

Sameer Hassan

List of Publications by Year in descending order

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33
papers

343
citations

932766

10
h-index

887659

17
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34
all docs

34
docs citations

34
times ranked

497
citing authors

#	ARTICLE	IF	CITATIONS
1	Synonymous Codon Usage Analysis of Thirty Two Mycobacteriophage Genomes. <i>Advances in Bioinformatics</i> , 2009, 2009, 1-11.	5.7	48
2	Advances in Designing and Developing Vaccines, Drugs and Therapeutic Approaches to Counter Human Papilloma Virus. <i>Frontiers in Immunology</i> , 2018, 9, 2478.	2.2	41
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.	0.7	35
4	Development and characterization of an EMS-mutagenized wheat population and identification of salt-tolerant wheat lines. <i>BMC Plant Biology</i> , 2020, 20, 18.	1.6	34
5	Andrographolide: A potent antituberculosis compound that targets Aminoglycoside 2- N -acetyltransferase in <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Graphics and Modelling</i> , 2015, 61, 133-140.	1.3	31
6	Insights into RpoB clinical mutants in mediating rifampicin resistance in <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Graphics and Modelling</i> , 2016, 67, 20-32.	1.3	14
7	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.	1.1	14
8	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.	1.3	13
9	Insight to pyrazinamide resistance in <i>Mycobacterium tuberculosis</i> by molecular docking. <i>Bioinformation</i> , 2009, 4, 24-29.	0.2	12
10	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, 11-19.	1.3	11
11	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.	1.1	8
12	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.	1.5	8
13	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.	0.5	7
14	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> , 2022, 40, 7191-7204.	2.0	7
15	Homology modeling, substrate docking, and molecular simulation studies of mycobacteriophage Che12 lysin A. <i>Journal of Molecular Modeling</i> , 2016, 22, 180.	0.8	6
16	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.	0.8	6
17	Exploring the conformational landscapes of HIV protease structural ensembles using principal component analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 990-1000.	1.5	6
18	Protein-protein interaction of Rv0148 with Htdy and its predicted role towards drug resistance in <i>Mycobacterium tuberculosis</i> . <i>BMC Microbiology</i> , 2020, 20, 93.	1.3	6

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19	Lytic Efficiency of Mycobacteriophages. <i>The Open Systems Biology Journal</i> , 2010, 3, 21-28.	0.7	6
20	MtbSDâ€“A comprehensive structural database for Mycobacterium tuberculosis. <i>Tuberculosis</i> , 2011, 91, 556-562.	0.8	5
21	Computational approach identifies protein off-targets for Isoniazid-NAD adduct: hypothesizing a possible drug resistance mechanism in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 1-14.	2.0	5
22	Binding of activated isoniazid with acetyl-CoA carboxylase from Mycobacterium tuberculosis. <i>Bioinformatics</i> , 2011, 7, 107-111.	0.2	5
23	Tape measure protein having MT3 motif facilitates phage entry into stationary phase cells of Mycobacterium tuberculosis. <i>Computational Biology and Chemistry</i> , 2008, 32, 367-369.	1.1	4
24	Computational analysis of drug like candidates against Neuraminidase of Human Influenza A virus subtypes. <i>Informatics in Medicine Unlocked</i> , 2020, 18, 100284.	1.9	4
25	Mycobacteriophage Genome Database. <i>Bioinformatics</i> , 2011, 6, 393-394.	0.2	3
26	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.	1.6	2
27	Computational structural analysis of proteins of Mycobacterium tuberculosis and a resource for identifying off-targets. <i>Journal of Molecular Modeling</i> , 2012, 18, 3993-4004.	0.8	1
28	A user-friendly web portal for analyzing conformational changes in structures of Mycobacterium tuberculosis. <i>Journal of Molecular Modeling</i> , 2015, 21, 252.	0.8	1
29	In silico sequence and structure analysis for mycobacteriophages. <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2012, 2, S377-S379.	0.5	0
30	Functional assignment of the 64 mycobacteriophages into gene families. <i>Asian Pacific Journal of Tropical Biomedicine</i> , 2012, 2, S383-S385.	0.5	0
31	Comparative codon usage analysis of HIV-1 and HIV-2 genomes. <i>BMC Infectious Diseases</i> , 2014, 14, .	1.3	0
32	Multifaced pknE: Apoptosis Inhibition, HIV Co-Infection, Host Signaling Cross-Talk and in Orchestrating the Physiology of Mycobacterium tuberculosis. <i>Journal of Microbial & Biochemical Technology</i> , 2016, 8, .	0.2	0
33	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.	0.5	0