Abhishek Sengupta

List of Publications by Year
in descending order

14 papers	56 citations	2258059 3 h-index	2053705 5 g-index
15 all docs	15 docs citations	15 times ranked	49 citing authors

#	Article	IF	Citations
1	PluriMetNet: A dynamic electronic model decrypting the metabolic variations in human embryonic stem cells (hESCs) at fluctuating oxygen concentrations. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4570-4578.	3.5	1
2	Agro-morphological variability and genetic diversity in linseed (Linum usitatissimum L.) germplasm accessions with emphasis on flowering and maturity time. Genetic Resources and Crop Evolution, 2022, 69, 315-333.	1.6	16
3	Proteome analysis using machine learning approaches and its applications to diseases. Advances in Protein Chemistry and Structural Biology, 2021, 127, 161-216.	2.3	2
4	In-Silico Structure-Based Drug Discovery of Candidate Drugs against Novel Protein Receptor Complex Nsp10-Nsp16 of SARS-CoV-2 using Drug Repurposing Approach. Coronaviruses, 2021, 2, 255-264.	0.3	1
5	VIRdb 2.0: Interactive analysis of comorbidity conditions associated with vitiligo pathogenesis using co-expression network-based approach. F1000Research, 2020, 9, 1055.	1.6	0
6	VIRdb: a comprehensive database for interactive analysis of genes/proteins involved in the pathogenesis of vitiligo. PeerJ, 2020, 8, e9119.	2.0	3
7	VIRdb 2.0: Interactive analysis of comorbidity conditions associated with vitiligo pathogenesis using co-expression network-based approach. F1000Research, 2020, 9, 1055.	1.6	1
8	Metabolomics. , 2018, , 75-97.		6
9	Identification of target analogues of E3 ubiquitin ligase involved in the incidence of breast cancer: A rational drug designing approach. , 2018, , .		0
10	Construction of Discrete Model of Human Pluripotency in Predicting Lineage-Specific Outcomes and Targeted Knockdowns of Essential Genes. Scientific Reports, 2018, 8, 11031.	3.3	3
11	Transcription Factor Information System (TFIS): A Tool for Detection of Transcription Factor Binding Sites. Interdisciplinary Sciences, Computational Life Sciences, 2017, 9, 378-391.	3.6	4
12	Glucose concentration varies logarithmically under both glycemic conditions in a computationally reconstructed human energy pool network (HEPNet). , 2016, , .		0
13	In silico Identification of Ergosterol as a Novel Fungal Metabolite Enhancing RuBisCO Activity in Lycopersicum esculentum. Interdisciplinary Sciences, Computational Life Sciences, 2016, 8, 229-240.	3.6	3
14	HEPNet: A Knowledge Base Model of Human Energy Pool Network for Predicting the Energy Availability Status of an Individual. PLoS ONE, 2015, 10, e0127918.	2.5	2