

# Sameer Hassan

## List of Publications by Citations

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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	Comparative codon usage analysis of HIV-1 and HIV-2 genomes. <i>BMC Infectious Diseases</i> , <b>2014</b> , 14, E2	4	78
31	Construction and evaluation of luciferase reporter phages for the detection of active and non-replicating tubercle bacilli. <i>Journal of Microbiological Methods</i> , <b>2008</b> , 73, 18-25	2.8	28
30	Advances in Designing and Developing Vaccines, Drugs and Therapeutic Approaches to Counter Human Papilloma Virus. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 2478	8.4	28
29	Andrographolide: A potent antituberculosis compound that targets Aminoglycoside 2bN-acetyltransferase in Mycobacterium tuberculosis. <i>Journal of Molecular Graphics and Modelling</i> , <b>2015</b> , 61, 133-40	2.8	25
28	Synonymous codon usage analysis of thirty two mycobacteriophage genomes. <i>Advances in Bioinformatics</i> , <b>2009</b> , 316936	5.5	24
27	Development and characterization of an EMS-mutagenized wheat population and identification of salt-tolerant wheat lines. <i>BMC Plant Biology</i> , <b>2020</b> , 20, 18	5.3	14
26	Insight to pyrazinamide resistance in Mycobacterium tuberculosis by molecular docking. <i>Bioinformation</i> , <b>2009</b> , 4, 24-9	1.1	12
25	Insights into RpoB clinical mutants in mediating rifampicin resistance in Mycobacterium tuberculosis. <i>Journal of Molecular Graphics and Modelling</i> , <b>2016</b> , 67, 20-32	2.8	10
24	Homology modelling, docking, pharmacophore and site directed mutagenesis analysis to identify the critical amino acid residue of PknI from Mycobacterium tuberculosis. <i>Journal of Molecular Graphics and Modelling</i> , <b>2014</b> , 52, 11-9	2.8	9
23	In silico and experimental validation of protein-protein interactions between PknI and Rv2159c from Mycobacterium tuberculosis. <i>Journal of Molecular Graphics and Modelling</i> , <b>2015</b> , 62, 283-293	2.8	8
22	In silico analysis of mycobacteriophage Che12 genome: characterization of genes required to lysogenise Mycobacterium tuberculosis. <i>Computational Biology and Chemistry</i> , <b>2007</b> , 31, 82-91	3.6	6
21	In silico based screening of WRKY genes for identifying functional genes regulated by WRKY under salt stress. <i>Computational Biology and Chemistry</i> , <b>2019</b> , 83, 107131	3.6	5
20	Binding of activated isoniazid with acetyl-CoA carboxylase from Mycobacterium tuberculosis. <i>Bioinformation</i> , <b>2011</b> , 7, 107-11	1.1	5
19	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> , <b>2020</b> , 38, 1697-1710	3.6	4
18	Homology modeling, substrate docking, and molecular simulation studies of mycobacteriophage Che12 lysin A. <i>Journal of Molecular Modeling</i> , <b>2016</b> , 22, 180	2	4
17	MtbSD--a comprehensive structural database for Mycobacterium tuberculosis. <i>Tuberculosis</i> , <b>2011</b> , 91, 556-62	2.6	4
16	Lytic Efficiency of Mycobacteriophages <b>2010</b> , 3, 21-28		4

15	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> , <b>2020</b> , 11, 1182	5.7	3
14	Exploring the conformational landscapes of HIV protease structural ensembles using principal component analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2018</b> , 86, 990-1000	4.2	3
13	Homology modeling of Homo sapiens lipoic acid synthase: Substrate docking and insights on its binding mode. <i>Journal of Theoretical Biology</i> , <b>2017</b> , 420, 259-266	2.3	3
12	Tape measure protein having MT3 motif facilitates phage entry into stationary phase cells of Mycobacterium tuberculosis. <i>Computational Biology and Chemistry</i> , <b>2008</b> , 32, 367-9	3.6	3
11	Mycobacteriophage genome database. <i>Bioinformatics</i> , <b>2011</b> , 6, 393-4	1.1	3
10	Biased Nucleotide Composition and Differential Codon Usage Pattern in HIV-1 and HIV-2. <i>AIDS Research and Human Retroviruses</i> , <b>2017</b> , 33, 298-307	1.6	2
9	Computational analysis of drug like candidates against Neuraminidase of Human Influenza A virus subtypes. <i>Informatics in Medicine Unlocked</i> , <b>2020</b> , 18, 100284	5.3	2
8	Protein-protein interaction of Rv0148 with Htdy and its predicted role towards drug resistance in Mycobacterium tuberculosis. <i>BMC Microbiology</i> , <b>2020</b> , 20, 93	4.5	2
7	Computational structural analysis of proteins of Mycobacterium tuberculosis and a resource for identifying off-targets. <i>Journal of Molecular Modeling</i> , <b>2012</b> , 18, 3993-4004	2	1
6	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> , <b>2021</b> , 1-14	3.6	0
5	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> , <b>2022</b> , 14, 5061	3.6	0
4	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> , <b>2017</b> , 33, 900-901	1.6	
3	A user-friendly web portal for analyzing conformational changes in structures of Mycobacterium tuberculosis. <i>Journal of Molecular Modeling</i> , <b>2015</b> , 21, 252	2	
2	In silico sequence and structure analysis for mycobacteriophages. <i>Asian Pacific Journal of Tropical Biomedicine</i> , <b>2012</b> , 2, S377-S379	1.4	
1	Functional assignment of the 64 mycobacteriophages into gene families. <i>Asian Pacific Journal of Tropical Biomedicine</i> , <b>2012</b> , 2, S383-S385	1.4	