

Sameer Hassan

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

32
papers

290
citations

9
h-index

16
g-index

34
ext. papers

385
ext. citations

3.1
avg, IF

3.07
L-index

#	Paper	IF	Citations
32	Effects of Increasing Salinity by Drip Irrigation on Total Grain Weight Show High Yield Potential of Putative Salt-Tolerant Mutagenized Wheat Lines. <i>Sustainability</i> , 2022 , 14, 5061	3.6	0
31	Evolution and identification of DREB transcription factors in the wheat genome: modeling, docking and simulation of DREB proteins associated with salt stress. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-14	3.6	0
30	Computational approach identifies protein off-targets for Isoniazid-NAD adduct: hypothesizing a possible drug resistance mechanism in. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 1697-1710	3.6	4
29	Wild-Type MIC Distribution for Re-evaluating the Critical Concentration of Anti-TB Drugs and Pharmacodynamics Among Tuberculosis Patients From South India. <i>Frontiers in Microbiology</i> , 2020 , 11, 1182	5.7	3
28	Development and characterization of an EMS-mutagenized wheat population and identification of salt-tolerant wheat lines. <i>BMC Plant Biology</i> , 2020 , 20, 18	5.3	14
27	Computational analysis of drug like candidates against Neuraminidase of Human Influenza A virus subtypes. <i>Informatics in Medicine Unlocked</i> , 2020 , 18, 100284	5.3	2
26	Protein-protein interaction of Rv0148 with Htdy and its predicted role towards drug resistance in Mycobacterium tuberculosis. <i>BMC Microbiology</i> , 2020 , 20, 93	4.5	2
25	In silico based screening of WRKY genes for identifying functional genes regulated by WRKY under salt stress. <i>Computational Biology and Chemistry</i> , 2019 , 83, 107131	3.6	5
24	Exploring the conformational landscapes of HIV protease structural ensembles using principal component analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86, 990-1000	4.2	3
23	Advances in Designing and Developing Vaccines, Drugs and Therapeutic Approaches to Counter Human Papilloma Virus. <i>Frontiers in Immunology</i> , 2018 , 9, 2478	8.4	28
22	Differential Codon Usage Pattern of HIV-1 tat Gene in Those with Slower and Faster Rates of Disease Progression. <i>AIDS Research and Human Retroviruses</i> , 2017 , 33, 900-901	1.6	
21	Biased Nucleotide Composition and Differential Codon Usage Pattern in HIV-1 and HIV-2. <i>AIDS Research and Human Retroviruses</i> , 2017 , 33, 298-307	1.6	2
20	Homology modeling of Homo sapiens lipoic acid synthase: Substrate docking and insights on its binding mode. <i>Journal of Theoretical Biology</i> , 2017 , 420, 259-266	2.3	3
19	Homology modeling, substrate docking, and molecular simulation studies of mycobacteriophage Che12 lysin A. <i>Journal of Molecular Modeling</i> , 2016 , 22, 180	2	4
18	Insights into RpoB clinical mutants in mediating rifampicin resistance in Mycobacterium tuberculosis. <i>Journal of Molecular Graphics and Modelling</i> , 2016 , 67, 20-32	2.8	10
17	Andrographolide: A potent antituberculosis compound that targets Aminoglycoside 2bN-acetyltransferase in Mycobacterium tuberculosis. <i>Journal of Molecular Graphics and Modelling</i> , 2015 , 61, 133-40	2.8	25
16	A user-friendly web portal for analyzing conformational changes in structures of Mycobacterium tuberculosis. <i>Journal of Molecular Modeling</i> , 2015 , 21, 252	2	

15	In silico and experimental validation of protein-protein interactions between PknI and Rv2159c from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Graphics and Modelling</i> , 2015 , 62, 283-293	2.8	8
14	Comparative codon usage analysis of HIV-1 and HIV-2 genomes. <i>BMC Infectious Diseases</i> , 2014 , 14, E2	4	78
13	Homology modelling, docking, pharmacophore and site directed mutagenesis analysis to identify the critical amino acid residue of PknI from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Graphics and Modelling</i> , 2014 , 52, 11-9	2.8	9
12	In silico sequence and structure analysis for mycobacteriophages. <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2012 , 2, S377-S379	1.4	
11	Functional assignment of the 64 mycobacteriophages into gene families. <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2012 , 2, S383-S385	1.4	
10	Computational structural analysis of proteins of <i>Mycobacterium tuberculosis</i> and a resource for identifying off-targets. <i>Journal of Molecular Modeling</i> , 2012 , 18, 3993-4004	2	1
9	MtbSD--a comprehensive structural database for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2011 , 91, 556-62	2.6	4
8	Mycobacteriophage genome database. <i>Bioinformatics</i> , 2011 , 6, 393-4	1.1	3
7	Binding of activated isoniazid with acetyl-CoA carboxylase from <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2011 , 7, 107-11	1.1	5
6	Lytic Efficiency of Mycobacteriophages 2010 , 3, 21-28		4
5	Synonymous codon usage analysis of thirty two mycobacteriophage genomes. <i>Advances in Bioinformatics</i> , 2009 , 316936	5.5	24
4	Insight to pyrazinamide resistance in <i>Mycobacterium tuberculosis</i> by molecular docking. <i>Bioinformatics</i> , 2009 , 4, 24-9	1.1	12
3	Construction and evaluation of luciferase reporter phages for the detection of active and non-replicating tubercle bacilli. <i>Journal of Microbiological Methods</i> , 2008 , 73, 18-25	2.8	28
2	Tape measure protein having MT3 motif facilitates phage entry into stationary phase cells of <i>Mycobacterium tuberculosis</i> . <i>Computational Biology and Chemistry</i> , 2008 , 32, 367-9	3.6	3
1	In silico analysis of mycobacteriophage Che12 genome: characterization of genes required to lysogenise <i>Mycobacterium tuberculosis</i> . <i>Computational Biology and Chemistry</i> , 2007 , 31, 82-91	3.6	6