Masroor Ellahi Babar

List of Publications by Year
in descending order

12 papers	520 citations	1478505 6 h-index	1199594 12 g-index
13 all docs	13 docs citations	13 times ranked	1035 citing authors

#	Article	IF	Citations
1	Isolation and genetic characterization of virulent strains of avian paramyxovirus-1 from multiple avian species in Azad Jammu and Kashmir 2017â€"2018. Brazilian Journal of Microbiology, 2020, 51, 385-394.	2.0	7
2	In Silico Analysis of Hepatitis B Virus Genotype D Subgenotype D1 Circulating in Pakistan, China, and India. Evolutionary Bioinformatics, 2019, 15, 117693431986133.	1.2	2
3	SAliBASE: A Database of Simulated Protein Alignments. Evolutionary Bioinformatics, 2019, 15, 117693431882108.	1.2	4
4	Isolation and Characterization of Avian Influenza H9N2 Viruses from Different Avian Species in Pakistan 2016â€"17. Avian Diseases, 2019, 63, 721.	1.0	5
5	A Comprehensive Study of De Novo Genome Assemblers: Current Challenges and Future Prospective. Evolutionary Bioinformatics, 2018, 14, 117693431875865.	1.2	37
6	Pathotyping and genetic characterization of avian avulavirus-1 from domestic and wild waterfowl, geese and black swans in Pakistan, 2014 to 2017. Archives of Virology, 2018, 163, 2513-2518.	2.1	19
7	Microsatellite based genetic variation among the buffalo breed populations in Pakistan. Journal of Veterinary Research (Poland), 2017, 61, 535-542.	1.0	8
8	Expression Profi ling of Hspb1 and Tp53 Genes through RT-qPCR in Different Cancer Types of Canis familiaris. Iranian Journal of Biotechnology, 2017, 15, 186-193.	0.3	2
9	Hspb1 and Tp53 Mutation and Expression Analysis in Cat Mammary Tumors. Iranian Journal of Biotechnology, 2016, 14, 202-212.	0.3	2
10	IVisTMSA: Interactive Visual Tools for Multiple Sequence Alignments. Evolutionary Bioinformatics, 2015, 11, EBO.S18980.	1.2	6
11	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	3.5	391
12	Evaluating the Accuracy and Efficiency of Multiple Sequence Alignment Methods. Evolutionary Bioinformatics, 2014, 10, EBO.S19199.	1.2	37