from Biomolecular Data. IEEE/ACM 14 3.0 57 Transactions on Computational Biology and Bioinformatics, 2013, 10, 657-670. SCÂ3: Triple Spectral Clustering-Based Consensus Clustering Framework for Class Discovery from Cancer Gene Expression Profiles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1751-1765. Representative Distance: A New Similarity Measure for Class Discovery From Gene Expression Data. IEEE 16 3.3 14 Transactions on Nanobioscience, 2012, 11, 341-351.