

Nicholas Di Paola

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

826
citations

623734

14
h-index

552781

26
g-index

29
all docs

29
docs citations

29
times ranked

1529
citing authors

#	ARTICLE	IF	CITATIONS
1	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	2.1	184
2	Biological and phylogenetic characteristics of West African lineages of West Nile virus. PLoS Neglected Tropical Diseases, 2017, 11, e0006078.	3.0	83
3	Medical countermeasures during the 2018 Ebola virus disease outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo: a rapid genomic assessment. Lancet Infectious Diseases, The, 2019, 19, 648-657.	9.1	62
4	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	2.1	62
5	ICTV Virus Taxonomy Profile: Nairoviridae. Journal of General Virology, 2020, 101, 798-799.	2.9	56
6	“Super-Spreaders” and Person-to-Person Transmission of Andes Virus in Argentina. New England Journal of Medicine, 2020, 383, 2230-2241.	27.0	52
7	Usutu Virus Isolated from Rodents in Senegal. Viruses, 2019, 11, 181.	3.3	37
8	Integration of genomic sequencing into the response to the Ebola virus outbreak in Nord Kivu, Democratic Republic of the Congo. Nature Medicine, 2021, 27, 710-716.	30.7	35
9	Lassa virus circulating in Liberia: a retrospective genomic characterisation. Lancet Infectious Diseases, The, 2019, 19, 1371-1378.	9.1	30
10	Viral genomics in Ebola virus research. Nature Reviews Microbiology, 2020, 18, 365-378.	28.6	30
11	2018 Ebola virus disease outbreak in Équateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. Lancet Infectious Diseases, The, 2019, 19, 641-647.	9.1	27
12	Shedding of Marburg Virus in Naturally Infected Egyptian Rousette Bats, South Africa, 2017. Emerging Infectious Diseases, 2020, 26, 3051-3055.	4.3	23
13	Molecular epidemiological study on Infectious Pancreatic Necrosis Virus isolates from aquafarms in Scotland over three decades. Journal of General Virology, 2018, 99, 1567-1581.	2.9	18
14	Novel Filoviruses, Hantavirus, and Rhabdovirus in Freshwater Fish, Switzerland, 2017. Emerging Infectious Diseases, 2021, 27, 3082-3091.	4.3	16
15	“Jingchuvirales”: a New Taxonomical Framework for a Rapidly Expanding Order of Unusual Monjiviricete Viruses Broadly Distributed among Arthropod Subphyla. Applied and Environmental Microbiology, 2022, 88, AEM0195421.	3.1	16
16	An Outbreak of Human Parvovirus B19 Hidden by Dengue Fever. Clinical Infectious Diseases, 2019, 68, 810-817.	5.8	11
17	Does adaptation to vertebrate codon usage relate to flavivirus emergence potential?. PLoS ONE, 2018, 13, e0191652.	2.5	11
18	History and classification of Aigai virus (formerly Crimean–Congo haemorrhagic fever virus genotype) Tj ETQq0 0,0,rgBT /Overlock 10	2.9	11

#	ARTICLE	IF	CITATIONS
19	A Model for the Production of Regulatory Grade Viral Hemorrhagic Fever Exposure Stocks: From Field Surveillance to Advanced Characterization of SFTSV. <i>Viruses</i> , 2020, 12, 958.	3.3	5
20	Molecular analysis of the 2012 Bundibugyo virus disease outbreak. <i>Cell Reports Medicine</i> , 2021, 2, 100351.	6.5	4
21	Delayed viral clearance despite high number of activated T cells during the acute phase in Argentinean patients with hantavirus pulmonary syndrome. <i>EBioMedicine</i> , 2022, 75, 103765.	6.1	3
22	Complete Genome Sequences of Two Human Parainfluenza Virus Type 3 Isolates Collected in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
23	Complete Genome Sequence of a Human Metapneumovirus Isolate Collected in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
24	On-Demand Patient-Specific Phenotype-to-Genotype Ebola Virus Characterization. <i>Viruses</i> , 2021, 13, 2010.	3.3	1
25	Rabies surveillance in Senegal 2001 to 2015 uncovers first infection of a honey badger. <i>Transboundary and Emerging Diseases</i> , 2022, , .	3.0	1
26	Complete Genome Sequences of Five Human Respiratory Syncytial Virus Isolates Collected in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
27	Where there is no overlap, there is a gap. <i>Revista Da Sociedade Brasileira De Medicina Tropical</i> , 2014, 47, 675-676.	0.9	0