Tapobrata Lahiri

List of Publications by Year
in descending order

28	101	1684188	1588992
28 papers	**101** citations	**5** h-index	**8** g-index
29 all docs	**29** docs citations	**29** times ranked	**129** citing authors

#	Article	IF	Citations
1	A comparative study on the molecular descriptors for predicting drug-likeness of small molecules. Bioinformation, 2009, 3, 384-388.	0.5	28
2	Exploring geometric properties of gold nanoparticles using TEM images to explain their chaperone like activity for citrate synthase. Bioinformation, 2011, 7, 320-323.	0.5	7
3	Protein structure validation using a semi-empirical method. Bioinformation, 2012, 8, 984-987.	0.5	6
4	Multilamellar Vesicular Clusters of Phosphatidylcholine and Their Sensitivity to Spectrin: A Study by Fractal Analysis. Journal of Structural Biology, 1998, 123, 179-186.	2.8	5
5	Onset of Percolation and Fractal Classification Scheme for Multilamellar Lipid Vesicles. Journal of Colloid and Interface Science, 1999, 211, 89-95.	9.4	5
6	PCV: An Alignment Free Method for Finding Homologous Nucleotide Sequences and its Application in Phylogenetic Study. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 173-183.	3.6	5
7	An ANN-GA model based promoter prediction in Arabidopsis thaliana using tilling microarray data. Bioinformation, 2011, 6, 240-243.	0.5	5
8	A Novel Strategy for Designing Efficient Multiple Classifier. Lecture Notes in Computer Science, 2005, , 713-720.	1.3	5
9	Segmentation of Ill-Defined Objects by Convoluting Context Window of Each Pixel with a Non-Parametric Function. International Journal of Computer Vision and Image Processing, 2013, 3, 33-41.	0.4	5
10	FGO: A novel ontology for identification of ligand functional group. Bioinformation, 2007, 2, 113-118.	0.5	4
11	An improved protein structure evaluation using a semi-empirically derived structure property. BMC Structural Biology, 2018, 18, 16.	2.3	3
12	ProtPCV: A Fixed Dimensional Numerical Representation of Protein Sequence to Significantly Reduce Sequence Search Time. Interdisciplinary Sciences, Computational Life Sciences, 2020, 12, 276-287.	3.6	3
13	Surface characterization of proteins using multi-fractal property of heat-denatured aggregates. Bioinformation, 2008, 2, 379-383.	0.5	3
14	Functional group based Ligand binding affinity scoring function at atomic environmental level. Bioinformation, 2009, 3, 268-274.	0.5	3
15	Neurocognitive derivation of protein surface property from protein aggregate parameters. Bioinformation, 2011, 6, 158-161.	0.5	3
16	Significant Enhancement of Object Recognition Efficiency Using Human Cognition based Decision Clustering. International Journal of Computer Vision and Image Processing, 2013, 3, 1-15.	0.4	3
17	Clustering of signal components within most likely ECG episodes to analyze the ECG-waves. Pattern Recognition and Image Analysis, 2009, 19, 30-34.	1.0	2
18	Surface roughness index, a novel approach to compare protein surfaces. , 0, , .		1

#	Article	IF	Citations
19	Evaluation of protein surface roughness index using its heat denatured aggregates. Nature Precedings, 2009, , .	0.1	1
20	Theoretical model of circular RNA prediction and classification. , 2016, , .		1
21	An Improved Protein Surface Extraction Method Using Rotating Cylinder Probe. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 65-71.	3.6	1
22	A Critical Note on Symmetry Contact Artifacts and the Evaluation of the Quality of Homology Models. Symmetry, 2018, 10, 25.	2.2	1
23	APT: An Automated Probe Tracker from gene expression data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	1
24	Models of circular RNA biogenesis. , 2015, , .		0
25	A new search subspace to compensate failure of cavity-based localization of ligand-binding sites. Computational Biology and Chemistry, 2017, 68, 6-11.	2.3	0
26	EcircPred: Sequence and secondary structural property based computational identification of exonic circular RNAs. Computational Biology and Chemistry, 2018, 77, 28-35.	2.3	0
27	Statistics of Unrelated Sequence Properties to Improve Prediction of B-Cell Based Linear Epitopes. , 2018, , .		0
28	Digital signal processing-based approach to identify splicing mutations for detecting genetic diseases. Journal of Radio Electronics, 2021, 2021, .	0.1	0