

Atul Kumar Upadhyay

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

191
citations

1307594

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31
all docs

31
docs citations

31
times ranked

232
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural insights into the amino acid usage variations in the profilin gene family. <i>Amino Acids</i> , 2022, 54, 411-419.	2.7	3
2	T-cell epitope-based vaccine designing against Orthohantavirus: a causative agent of deadly cardio-pulmonary disease. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2022, 11, 2.	2.1	17
3	Development, In-Vitro Characterization and Preclinical Evaluation of Esomeprazole-Encapsulated Proniosomal Formulation for the Enhancement of Anti-Ulcer Activity. <i>Molecules</i> , 2022, 27, 2748.	3.8	3
4	Food Allergens and Related Computational Biology Approaches: A Requisite for a Healthy Life. , 2021, , 145-160.		2
5	An Upsurge of the novel sub-acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic: A systematic review. <i>Romanian Biotechnological Letters</i> , 2021, 26, 2195-2206.	0.5	0
6	Screening of potent drug inhibitors against SARS-CoV-2 RNA polymerase: an in silico approach. <i>3 Biotech</i> , 2021, 11, 93.	2.2	11
7	Bioinformatics Tools and Databases for Genomics-assisted Breeding and Population Genetics of Plants: A Review. <i>Current Bioinformatics</i> , 2021, 16, 766-773.	1.5	2
8	In-Silico Prediction of Peptide Based Vaccine Against Zika Virus. <i>International Journal of Peptide Research and Therapeutics</i> , 2020, 26, 85-91.	1.9	11
9	The transcriptome enables the identification of candidate genes behind medicinal value of Drumstick tree (<i>Moringa oleifera</i>). <i>Genomics</i> , 2020, 112, 621-628.	2.9	22
10	A knowledge-driven protocol for prediction of proteins of interest with an emphasis on biosynthetic pathways. <i>MethodsX</i> , 2020, 7, 101053.	1.6	4
11	Dataset for the combined transcriptome assembly of <i>M. oleifera</i> and functional annotation. <i>Data in Brief</i> , 2020, 30, 105416.	1.0	4
12	Quantitative Genetics and the Genetic Basis for Polyphenolics Trait in Plants. , 2020, , 501-515.		0
13	Genome-wide Identification and Annotation of metabolite producing Gene Clusters in Rice Genome. <i>Research Journal of Pharmacy and Technology</i> , 2020, 13, 1744.	0.8	0
14	Computational approach to understand fungal secondary metabolites and responsible biological molecules. , 2020, , 105-114.		0
15	Genome-Wide Analysis of Domain-Swap Predicted Products in the Genome of Anti-Stress Medicinal Plant: <i>Ocimum tenuiflorum</i> . <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221882136.	2.0	1
16	Transcriptome analysis reveals plasticity in gene regulation due to environmental cues in <i>Primula sikkimensis</i> , a high altitude plant species. <i>BMC Genomics</i> , 2019, 20, 989.	2.8	10
17	Understanding Cellular and Molecular Events of Skin Aging and Cancer: An Integrative Perspective. , 2019, , 11-28.		1
18	Genome-wide prediction and analysis of siRNA as potential antiviral agent against Hepatitis-C virus. , 2018, , .		0

#	ARTICLE	IF	CITATIONS
19	Computational Tools and Databases of Microbes and Its Bioprospecting for Sustainable Development. , 2018, , 385-397.		0
20	Computational Approaches to Understand the Genome and Protein Sequences of Fungi. , 2018, , 635-649.		0
21	Niosomes: A Novel Trend in Drug Delivery. Research Journal of Pharmacy and Technology, 2018, 11, 5205.	0.8	9
22	MOLECULAR MODELING AND ANALYSIS OF KEY PROTEINS IN CYTOKININ MEDIATED LEAF SENESCENCE OF WHEAT. , 2017, 73, .		0
23	HYPERTENSION AND GENETIC POLYMORPHISM OF ACE AND ADD1 GENE IN NORTH INDIAN POPULATION. , 2017, 73, .		0
24	Genome-Wide Identification and Analysis of Putative Rhomboid Gene Enhancers in Multiple Drosophila Species. Immunome Research, 2017, 13, .	0.1	1
25	Genome-Wide Prediction and Analysis of 3D-Domain Swapped Proteins in the Human Genome from Sequence Information. PLoS ONE, 2016, 11, e0159627.	2.5	5
26	Genome sequencing of herb Tulsi (<i>Ocimum tenuiflorum</i>) unravels key genes behind its strong medicinal properties. BMC Plant Biology, 2015, 15, 212.	3.6	80
27	3PFDB+: improved search protocol and update for the identification of representatives of protein sequence domain families. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau026.	3.0	5
28	IDENTIFICATION AND CONFORMATIONAL ANALYSIS OF HINGE REGIONS IN PROTEINS THAT UNDERGO DOMAIN SWAPPING. , 2013, , 320-332.		0
29	A bioinformatics pipeline for sequence to structure: A case study with a Cml patient undergoing treatment with imatinib. , 2013, , .		0