

Hirak Jyoti Chakraborty

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

244
citations

1162367

8
h-index

996533

15
g-index

19
all docs

19
docs citations

19
times ranked

256
citing authors

#	ARTICLE	IF	CITATIONS
1	Trh positive strain of <i>Vibrio parahaemolyticus</i> induce immunity by modulating MAPK pathway: A molecular pathogenic insight in immune-related gene regulation. <i>Microbial Pathogenesis</i> , 2022, 164, 105436.	1.3	4
2	Metagenomics study in aquatic resource management: Recent trends, applied methodologies and future needs. <i>Gene Reports</i> , 2021, 25, 101372.	0.4	9
3	Metagenomic Analysis Reveals Bacterial and Fungal Diversity and Their Bioremediation Potential From Sediments of River Ganga and Yamuna in India. <i>Frontiers in Microbiology</i> , 2020, 11, 556136.	1.5	44
4	Metagenomic study focusing on antibiotic resistance genes from the sediments of River Yamuna. <i>Gene</i> , 2020, 758, 144951.	1.0	33
5	Structural Characterization of Open Reading Frame-Encoded Functional Genes from Tilapia Lake Virus (TiLV). <i>Molecular Biotechnology</i> , 2019, 61, 945-957.	1.3	26
6	Employing virtual screening and molecular dynamics simulations for identifying hits against the active cholera toxin. <i>Toxicon</i> , 2019, 170, 1-9.	0.8	4
7	Prediction and characterisation of lantibiotic structures with molecular modelling and molecular dynamics simulations. <i>Scientific Reports</i> , 2019, 9, 7169.	1.6	10
8	De novo whole transcriptome profiling of <i>Edwardsiella tarda</i> isolated from infected fish (<i>Labeo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	1.0	9
9	Therapeutic value of steroidal alkaloids in cancer: Current trends and future perspectives. <i>International Journal of Cancer</i> , 2019, 145, 1731-1744.	2.3	63
10	Computational characterization and molecular dynamics simulation of the thermostable direct hemolysin-related hemolysin (TRH) amplified from <i>Vibrio parahaemolyticus</i> . <i>Microbial Pathogenesis</i> , 2019, 127, 172-182.	1.3	8
11	Insights into the aquaporin 4 of zebrafish (<i>Danio rerio</i>) through evolutionary analysis, molecular modeling and structural dynamics. <i>Gene Reports</i> , 2018, 11, 101-109.	0.4	11
12	In Silico Structural Studies and Molecular Docking Analysis of Delta6-desaturase in HUFA Biosynthetic Pathway. <i>Animal Biotechnology</i> , 2018, 29, 161-173.	0.7	9
13	Protein Structure Prediction. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2018, , 48-79.	0.2	3
14	Protein Docking and Drug Design. <i>Advances in Bioinformatics and Biomedical Engineering Book Series</i> , 2018, , 207-241.	0.2	0
15	Targeting the dengue $\hat{2}$ -OG with serotype-specific alkaloid virtual leads. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 73, 129-142.	1.3	7
16	Intelligent Access to Sequence and Structure Databases (IASSD) â€“ an interface for accessing information from major web databases. <i>Bioinformation</i> , 2014, 10, 764-766.	0.2	1
17	Identification of regulatory sequence signatures in microRNA precursors implicated in neurological disorders. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2013, 04, 26-33.	0.3	3
18	Phylogenetic signatures of functional conservedness in lantibiotics- an in-silico regulomics study. <i>Indian Journal of Medical Research</i> , 2010, 2, 5-11.	0.0	0

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19	Identifying Overlapping Phylogenetic and Geographic Roots of HIV "1 Evolution through Computational Analyses. International Letters of Natural Sciences, 0, 7, 23-29.	1.0	0