

Kyriaki Nomikou

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

5,396
citations

156536

32
h-index

107981

68
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76
all docs

76
docs citations

76
times ranked

9362
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined epidemiological and genomic analysis of nosocomial SARS-CoV-2 infection early in the pandemic and the role of unidentified cases in transmission. <i>Clinical Microbiology and Infection</i> , 2022, 28, 93-100.	2.8	21
2	Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 35-42.	4.6	612
3	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	5.8	10
4	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
5	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	5.9	88
6	A plasmid DNA-launched SARS-CoV-2 reverse genetics system and coronavirus toolkit for COVID-19 research. <i>PLoS Biology</i> , 2021, 19, e3001091.	2.6	163
7	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	13.5	541
8	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	4.7	269
9	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	2.9	375
10	Genetic epidemiology of SARS-CoV-2 transmission in renal dialysis units – A high risk community-hospital interface. <i>Journal of Infection</i> , 2021, 83, 96-103.	1.7	12
11	Genomic reconstruction of the SARS-CoV-2 epidemic in England. <i>Nature</i> , 2021, 600, 506-511.	13.7	80
12	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>iScience</i> , 2021, 24, 103353.	1.9	57
13	Elevated temperature inhibits SARS-CoV-2 replication in respiratory epithelium independently of IFN-mediated innate immune defenses. <i>PLoS Biology</i> , 2021, 19, e3001065.	2.6	26
14	Diversity of Transmission Outcomes Following Co-Infection of Sheep with Strains of Bluetongue Virus Serotype 1 and 8. <i>Microorganisms</i> , 2020, 8, 851.	1.6	5
15	“Frozen evolution” of an RNA virus suggests accidental release as a potential cause of arbovirus re-emergence. <i>PLoS Biology</i> , 2020, 18, e3000673.	2.6	15
16	Contrasting selective patterns across the segmented genome of bluetongue virus in a global reassortment hotspot. <i>Virus Evolution</i> , 2019, 5, vez027.	2.2	17
17	A low-passage insect-cell isolate of bluetongue virus uses a macropinocytosis-like entry pathway to infect natural target cells derived from the bovine host. <i>Journal of General Virology</i> , 2019, 100, 568-582.	1.3	10
18	BTV-GLUE: a new bioinformatic resource for genomic studies of Bluetongue virus. <i>Access Microbiology</i> , 2019, 1, .	0.2	0

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19	Bluetongue virus spread in Europe is a consequence of climatic, landscape and vertebrate host factors as revealed by phylogeographic inference. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170919.	1.2	55
20	Identification of the Genome Segments of Bluetongue Virus Serotype 26 (Isolate KUW2010/02) that Restrict Replication in a <i>Culicoides sonorensis</i> Cell Line (KC Cells). <i>PLoS ONE</i> , 2016, 11, e0149709.	1.1	22
21	Genome Sequence of <i>Bluetongue virus</i> Serotype 17 Isolated in Brazil in 2014. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
22	Full-Genome Sequencing as a Basis for Molecular Epidemiology Studies of Bluetongue Virus in India. <i>PLoS ONE</i> , 2015, 10, e0131257.	1.1	52
23	Genome Sequence of Bluetongue Virus Type 2 from India: Evidence for Reassortment between Outer Capsid Protein Genes. <i>Genome Announcements</i> , 2015, 3, .	0.8	13
24	A quantitative real-time reverse transcription PCR (qRT-PCR) assay to detect genome segment 9 of all 26 bluetongue virus serotypes. <i>Journal of Virological Methods</i> , 2015, 213, 118-126.	1.0	25
25	Evaluation of adaptive immune responses and heterologous protection induced by inactivated bluetongue virus vaccines. <i>Vaccine</i> , 2015, 33, 512-518.	1.7	23
26	Widespread Reassortment Shapes the Evolution and Epidemiology of Bluetongue Virus following European Invasion. <i>PLoS Pathogens</i> , 2015, 11, e1005056.	2.1	117
27	Full Genome Sequence of a Western Reference Strain of Bluetongue Virus Serotype 16 from Nigeria. <i>Genome Announcements</i> , 2013, 1, .	0.8	2
28	Reassortment between Two Serologically Unrelated Bluetongue Virus Strains Is Flexible and Can Involve any Genome Segment. <i>Journal of Virology</i> , 2013, 87, 543-557.	1.5	107
29	Serosurveillance of orbiviruses in wild cervids from Spain. <i>Veterinary Record</i> , 2013, 172, 508-509.	0.2	5
30	Full Genome Sequencing of Corriparta Virus, Identifies California Mosquito Pool Virus as a Member of the Corriparta virus Species. <i>PLoS ONE</i> , 2013, 8, e70779.	1.1	12
31	Epizootiological investigation of the most important infectious equine diseases in Greece. <i>OIE Revue Scientifique Et Technique</i> , 2013, 32, 775-787.	0.5	11
32	Reply to "Intercontinental Movement of Bluetongue Virus and Potential Consequences to Trade". <i>Journal of Virology</i> , 2012, 86, 8342-8343.	1.5	6
33	Genome Sequence of a Reassortant Strain of Bluetongue Virus Serotype 23 from Western India. <i>Journal of Virology</i> , 2012, 86, 7011-7012.	1.5	13
34	The Genome Sequence of Bluetongue Virus Type 10 from India: Evidence for Circulation of a Western Topotype Vaccine Strain. <i>Journal of Virology</i> , 2012, 86, 5971-5972.	1.5	17
35	Full Genome Sequence of Bluetongue Virus Serotype 1 from India. <i>Journal of Virology</i> , 2012, 86, 4717-4718.	1.5	9
36	Complete Genome Sequence Analysis of a Reference Strain of Bluetongue Virus Serotype 16. <i>Journal of Virology</i> , 2012, 86, 10255-10256.	1.5	11

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37	Complete Genome Sequence of an Isolate of Bluetongue Virus Serotype 2, Demonstrating Circulation of a Western Topotype in Southern India. <i>Journal of Virology</i> , 2012, 86, 5404-5405.	1.5	18
38	The Genome Sequence of a Reassortant Bluetongue Virus Serotype 3 from India. <i>Journal of Virology</i> , 2012, 86, 6375-6376.	1.5	20
39	The Genome Sequence of Bluetongue Virus Type 2 from India: Evidence for Reassortment between Eastern and Western Topotype Field Strains. <i>Journal of Virology</i> , 2012, 86, 5967-5968.	1.5	30
40	Identification and Differentiation of the Twenty Six Bluetongue Virus Serotypes by RT-PCR Amplification of the Serotype-Specific Genome Segment 2. <i>PLoS ONE</i> , 2012, 7, e32601.	1.1	125
41	Full Genome Sequencing and Genetic Characterization of Eubenberg Viruses Identify Pata Virus as a Distinct Species within the Genus Orbivirus. <i>PLoS ONE</i> , 2012, 7, e31911.	1.1	31
42	Molecular epidemiology of bluetongue virus serotype 1 isolated in 2006 from Algeria. <i>Research in Veterinary Science</i> , 2011, 91, 486-497.	0.9	19
43	Isolation and Phylogenetic Grouping of Equine Encephalosis Virus in Israel. <i>Emerging Infectious Diseases</i> , 2011, 17, 1883-1886.	2.0	19
44	Serotype Specific Primers and Gel-Based RT-PCR Assays for "Typing" African Horse Sickness Virus: Identification of Strains from Africa. <i>PLoS ONE</i> , 2011, 6, e25686.	1.1	13
45	Complete Genome Characterisation of a Novel 26th Bluetongue Virus Serotype from Kuwait. <i>PLoS ONE</i> , 2011, 6, e26147.	1.1	151
46	RNA segment 9 exists as a duplex concatemer in an Australian strain of epizootic haemorrhagic disease virus (EHDV): Genetic analysis and evidence for the presence of concatemers as a normal feature of orbivirus replication. <i>Virology</i> , 2011, 420, 164-171.	1.1	15
47	Novel Bluetongue Virus Serotype from Kuwait. <i>Emerging Infectious Diseases</i> , 2011, 17, 886-889.	2.0	190
48	Full Genome Characterisation of Bluetongue Virus Serotype 6 from the Netherlands 2008 and Comparison to Other Field and Vaccine Strains. <i>PLoS ONE</i> , 2010, 5, e10323.	1.1	119
49	RT-PCR Assays for Seven Serotypes of Epizootic Haemorrhagic Disease Virus & Their Use to Type Strains from the Mediterranean Region and North America. <i>PLoS ONE</i> , 2010, 5, e12782.	1.1	42
50	Multiple Serotypes of Bluetongue Virus in Sheep and Cattle, Israel. <i>Emerging Infectious Diseases</i> , 2010, 16, 2003-2004.	2.0	29
51	Bluetongue virus diagnosis. , 2009, , 365-395.		4
52	Molecular epidemiology studies of bluetongue virus. , 2009, , 135-166.		28
53	Evolution and Phylogenetic Analysis of Full-Length VP3 Genes of Eastern Mediterranean Bluetongue Virus Isolates. <i>PLoS ONE</i> , 2009, 4, e6437.	1.1	33
54	Communication of bluetongue mitigation techniques. <i>Veterinary Record</i> , 2009, 165, 636-636.	0.2	0

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55	Emergence of Bluetongue Serotypes in Europe, Part 2: The Occurrence of a BTV-11 Strain in Belgium. <i>Transboundary and Emerging Diseases</i> , 2009, 56, 355-361.	1.3	51
56	Engineering of the membrane of fibroblast cells with virus-specific antibodies: A novel biosensor tool for virus detection. <i>Biosensors and Bioelectronics</i> , 2008, 24, 1027-1030.	5.3	39
57	Sequence analysis of bluetongue virus serotype 8 from the Netherlands 2006 and comparison to other European strains. <i>Virology</i> , 2008, 377, 308-318.	1.1	172
58	The epidemiology of sheep pox in Greece from 1987 to 2007. <i>OIE Revue Scientifique Et Technique</i> , 2008, 27, 899-905.	0.5	17
59	Molecular epidemiology of bluetongue virus serotype 4 isolated in the Mediterranean Basin between 1979 and 2004. <i>Virus Research</i> , 2007, 125, 191-197.	1.1	38
60	Quantifying the wind dispersal of <i>Culicoides</i> species in Greece and Bulgaria. <i>Geospatial Health</i> , 2007, 1, 177.	0.3	73
61	Differential effect of the shape of calcium alginate matrices on the physiology of immobilized neuroblastoma N2a and Vero cells: A comparative study. <i>Biosensors and Bioelectronics</i> , 2007, 23, 543-548.	5.3	16
62	Incriminating bluetongue virus vectors with climate envelope models. <i>Journal of Applied Ecology</i> , 2007, 44, 1231-1242.	1.9	43
63	Development of a novel, multi-analyte biosensor system for assaying cell division: Identification of cell proliferation/death precursor events. <i>Biosensors and Bioelectronics</i> , 2006, 21, 1365-1373.	5.3	23
64	Phylogenetic correlation of Greek and Italian orf virus isolates based on VIR gene. <i>Veterinary Microbiology</i> , 2006, 116, 310-316.	0.8	27
65	Laboratory diagnosis of contagious ecthyma: Comparison of different PCR protocols with virus isolation in cell culture. <i>Journal of Virological Methods</i> , 2006, 134, 119-124.	1.0	48
66	VP2-segment Sequence Analysis of Some Isolates of Bluetongue Virus Recovered in the Mediterranean Basin During the 1998-2003 Outbreak. <i>Zoonoses and Public Health</i> , 2005, 52, 372-379.	1.4	22
67	Molecular analysis of the NS3/NS3A gene of Bluetongue virus isolates from the 1979 and 1998-2001 epizootics in Greece and their segregation into two distinct groups. <i>Virus Research</i> , 2005, 114, 6-14.	1.1	33
68	Study on the mechanism of Bioelectric Recognition Assay: evidence for immobilized cell membrane interactions with viral fragments. <i>Biosensors and Bioelectronics</i> , 2004, 20, 907-916.	5.3	21
69	Bluetongue virus diagnosis of clinical cases by a duplex reverse transcription-PCR: a comparison with conventional methods. <i>Journal of Virological Methods</i> , 2001, 98, 77-89.	1.0	38
70	Detection of sheep poxvirus in skin biopsy samples by a multiplex polymerase chain reaction. <i>Journal of Virological Methods</i> , 2000, 84, 161-167.	1.0	41
71	Sheep poxvirus identification from clinical specimens by PCR, cell culture, immunofluorescence and agar gel immunoprecipitation assay. <i>Molecular and Cellular Probes</i> , 2000, 14, 305-310.	0.9	40
72	Sheep poxvirus identification by PCR in cell cultures. <i>Journal of Virological Methods</i> , 1999, 77, 75-79.	1.0	42

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73	Duration of bluetongue viraemia and serological responses in experimentally infected European breeds of sheep and goats. <i>Veterinary Microbiology</i> , 1999, 64, 277-285.	0.8	74