NÃ- dia Sequeira TrovÃ£o

List of Publications by Year
in descending order

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39

papers

987

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516561

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43

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43

docs citations

43

times ranked

1783

citing authors

#	Article	IF	Citations
1	SARS-CoV-2 introductions and early dynamics of the epidemic in Portugal. Communications Medicine, 2022, 2, .	1.9	5
2	The emergence and transmission dynamics of HIV-1 CRF07_BC in Mainland China. Virus Evolution, 2022, 8, veac014.	2.2	5
3	Evolutionary history and introduction of SARS-CoV-2 Alpha VOC/B.1.1.7 in Pakistan through international travelers. Virus Evolution, 2022, 8, veac020.	2.2	8
4	Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. Virus Evolution, 2022, 8, .	2.2	4
5	Insect-specific viruses in the Parvoviridae family: Genetic lineage characterization and spatiotemporal dynamics of the recently established Brevihamaparvovirus genus. Virus Research, 2022, 313, 198728.	1.1	1
6	Readdressing the genetic diversity and taxonomy of the Mesoniviridae family, as well as its relationships with other nidoviruses and putative mesonivirus-like viral sequences. Virus Research, 2022, 313, 198727.	1.1	0
7	A comprehensive SARS-CoV-2 and COVID-19 review, Part 1: Intracellular overdrive for SARS-CoV-2 infection. European Journal of Human Genetics, 2022, 30, 889-898.	1.4	30
8	Ecological divergence of wild birds drives avian influenza spillover and global spread. PLoS Pathogens, 2022, 18, e1010062.	2.1	45
9	SARS-CoV-2 antibody prevalence in a pediatric cohort of unvaccinated children in MÃ©rida, YucatÃ¡n, MÃ©xico. PLOS Global Public Health, 2022, 2, e0000354.	0.5	0
10	Origins and Evolution of Seasonal Human Coronaviruses. Viruses, 2022, 14, 1551.	1.5	6
11	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimoreâ€“Washington metropolitan area. JCI Insight, 2021, 6, .	2.3	31
12	Proposal for Human Respiratory Syncytial Virus Nomenclature below the Species Level. Emerging Infectious Diseases, 2021, 27, 1-9.	2.0	20
13	Genetic and evolutionary analysis of SARS-CoV-2 circulating in the region surrounding Islamabad, Pakistan. Infection, Genetics and Evolution, 2021, 94, 105003.	1.0	7
14	Genetic lineage characterization and spatiotemporal dynamics of classical insect-specific flaviviruses: outcomes and limitations. Virus Research, 2021, 303, 198507.	1.1	1
15	Molecular characterization of respiratory syncytial viruses circulating in a paediatric cohort in Amman, Jordan. Microbial Genomics, 2021, 7, .	1.0	8
16	The Evolutionary Dynamics of Influenza A Viruses Circulating in Mallards in Duck Hunting Preserves in Maryland, USA. Microorganisms, 2021, 9, 40.	1.6	3
17	Molecular epidemiology, phylogenetic analysis and genotype distribution of hepatitis B virus in Saudi Arabia: Predominance of genotype D1. Infection, Genetics and Evolution, 2020, 77, 104051.	1.0	10
18	Evolution of highly pathogenic H7N3 avian influenza viruses in Mexico. Zoonoses and Public Health, 2020, 67, 318-323.	0.9	3

#	Article	IF	Citations
19	Beyond clinical trials: Evolutionary and epidemiological considerations for development of a universal influenza vaccine. PLoS Pathogens, 2020, 16, e1008583.	2.1	22
20	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	3.3	68
21	When Pigs Fly: Pandemic influenza enters the 21st century. PLoS Pathogens, 2020, 16, e1008259.	2.1	16
22	Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in Africanâ€“Belgian chronic carriers. International Journal of Infectious Diseases, 2020, 93, 98-101.	1.5	11
23	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. Emerging Infectious Diseases, 2019, 25, 691-700.	2.0	18
24	Evolution of rotavirus C in humans and several domestic animal species. Zoonoses and Public Health, 2019, 66, 546-557.	0.9	20
25	Human Influenza A Virus Hemagglutinin Glycan Evolution Follows a Temporal Pattern to a Glycan Limit. MBio, 2019, 10, .	1.8	74
26	Cover Image, Volume 66, Issue 5. Zoonoses and Public Health, 2019, 66, i.	0.9	0
27	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. Emerging Infectious Diseases, 2019, 25, .	2.0	0
28	The transmission dynamics and diversity of human metapneumovirus in Peru. Influenza and Other Respiratory Viruses, 2018, 12, 508-513.	1.5	6
29	On the importance of negative controls in viral landscape phylogeography. Virus Evolution, 2018, 4, vey023.	2.2	29
30	Emergence and Evolution of Novel Reassortant Influenza A Viruses in Canines in Southern China. MBio, 2018, 9, .	1.8	41
31	15 year fulminant hepatitis B follow-up in Belgium: Viral evolution and signature of demographic change. Infection, Genetics and Evolution, 2017, 49, 221-225.	1.0	8
32	The emergence and evolution of influenza A (H1Î±) viruses in swine in Canada and the United States. Journal of General Virology, 2017, 98, 2663-2675.	1.3	23
33	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. Viruses, 2016, 8, 12.	1.5	13
34	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. ELife, 2016, 5, .	2.8	237
35	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. Journal of Virology, 2016, 90, 10963-10971.	1.5	22
36	Host ecology determines the dispersal patterns of a plant virus. Virus Evolution, 2015, 1, vev016.	2.2	59

#	ARTICLE	IF	CITATIONS
37	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. Genome Biology and Evolution, 2015, 7, 2473-2483.	1.1	43
38	Bayesian Inference Reveals Host-Specific Contributions to the Epidemic Expansion of Influenza A H5N1. Molecular Biology and Evolution, 2015, 32, msv185.	3.5	46
39	Trends and Predictors of Transmitted Drug Resistance (TDR) and Clusters with TDR in a Local Belgian HIV-1 Epidemic. PLoS ONE, 2014, 9, e101738.	1.1	36