

Mahmudul Hasan

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

650
citations

686830

13
h-index

642321

23
g-index

51
all docs

51
docs citations

51
times ranked

894
citing authors

#	ARTICLE	IF	CITATIONS
1	Plants Metabolites: Possibility of Natural Therapeutics Against the COVID-19 Pandemic. <i>Frontiers in Medicine</i> , 2020, 7, 444.	1.2	119
2	Reverse vaccinology approach to design a novel multi-epitope subunit vaccine against avian influenza A (H7N9) virus. <i>Microbial Pathogenesis</i> , 2019, 130, 19-37.	1.3	72
3	Prediction of potential inhibitors for RNA-dependent RNA polymerase of SARS-CoV-2 using comprehensive drug repurposing and molecular docking approach. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1787-1797.	3.6	57
4	Vaccinomics strategy for developing a unique multi-epitope monovalent vaccine against Marburg marburgvirus. <i>Infection, Genetics and Evolution</i> , 2019, 70, 140-157.	1.0	49
5	Immunoinformatics approaches for designing a novel multi epitope peptide vaccine against human norovirus (Norwalk virus). <i>Infection, Genetics and Evolution</i> , 2019, 74, 103936.	1.0	43
6	Contriving a chimeric polyvalent vaccine to prevent infections caused by herpes simplex virus (type-1) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Dynamics, 2020, 38, 2898-2915.	2.0	43
7	Revisiting potential druggable targets against <scp>SARSâ€CoV</scp>â€2 and repurposing therapeutics under preclinical study and clinical trials: A comprehensive review. <i>Drug Development Research</i> , 2020, 81, 919-941.	1.4	35
8	Prospects of nutritional interventions in the care of COVID-19 patients. <i>Heliyon</i> , 2021, 7, e06285.	1.4	22
9	Genome based evolutionary lineage of SARS-CoV-2 towards the development of novel chimeric vaccine. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104517.	1.0	17
10	Multidrug Antimicrobial Resistance and Molecular Detection of mcr-1 Gene in Salmonella Species Isolated from Chicken. <i>Animals</i> , 2021, 11, 206.	1.0	16
11	Comprehensive genome based analysis of <i>Vibrio parahaemolyticus</i> for identifying novel drug and vaccine molecules: Subtractive proteomics and vaccinomics approach. <i>PLoS ONE</i> , 2020, 15, e0237181.	1.1	15
12	Main protease inhibitors and drug surface hotspots for the treatment of COVID-19: A drug repurposing and molecular docking approach. <i>Biomedicine and Pharmacotherapy</i> , 2021, 140, 111742.	2.5	15
13	Subtractive genomics approach towards the identification of novel therapeutic targets against human <i>Bartonella bacilliformis</i> . <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100385.	1.9	13
14	A Revisit to the Research Updates of Drugs, Vaccines, and Bioinformatics Approaches in Combating COVID-19 Pandemic. <i>Frontiers in Molecular Biosciences</i> , 2021, 7, 585899.	1.6	12
15	Identification and host response interaction study of SARS-CoV-2 encoded miRNA-like sequences: an in silico approach. <i>Computers in Biology and Medicine</i> , 2021, 134, 104451.	3.9	10
16	In Silico Characterization and Motif Election of Neurotoxins from Snake Venom. <i>American Journal of Biochemistry and Biotechnology</i> , 2015, 11, 84-91.	0.1	9
17	Ancestral origin, antigenic resemblance and epidemiological insights of novel coronavirus (SARS-CoV-2): Global burden and Bangladesh perspective. <i>Infection, Genetics and Evolution</i> , 2020, 84, 104440.	1.0	9
18	Combination of highly antigenic nucleoproteins to inaugurate a cross-reactive next generation vaccine candidate against Arenaviridae family. <i>Heliyon</i> , 2021, 7, e07022.	1.4	9

#	ARTICLE	IF	CITATIONS
19	Major Insights in Dynamics of Host Response to SARS-CoV-2: Impacts and Challenges. <i>Frontiers in Microbiology</i> , 2021, 12, 637554.	1.5	8
20	Kinetics, detergent compatibility and feather-degrading capability of alkaline protease from <i>Bacillus subtilis</i> AKAL7 and <i>Exiguobacterium indicum</i> AKAL11 produced with fermentation of organic municipal solid wastes. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2020, 55, 1339-1348.	0.9	7
21	In silico identification of conserved miRNAs in the genome of fibre biogenesis crop <i>Corchorus capsularis</i> . <i>Heliyon</i> , 2021, 7, e06705.	1.4	7
22	First molecular characterization and phylogenetic analysis of the VP2 gene of feline panleukopenia virus in Bangladesh. <i>Archives of Virology</i> , 2021, 166, 2273-2278.	0.9	7
23	Designing potential siRNA molecules for silencing the gene of the nucleocapsid protein of Nipah virus: A computational investigation. <i>Infection, Genetics and Evolution</i> , 2022, 102, 105310.	1.0	7
24	Antiviral peptides from aquatic organisms: Functionality and potential inhibitory effect on SARS-CoV-2. <i>Aquaculture</i> , 2021, 541, 736783.	1.7	5
25	Molecular Detection of Colistin Resistance <i>mcr-1</i> Gene in Multidrug-Resistant <i>Escherichia coli</i> Isolated from Chicken. <i>Antibiotics</i> , 2022, 11, 97.	1.5	5
26	In Silico Identification and Functional Characterization of Conserved miRNAs in the Genome of <i>Cryptosporidium parvum</i> . <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110276.	1.0	4
27	In silico analysis to elect superior bacterial alkaline protease for detergent and leather industries. <i>Journal of Advances in Biotechnology</i> , 2016, 5, 685-698.	0.1	4
28	Proteome Exploration of <i>Legionella pneumophila</i> To Identify Novel Therapeutics: a Hierarchical Subtractive Genomics and Reverse Vaccinology Approach. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
29	Genome-wide Characterization Deciphers Distinct Properties of Aquaporins in Six <i>Phytophthora</i> Species. <i>Current Bioinformatics</i> , 2021, 16, 880-898.	0.7	2
30	Comprehensive in silico Study of GLUT10: Prediction of Possible Substrate Binding Sites and Interacting Molecules. <i>Current Pharmaceutical Biotechnology</i> , 2020, 21, 117-130.	0.9	2
31	Genomic diversity and molecular dynamics interaction on mutational variances among RB domains of SARS-CoV-2 interplay drug inactivation. <i>Infection, Genetics and Evolution</i> , 2021, , 105128.	1.0	2
32	Genomic attributes and recent advances in detection of white spot syndrome virus in shrimp: a review. <i>Marine Biology Research</i> , 0, , 1-21.	0.3	2
33	First report of <i>Epuraea</i> sp. (Coleoptera: Nitidulidae) on bottle gourd (<i>Lagenaria siceraria</i>) in north eastern part of Bangladesh. <i>International Journal of Tropical Insect Science</i> , 2022, 42, 1349-1355.	0.4	1
34	In Silico Investigation of Conserved miRNAs and Their Targets From the Expressed Sequence Tags in <i>Neospora Caninum</i> Genome. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110467.	1.0	1
35	The PH Domain and C-Terminal polyD Motif of Phafin2 Exhibit a Unique Concurrence in Animals. <i>Membranes</i> , 2022, 12, 696.	1.4	1
36	Molecular detection and phylogenetic analysis of Canine Parvovirus (CPV) in diarrheic pet dogs in Bangladesh. <i>Veterinary and Animal Science</i> , 2021, 14, 100224.	0.6	0

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37	Prediction and expression analysis of deleterious nonsynonymous SNPs of Arabidopsis ACD11 gene by combining computational algorithms and molecular docking approach. PLoS Computational Biology, 2022, 18, e1009539.	1.5	0