

Oommen K Mathew

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

559
citations

933447

10
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

836
citing authors

#	ARTICLE	IF	CITATIONS
1	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	0
2	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
3	The Indian cobra reference genome and transcriptome enables comprehensive identification of venom toxins. <i>Nature Genetics</i> , 2020, 52, 106-117.	21.4	139
4	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
5	Sepsis in the era of data-driven medicine: personalizing risks, diagnoses, treatments and prognoses. <i>Briefings in Bioinformatics</i> , 2020, 21, 1182-1195.	6.5	29
6	Phenotypic expression and clinical outcomes in a South Asian PRKAC2 cardiomyopathy cohort. <i>Scientific Reports</i> , 2020, 10, 20610.	3.3	10
7	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
8	Draft Genome Sequence of Plant Growth-Promoting Endophytic Microbacterium <i>hydrothermale</i> BPSAC84, Isolated from the Medicinal Plant <i>Mirabilis jalapa</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	17
9	Draft Genome Sequence of <i>Streptomyces thermocarboxyus</i> BPSAC147, a Potentially Plant Growth-Promoting Endophytic Bacterium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
10	PASS2 version 6: a database of structure-based sequence alignments of protein domain superfamilies in accordance with SCOPe. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	2
11	Draft Genome Sequence of Freshwater-Derived <i>Streptomyces</i> sp. Strain BPSDS2, Isolated from Damte Stream, Northeast India. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
12	A comparative study of Bisulphite-seq analysis pipeline. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 233-233.	0.3	0
13	Pipeline to upgrade the genome annotations. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 236-236.	0.3	0
14	PIMADb: A Database of Protein-Protein Interactions in Huge Macromolecular Assemblies. <i>Bioinformatics and Biology Insights</i> , 2016, 10, BBI.S38416.	2.0	4
15	RStrucFam: a web server to associate structure and cognate RNA for RNA-binding proteins from sequence information. <i>BMC Bioinformatics</i> , 2016, 17, 411.	2.6	9
16	PASS2 database for the structure-based sequence alignment of distantly related SCOP domain superfamilies: update to version 5 and added features. <i>Nucleic Acids Research</i> , 2016, 44, D410-D414.	14.5	4
17	An Approach to Function Annotation for Proteins of Unknown Function (PUFs) in the Transcriptome of Indian Mulberry. <i>PLoS ONE</i> , 2016, 11, e0151323.	2.5	40
18	PIMA: Protein-Protein Interactions in Macromolecular Assembly - a web server for its Analysis and Visualization. <i>Bioinformatics</i> , 2016, 12, 9-11.	0.5	19

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19	Genome sequencing of herb Tulsi (<i>Ocimum tenuiflorum</i>) unravels key genes behind its strong medicinal properties. <i>BMC Plant Biology</i> , 2015, 15, 212.	3.6	80
20	DOCKSCORE: a webserver for ranking protein-protein docked poses. <i>BMC Bioinformatics</i> , 2015, 16, 127.	2.6	33
21	POEAS: Automated Plant Phenomic Analysis Using Plant Ontology. <i>Bioinformatics and Biology Insights</i> , 2014, 8, BBI.S19057.	2.0	6
22	LenVarDB: database of length-variant protein domains. <i>Nucleic Acids Research</i> , 2014, 42, D246-D250.	14.5	4
23	STIFDB2: An Updated Version of Plant Stress-Responsive Transcription Factor DataBase with Additional Stress Signals, Stress-Responsive Transcription Factor Binding Sites and Stress-Responsive Genes in <i>Arabidopsis</i> and <i>Rice</i> . <i>Plant and Cell Physiology</i> , 2013, 54, e8-e8.	3.1	130