

Nã-dia Sequeira Trovã£o

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3403929/publications.pdf>

Version: 2024-02-01

39
papers

987
citations

516561

16
h-index

477173

29
g-index

43
all docs

43
docs citations

43
times ranked

1783
citing authors

#	ARTICLE	IF	CITATIONS
1	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, .	2.8	237
2	Human Influenza A Virus Hemagglutinin Glycan Evolution Follows a Temporal Pattern to a Glycan Limit. <i>MBio</i> , 2019, 10, .	1.8	74
3	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
4	Host ecology determines the dispersal patterns of a plant virus. <i>Virus Evolution</i> , 2015, 1, vev016.	2.2	59
5	Bayesian Inference Reveals Host-Specific Contributions to the Epidemic Expansion of Influenza A H5N1. <i>Molecular Biology and Evolution</i> , 2015, 32, msv185.	3.5	46
6	Ecological divergence of wild birds drives avian influenza spillover and global spread. <i>PLoS Pathogens</i> , 2022, 18, e1010062.	2.1	45
7	Genome-Wide Evolutionary Analyses of G1P[8] Strains Isolated Before and After Rotavirus Vaccine Introduction. <i>Genome Biology and Evolution</i> , 2015, 7, 2473-2483.	1.1	43
8	Emergence and Evolution of Novel Reassortant Influenza A Viruses in Canines in Southern China. <i>MBio</i> , 2018, 9, .	1.8	41
9	Trends and Predictors of Transmitted Drug Resistance (TDR) and Clusters with TDR in a Local Belgian HIV-1 Epidemic. <i>PLoS ONE</i> , 2014, 9, e101738.	1.1	36
10	Genomic diversity of SARS-CoV-2 during early introduction into the Baltimoreâ€“Washington metropolitan area. <i>JCI Insight</i> , 2021, 6, .	2.3	31
11	A comprehensive SARS-CoV-2 and COVID-19 review, Part 1: Intracellular overdrive for SARS-CoV-2 infection. <i>European Journal of Human Genetics</i> , 2022, 30, 889-898.	1.4	30
12	On the importance of negative controls in viral landscape phylogeography. <i>Virus Evolution</i> , 2018, 4, vey023.	2.2	29
13	The emergence and evolution of influenza A (H1N1) viruses in swine in Canada and the United States. <i>Journal of General Virology</i> , 2017, 98, 2663-2675.	1.3	23
14	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. <i>Journal of Virology</i> , 2016, 90, 10963-10971.	1.5	22
15	Beyond clinical trials: Evolutionary and epidemiological considerations for development of a universal influenza vaccine. <i>PLoS Pathogens</i> , 2020, 16, e1008583.	2.1	22
16	Evolution of rotavirus C in humans and several domestic animal species. <i>Zoonoses and Public Health</i> , 2019, 66, 546-557.	0.9	20
17	Proposal for Human Respiratory Syncytial Virus Nomenclature below the Species Level. <i>Emerging Infectious Diseases</i> , 2021, 27, 1-9.	2.0	20
18	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. <i>Emerging Infectious Diseases</i> , 2019, 25, 691-700.	2.0	18

#	ARTICLE	IF	CITATIONS
19	When Pigs Fly: Pandemic influenza enters the 21st century. <i>PLoS Pathogens</i> , 2020, 16, e1008259.	2.1	16
20	Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. <i>Viruses</i> , 2016, 8, 12.	1.5	13
21	Novel hepatitis B virus subgenotype A8 and quasi-subgenotype D12 in African-Belgian chronic carriers. <i>International Journal of Infectious Diseases</i> , 2020, 93, 98-101.	1.5	11
22	Molecular epidemiology, phylogenetic analysis and genotype distribution of hepatitis B virus in Saudi Arabia: Predominance of genotype D1. <i>Infection, Genetics and Evolution</i> , 2020, 77, 104051.	1.0	10
23	15 year fulminant hepatitis B follow-up in Belgium: Viral evolution and signature of demographic change. <i>Infection, Genetics and Evolution</i> , 2017, 49, 221-225.	1.0	8
24	Molecular characterization of respiratory syncytial viruses circulating in a paediatric cohort in Amman, Jordan. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
25	Evolutionary history and introduction of SARS-CoV-2 Alpha VOC/B.1.1.7 in Pakistan through international travelers. <i>Virus Evolution</i> , 2022, 8, veac020.	2.2	8
26	Genetic and evolutionary analysis of SARS-CoV-2 circulating in the region surrounding Islamabad, Pakistan. <i>Infection, Genetics and Evolution</i> , 2021, 94, 105003.	1.0	7
27	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 508-513.	1.5	6
28	Origins and Evolution of Seasonal Human Coronaviruses. <i>Viruses</i> , 2022, 14, 1551.	1.5	6
29	SARS-CoV-2 introductions and early dynamics of the epidemic in Portugal. <i>Communications Medicine</i> , 2022, 2, .	1.9	5
30	The emergence and transmission dynamics of HIV-1 CRF07_BC in Mainland China. <i>Virus Evolution</i> , 2022, 8, veac014.	2.2	5
31	Reconstruction of the origin and dispersal of the worldwide dominant Hepatitis B Virus subgenotype D1. <i>Virus Evolution</i> , 2022, 8, .	2.2	4
32	Evolution of highly pathogenic H7N3 avian influenza viruses in Mexico. <i>Zoonoses and Public Health</i> , 2020, 67, 318-323.	0.9	3
33	The Evolutionary Dynamics of Influenza A Viruses Circulating in Mallards in Duck Hunting Preserves in Maryland, USA. <i>Microorganisms</i> , 2021, 9, 40.	1.6	3
34	Genetic lineage characterization and spatiotemporal dynamics of classical insect-specific flaviviruses: outcomes and limitations. <i>Virus Research</i> , 2021, 303, 198507.	1.1	1
35	Insect-specific viruses in the Parvoviridae family: Genetic lineage characterization and spatiotemporal dynamics of the recently established <i>Brevihamaparvovirus</i> genus. <i>Virus Research</i> , 2022, 313, 198728.	1.1	1
36	Cover Image, Volume 66, Issue 5. <i>Zoonoses and Public Health</i> , 2019, 66, i.	0.9	0

#	ARTICLE	IF	CITATIONS
37	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. <i>Emerging Infectious Diseases</i> , 2019, 25, .	2.0	0
38	Readdressing the genetic diversity and taxonomy of the Mesoniviridae family, as well as its relationships with other nidoviruses and putative mesonivirus-like viral sequences. <i>Virus Research</i> , 2022, 313, 198727.	1.1	0
39	SARS-CoV-2 antibody prevalence in a pediatric cohort of unvaccinated children in Mérida, Yucatán, México. <i>PLOS Global Public Health</i> , 2022, 2, e0000354.	0.5	0