

Nick J Knowles

List of Publications by Year in descending order

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108
papers

6,496
citations

81839

39
h-index

69214

77
g-index

111
all docs

111
docs citations

111
times ranked

6417
citing authors

#	ARTICLE	IF	CITATIONS
1	Genotyping of foot-and-mouth disease viruses collected in Sudan between 2009 and 2018. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	2
2	Identification of diffusion routes of O/EA topotype of foot-and-mouth disease virus in Africa and Western Asia between 1974 and 2019 – a phylogeographic analysis. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	5
3	The first detection of a serotype O foot-and-mouth disease virus in Namibia. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	7
4	Foot-and-mouth disease viruses of the O/MEA/Ind2001e sublineage in Pakistan. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3126-3135.	1.3	10
5	Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 4346-4361.	3.5	14
6	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021, 166, 2633-2648.	0.9	219
7	A proposed division of the family Picornaviridae into subfamilies based on phylogenetic relationships and functional genomic organization. <i>Archives of Virology</i> , 2021, 166, 2927-2935.	0.9	11
8	Mutagenesis Mapping of RNA Structures within the Foot-and-Mouth Disease Virus Genome Reveals Functional Elements Localized in the Polymerase (3D ^{pol})-Encoding Region. <i>MSphere</i> , 2021, 6, e0001521.	1.3	3
9	The history of foot-and-mouth disease virus serotype C: the first known extinct serotype?. <i>Virus Evolution</i> , 2021, 7, .	2.2	35
10	Characterization of Foot-and-Mouth Disease Viruses in Zambia-Implications for the Epidemiology of the Disease in Southern Africa. <i>Viruses</i> , 2021, 13, 2195.	1.5	2
11	First detection of foot-and-mouth disease virus O/MEA/Ind2001e sublineage in Jordan. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 455-460.	1.3	4
12	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020, 165, 519-525.	0.9	51
13	Foot-and-mouth disease outbreaks in captive scimitar-horned oryx (<i>Oryx dammah</i>). <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1716-1724.	1.3	8
14	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). <i>Archives of Virology</i> , 2020, 165, 2737-2748.	0.9	202
15	Discovery of Lanama Virus, a Distinct Member of Species Kunsagivirus C (Picornavirales): Tj ETQq1 1 0.784314 rgBT 1.5 Overlock 5 Tf 5		
16	A vaccine-matching assessment of different genetic variants of serotype O foot-and-mouth disease virus isolated in Ethiopia between 2011 and 2014. <i>Archives of Virology</i> , 2020, 165, 1749-1757.	0.9	7
17	Molecular characterization of foot-and-mouth disease viruses circulating in Ethiopia between 2008 and 2019. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 2983-2992.	1.3	13
18	How to recognise and deal with dubious virus sequences?. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104242.	1.0	0

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19	Genome Sequences of Foot-and-Mouth Disease Virus O/ME-SA/Ind-2001e Strains Isolated in Pakistan. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	9
20	Characterization of the FMDV-serotype-O isolates collected during 1962 and 1997 discloses new topotypes, CEY-1 and WCSA-1, and six new lineages. <i>Scientific Reports</i> , 2019, 9, 14526.	1.6	4
21	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019, 164, 943-946.	0.9	102
22	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). <i>Archives of Virology</i> , 2019, 164, 2417-2429.	0.9	257
23	Foot-and-mouth disease in Southern Ghana: occurrence and molecular characterization of circulating viruses. <i>Tropical Animal Health and Production</i> , 2019, 51, 1667-1677.	0.5	4
24	Foot-and-mouth disease outbreaks due to an exotic virus serotype A lineage (A/AFRICA/Gâ€W) in Algeria in 2017. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 7-13.	1.3	12
25	Foot-and-mouth disease outbreaks due to an exotic serotype Asia 1 virus in Myanmar in 2017. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1067-1072.	1.3	14
26	ICTV Virus Taxonomy Profile: Caliciviridae. <i>Journal of General Virology</i> , 2019, 100, 1469-1470.	1.3	117
27	A traditional evolutionary history of foot-and-mouth disease viruses in Southeast Asia challenged by analyses of non-structural protein coding sequences. <i>Scientific Reports</i> , 2018, 8, 6472.	1.6	34
28	Development and evaluation of a novel real-time RT-PCR to detect foot-and-mouth disease viruses from the emerging A/ASIA/G-VII lineage. <i>Journal of Virological Methods</i> , 2018, 252, 37-41.	1.0	18
29	Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: the impact of recombination within the emerging O/ME-SA/Ind-2001 lineage. <i>Scientific Reports</i> , 2018, 8, 14693.	1.6	57
30	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). <i>Archives of Virology</i> , 2018, 163, 2601-2631.	0.9	567
31	Full Genome Sequencing Reveals New Southern African Territories Genotypes Bringing Us Closer to Understanding True Variability of Foot-and-Mouth Disease Virus in Africa. <i>Viruses</i> , 2018, 10, 192.	1.5	24
32	Foot-and-Mouth Disease in the Middle East Caused by an A/ASIA/G-VII Virus Lineage, 2015â€2016. <i>Emerging Infectious Diseases</i> , 2018, 24, 1073-1078.	2.0	26
33	Waves of endemic foot-and-mouth disease in eastern Africa suggest feasibility of proactive vaccination approaches. <i>Nature Ecology and Evolution</i> , 2018, 2, 1449-1457.	3.4	66
34	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017, 162, 1441-1446.	0.9	72
35	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). <i>Archives of Virology</i> , 2017, 162, 2505-2538.	0.9	506
36	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017, 18, 249.	1.2	42

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37	Development of a novel real-time RT-PCR assay to detect Seneca Valley virus-1 associated with emerging cases of vesicular disease in pigs. <i>Journal of Virological Methods</i> , 2017, 239, 34-37.	1.0	32
38	Development and evaluation of tailored specific real-time RT-PCR assays for detection of foot-and-mouth disease virus serotypes circulating in East Africa. <i>Journal of Virological Methods</i> , 2016, 237, 114-120.	1.0	28
39	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). <i>Archives of Virology</i> , 2016, 161, 2921-2949.	0.9	263
40	Genome Sequencing of Foot-and-Mouth Disease Virus Type O Isolate GRE/23/94. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
41	Bioinformatics and Molecular Analysis of the Evolutionary Relationship between Bovine Rhinitis A Viruses and Foot-And-Mouth Disease Virus. <i>Bioinformatics and Biology Insights</i> , 2015, 9s2, BBI.S37223.	1.0	5
42	Time Clustered Sampling Can Inflate the Inferred Substitution Rate in Foot-And-Mouth Disease Virus Analyses. <i>PLoS ONE</i> , 2015, 10, e0143605.	1.1	6
43	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2015). <i>Archives of Virology</i> , 2015, 160, 1837-1850.	0.9	126
44	A tortoise-infecting picornavirus expands the host range of the family Picornaviridae. <i>Archives of Virology</i> , 2015, 160, 1319-1323.	0.9	18
45	The impact of within-herd genetic variation upon inferred transmission trees for foot-and-mouth disease virus. <i>Infection, Genetics and Evolution</i> , 2015, 32, 440-448.	1.0	14
46	Rabovirus: a proposed new picornavirus genus that is phylogenetically basal to enteroviruses and sapeloviruses. <i>Archives of Virology</i> , 2015, 160, 2569-2575.	0.9	8
47	Viral meningitis epidemics and a single, recent, recombinant and anthroponotic origin of swine vesicular disease virus. <i>Evolution, Medicine and Public Health</i> , 2015, 2015, 289-303.	1.1	11
48	Near-Complete Genome Sequencing of Swine Vesicular Disease Virus Using the Roche GS FLX Sequencing Platform. <i>PLoS ONE</i> , 2014, 9, e97180.	1.1	3
49	A universal protocol to generate consensus level genome sequences for foot-and-mouth disease virus and other positive-sense polyadenylated RNA viruses using the Illumina MiSeq. <i>BMC Genomics</i> , 2014, 15, 828.	1.2	64
50	Phyldynamic reconstruction of O CATHAY topotype foot-and-mouth disease virus epidemics in the Philippines. <i>Veterinary Research</i> , 2014, 45, 90.	1.1	22
51	Patterns of Foot-and-Mouth Disease Virus Distribution in Africa. , 2014, , 21-38.		10
52	Novel antibody binding determinants on the capsid surface of serotype O foot-and-mouth disease virus. <i>Journal of General Virology</i> , 2014, 95, 1104-1116.	1.3	34
53	Characterization of a new picornavirus isolated from the freshwater fish <i>Lepomis macrochirus</i> . <i>Journal of General Virology</i> , 2014, 95, 601-613.	1.3	32
54	Development of tailored real-time RT-PCR assays for the detection and differentiation of serotype O, A and Asia-1 foot-and-mouth disease virus lineages circulating in the Middle East. <i>Journal of Virological Methods</i> , 2014, 207, 146-153.	1.0	41

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55	Characterization of sheep pox virus vaccine for cattle against lumpy skin disease virus. <i>Antiviral Research</i> , 2014, 109, 1-6.	1.9	106
56	Characteristics of a foot-and-mouth disease virus with a partial VP1 G-H loop deletion in experimentally infected cattle. <i>Veterinary Microbiology</i> , 2014, 169, 58-66.	0.8	13
57	Feline fecal virome reveals novel and prevalent enteric viruses. <i>Veterinary Microbiology</i> , 2014, 171, 102-111.	0.8	83
58	Comparative Complete Genome Analysis of Chicken and Turkey Megriviruses (Family Picornaviridae): Long 3' UTR Untranslated Regions with a Potential Second Open Reading Frame and Evidence for Possible Recombination. <i>Journal of Virology</i> , 2014, 88, 6434-6443.	1.5	26
59	Evolution of foot-and-mouth disease virus intra-sample sequence diversity during serial transmission in bovine hosts. <i>Veterinary Research</i> , 2013, 44, 12.	1.1	56
60	Positively Charged Residues at the Five-Fold Symmetry Axis of Cell Culture-Adapted Foot-and-Mouth Disease Virus Permit Novel Receptor Interactions. <i>Journal of Virology</i> , 2013, 87, 8735-8744.	1.5	26
61	Multiple introductions of serotype O foot-and-mouth disease viruses into East Asia in 2010-2011. <i>Veterinary Research</i> , 2013, 44, 76.	1.1	37
62	Reconstructing the origin and transmission dynamics of the 1967-68 foot-and-mouth disease epidemic in the United Kingdom. <i>Infection, Genetics and Evolution</i> , 2013, 20, 230-238.	1.0	20
63	Development of a universal RT-PCR for amplifying and sequencing the leader and capsid-coding region of foot-and-mouth disease virus. <i>Journal of Virological Methods</i> , 2013, 189, 70-76.	1.0	35
64	Reconstructing Geographical Movements and Host Species Transitions of Foot-and-Mouth Disease Virus Serotype SAT 2. <i>MBio</i> , 2013, 4, e00591-13.	1.8	50
65	Observing micro-evolutionary processes of viral populations at multiple scales. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120203.	1.8	29
66	Accumulation of nucleotide substitutions occurring during experimental transmission of foot-and-mouth disease virus. <i>Journal of General Virology</i> , 2013, 94, 108-119.	1.3	22
67	Two Closely Related Novel Picornaviruses in Cattle and Sheep in Hungary from 2008 to 2009, Proposed as Members of a New Genus in the Family Picornaviridae. <i>Journal of Virology</i> , 2012, 86, 13295-13302.	1.5	36
68	Natural interspecies recombinant bovine/porcine enterovirus in sheep. <i>Journal of General Virology</i> , 2012, 93, 1941-1951.	1.3	69
69	Genome Sequences of SAT 2 Foot-and-Mouth Disease Viruses from Egypt and Palestinian Autonomous Territories (Gaza Strip). <i>Journal of Virology</i> , 2012, 86, 8901-8902.	1.5	33
70	Reconstruction of the Transmission History of RNA Virus Outbreaks Using Full Genome Sequences: Foot-and-Mouth Disease Virus in Bulgaria in 2011. <i>PLoS ONE</i> , 2012, 7, e49650.	1.1	57
71	New technologies to diagnose and monitor infectious diseases of livestock: Challenges for sub-Saharan Africa. <i>Onderstepoort Journal of Veterinary Research</i> , 2012, 79, 456.	0.6	7
72	Southeast Asian Foot-and-Mouth Disease Viruses in Eastern Asia. <i>Emerging Infectious Diseases</i> , 2012, 18, 499-501.	2.0	73

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73	Comparative sequence analysis of representative foot-and-mouth disease virus genomes from Southeast Asia. <i>Virus Genes</i> , 2011, 43, 41-45.	0.7	34
74	Phylogeography of foot-and-mouth disease virus types O and A in Malaysia and surrounding countries. <i>Infection, Genetics and Evolution</i> , 2011, 11, 320-328.	1.0	49
75	Beyond the Consensus: Dissecting Within-Host Viral Population Diversity of Foot-and-Mouth Disease Virus by Using Next-Generation Genome Sequencing. <i>Journal of Virology</i> , 2011, 85, 2266-2275.	1.5	127
76	Recent spread of foot-and-mouth disease in the Far East. <i>Veterinary Record</i> , 2010, 166, 569-570.	0.2	23
77	Multiple Origins of Foot-and-Mouth Disease Virus Serotype Asia 1 Outbreaks, 2003-2007. <i>Emerging Infectious Diseases</i> , 2009, 15, 1046-1051.	2.0	104
78	Genetic Characterization of Foot-and-Mouth Disease Viruses, Ethiopia, 1981-2007. <i>Emerging Infectious Diseases</i> , 2009, 15, 1409-1417.	2.0	109
79	Equine Rhinitis A Virus and Its Low pH Empty Particle: Clues Towards an Aphthovirus Entry Mechanism?. <i>PLoS Pathogens</i> , 2009, 5, e1000620.	2.1	64
80	Molecular epidemiology of foot-and-mouth disease viruses from South East Asia 1998-2006: The Lao perspective. <i>Veterinary Microbiology</i> , 2009, 137, 178-183.	0.8	23
81	Complete sequence of a duck astrovirus associated with fatal hepatitis in ducklings. <i>Journal of General Virology</i> , 2009, 90, 1104-1108.	1.3	93
82	Genetic characterization and molecular epidemiology of foot-and-mouth disease viruses isolated from Afghanistan in 2003-2005. <i>Virus Genes</i> , 2008, 36, 401-413.	0.7	31
83	Picornavirales, a proposed order of positive-sense single-stranded RNA viruses with a pseudo-T=3 virion architecture. <i>Archives of Virology</i> , 2008, 153, 715-27.	0.9	237
84	Molecular and phylogenetic analyses of bovine rhinovirus type 2 shows it is closely related to foot-and-mouth disease virus. <i>Virology</i> , 2008, 373, 411-425.	1.1	41
85	Transmission Pathways of Foot-and-Mouth Disease Virus in the United Kingdom in 2007. <i>PLoS Pathogens</i> , 2008, 4, e1000050.	2.1	178
86	Comparative genomics of serotype Asia 1 foot-and-mouth disease virus isolates from India sampled over the last two decades. <i>Virus Research</i> , 2008, 136, 16-29.	1.1	27
87	Genomic characterization of novel marine vesiviruses from Steller sea lions (<i>Eumetopias jubatus</i>) from Alaska. <i>Virus Research</i> , 2008, 138, 26-35.	1.1	8
88	Phylogenetic Analysis of the Species <i>Theilovirus</i> : Emerging Murine and Human Pathogens. <i>Journal of Virology</i> , 2008, 82, 11545-11554.	1.5	63
89	DETECTION AND GENETIC CHARACTERIZATION OF PORCINE CIRCOVIRUS 2 ISOLATES FROM THE FIRST CASES OF POSTWEANING MULTISYSTEMIC AND WASTING SYNDROME IN WILD BOARS IN GREECE. <i>Journal of Wildlife Diseases</i> , 2008, 44, 864-870.	0.3	24
90	Abortions in dromedaries (<i>Camelus dromedarius</i>) caused by equine rhinitis A virus. <i>Journal of General Virology</i> , 2008, 89, 660-666.	1.3	19

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91	Complete genome sequence analysis of Seneca Valley virus-001, a novel oncolytic picornavirus. <i>Journal of General Virology</i> , 2008, 89, 1265-1275.	1.3	275
92	Molecular analysis of duck hepatitis virus type 1 indicates that it should be assigned to a new genus. <i>Virus Research</i> , 2007, 123, 190-203.	1.1	166
93	Development of a real-time reverse transcription polymerase chain reaction assay for detection of marine caliciviruses (genus Vesivirus). <i>Journal of Virological Methods</i> , 2007, 140, 166-173.	1.0	16
94	Foot-and-Mouth Disease Virus Serotype A in Egypt. <i>Emerging Infectious Diseases</i> , 2007, 13, 1593-1596.	2.0	56
95	Complete sequence and organization of the human adenovirus serotype 46 genome. <i>Virus Research</i> , 2006, 116, 119-128.	1.1	8
96	Pandemic Strain of Foot-and-Mouth Disease Virus Serotype O. <i>Emerging Infectious Diseases</i> , 2005, 11, 1887-1893.	2.0	147
97	Sequence analysis of the 5' untranslated region of swine vesicular disease virus reveals block deletions between the end of the internal ribosomal entry site and the initiation codon. <i>Journal of General Virology</i> , 2005, 86, 2753-2761.	1.3	8
98	Crystal Structure of Swine Vesicular Disease Virus and Implications for Host Adaptation. <i>Journal of Virology</i> , 2003, 77, 5475-5486.	1.5	25
99	Sequencing of Porcine Enterovirus Groups II and III Reveals Unique Features of Both Virus Groups. <i>Journal of Virology</i> , 2002, 76, 5813-5821.	1.5	87
100	Phylogenetic analysis of foot-and-mouth disease viruses isolated in Argentina. <i>Virus Genes</i> , 2001, 23, 175-181.	0.7	17
101	Emergence in Asia of Foot-and-Mouth Disease Viruses with Altered Host Range: Characterization of Alterations in the 3A Protein. <i>Journal of Virology</i> , 2001, 75, 1551-1556.	1.5	104
102	Evidence for Positive Selection in Foot-and-Mouth Disease Virus Capsid Genes From Field Isolates. <i>Genetics</i> , 2001, 157, 7-15.	1.2	126
103	Primary diagnosis of foot-and-mouth disease by reverse transcription polymerase chain reaction. <i>Journal of Virological Methods</i> , 2000, 89, 167-176.	1.0	118
104	Development of a reverse transcription polymerase chain reaction procedure for the detection of marine caliciviruses with potential application for nucleotide sequencing. <i>Journal of Virological Methods</i> , 1999, 82, 99-107.	1.0	22
105	Methods for the detection of non-random base substitution in virus genes: models of synonymous nucleotide substitution in picornavirus genes. <i>Virus Genes</i> , 1998, 16, 253-266.	0.7	9
106	Characterizing sequence variation in the VP1 capsid proteins of foot and mouth disease virus (serotype O) with respect to virion structure. <i>Journal of Molecular Evolution</i> , 1998, 46, 465-475.	0.8	22
107	Overview of Taxonomy. , 0, , 19-32.		3
108	Overview of Taxonomy. , 0, , 19-32.		4