

Anup Kumar Halder

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

112
citations

1684129

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1372553

10
g-index

14
all docs

14
docs citations

14
times ranked

101
citing authors

#	ARTICLE	IF	CITATIONS
1	Bio-inspired cryptosystem with DNA cryptography and neural networks. Journal of Systems Architecture, 2019, 94, 24-31.	4.3	27
2	Review of computational methods for virus-host protein interaction prediction: a case study on novel Ebola-human interactions. Briefings in Functional Genomics, 2018, 17, 381-391.	2.7	19
3	Drug repurposing for COVID-19 using computational screening: Is Fostamatinib/R406 a potential candidate?. Methods, 2022, 203, 564-574.	3.8	18
4	Aggregated network centrality shows non-random structure of genomic and proteomic networks. Methods, 2020, 181-182, 5-14.	3.8	11
5	S-Palmitoylation of Synaptic Proteins as a Novel Mechanism Underlying Sex-Dependent Differences in Neuronal Plasticity. International Journal of Molecular Sciences, 2021, 22, 6253.	4.1	7
6	HdK-means: Hadoop based parallel K-means clustering for big data. , 2017, , .		6
7	3gClust: Human Protein Cluster Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1-1.	3.0	6
8	Computational modeling of human-nCoV protein-protein interaction network. Methods, 2022, 203, 488-497.	3.8	5
9	A survey on Ebola genome and current trends in computational research on the Ebola virus. Briefings in Functional Genomics, 2018, 17, 374-380.	2.7	4
10	<i>JUPPI</i>: A Multi-Level Feature Based Method for PPI Prediction and a Refined Strategy for Performance Assessment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 531-542.	3.0	4
11	Prediction of Thyroid Cancer Genes Using an Ensemble of Post Translational Modification, Semantic and Structural Similarity Based Clustering Results. Lecture Notes in Computer Science, 2017, , 418-423.	1.3	3
12	RFCM-PALM: In-Silico Prediction of S-Palmitoylation Sites in the Synaptic Proteins for Male/Female Mouse Data. International Journal of Molecular Sciences, 2021, 22, 9901.	4.1	2
13	Analysis of Large-Scale Human Protein Sequences Using an Efficient Spark-Based DBSCAN Algorithm. Advances in Intelligent Systems and Computing, 2021, , 601-609.	0.6	0