

Marina Escalera-Zamudio

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

607
citations

687363

13
h-index

752698

20
g-index

28
all docs

28
docs citations

28
times ranked

1350
citing authors

#	ARTICLE	IF	CITATIONS
1	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
2	Molecular Anatomy of 2009 Influenza Virus A (H1N1). <i>Archives of Medical Research</i> , 2009, 40, 643-654.	3.3	60
3	A structural basis for antibody-mediated neutralization of Nipah virus reveals a site of vulnerability at the fusion glycoprotein apex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25057-25067.	7.1	53
4	The evolution of bat nucleic acid-sensing Toll-like receptors. <i>Molecular Ecology</i> , 2015, 24, 5899-5909.	3.9	43
5	Parallel molecular evolution and adaptation in viruses. <i>Current Opinion in Virology</i> , 2019, 34, 90-96.	5.4	35
6	The Potential Role of Endogenous Viral Elements in the Evolution of Bats as Reservoirs for Zoonotic Viruses. <i>Annual Review of Virology</i> , 2020, 7, 103-119.	6.7	34
7	A Novel Endogenous Betaretrovirus in the Common Vampire Bat (<i>Desmodus rotundus</i>) Suggests Multiple Independent Infection and Cross-Species Transmission Events. <i>Journal of Virology</i> , 2015, 89, 5180-5184.	3.4	32
8	Genomic Analysis of Early SARS-CoV-2 Variants Introduced in Mexico. <i>Journal of Virology</i> , 2020, 94, .	3.4	32
9	Bats, Primates, and the Evolutionary Origins and Diversification of Mammalian Gammaherpesviruses. <i>MBio</i> , 2016, 7, .	4.1	31
10	On the classification and evolution of endogenous retrovirus: human endogenous retroviruses may not be "human" after all. <i>Apmis</i> , 2016, 124, 44-51.	2.0	27
11	Leukocyte Profiles Reflect Geographic Range Limits in a Widespread Neotropical Bat. <i>Integrative and Comparative Biology</i> , 2019, 59, 1176-1189.	2.0	24
12	Parallel evolution in the emergence of highly pathogenic avian influenza A viruses. <i>Nature Communications</i> , 2020, 11, 5511.	12.8	23
13	The Alpha Variant (B.1.1.7) of SARS-CoV-2 Failed to Become Dominant in Mexico. <i>Microbiology Spectrum</i> , 2022, 10, e0224021.	3.0	21
14	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020, 94, .	3.4	17
15	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051.	4.9	14
16	Molecular Epidemiology of Influenza A/H3N2 Viruses Circulating in Mexico from 2003 to 2012. <i>PLoS ONE</i> , 2014, 9, e102453.	2.5	5
17	Viral Communities Among Sympatric Vampire Bats and Cattle. <i>EcoHealth</i> , 2018, 15, 132-142.	2.0	5
18	Genomic Characterization of SARS-CoV-2 Isolated from Patients with Distinct Disease Outcomes in Mexico. <i>Microbiology Spectrum</i> , 2022, , e0124921.	3.0	5

#	ARTICLE	IF	CITATIONS
19	Revealing the evolution of virulence in RNA viruses. <i>Virus Evolution</i> , 2019, 5, .	4.9	0