

Shifath Bin Syed

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

246
citations

1306789

7
h-index

1281420

11
g-index

15
all docs

15
docs citations

15
times ranked

315
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteome-wide screening for designing a multi-epitope vaccine against emerging pathogen <i>Elizabethkingia anophelis</i> using immunoinformatic approaches. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4850-4867.	2.0	90
2	Exploring Lassa Virus Proteome to Design a Multi-epitope Vaccine Through Immunoinformatics and Immune Simulation Analyses. International Journal of Peptide Research and Therapeutics, 2020, 26, 2089-2107.	0.9	44
3	Energy-optimized pharmacophore coupled virtual screening in the discovery of quorum sensing inhibitors of LasR protein of <i>Pseudomonas aeruginosa</i> . Journal of Biomolecular Structure and Dynamics, 2020, 38, 5374-5388.	2.0	22
4	Transcriptomic studies revealed pathophysiological impact of COVID-19 to predominant health conditions. Briefings in Bioinformatics, 2021, 22, .	3.2	17
5	Computational formulation and immune dynamics of a multi-peptide vaccine candidate against Crimean-Congo hemorrhagic fever virus. Molecular and Cellular Probes, 2021, 55, 101693.	0.9	16
6	A comprehensive screening of the whole proteome of hantavirus and designing a multi-epitope subunit vaccine for cross-protection against hantavirus: Structural vaccinology and immunoinformatics study. Microbial Pathogenesis, 2021, 150, 104705.	1.3	15
7	Inhibition of biofilm formation, quorum sensing and other virulence factors in <i>Pseudomonas aeruginosa</i> by polyphenols of <i>Gynura procumbens</i> leaves. Journal of Biomolecular Structure and Dynamics, 2022, 40, 5357-5371.	2.0	9
8	Community-acquired pneumonia: aetiology, antibiotic resistance and prospects of phage therapy. Journal of Chemotherapy, 2020, 32, 395-410.	0.7	7
9	COVID-19: The Catastrophe of Our Time. Journal of Advanced Biotechnology and Experimental Therapeutics, 2020, 3, 1.	0.4	7
10	Mycoremediation of reactive red HE7B dye by <i>Aspergillus salinarus</i> isolated from textile effluents. Current Research in Microbial Sciences, 2021, 2, 100056.	1.4	6
11	Comparative proteomic analysis to annotate the structural and functional association of the hypothetical proteins of <i>S. maltophilia</i> k279a and predict potential T and B cell targets for vaccination. PLoS ONE, 2021, 16, e0252295.	1.1	5