Patrick K Mitchell

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Multi-laboratory evaluation of the Illumina iSeq platform for whole genome sequencing of Salmonella, Escherichia coli and Listeria. Microbial Genomics, 2022, 8, .	2.0	3
2	Method comparison of targeted influenza A virus typing and whole-genome sequencing from respiratory specimens of companion animals. Journal of Veterinary Diagnostic Investigation, 2021, 33, 191-201.	1.1	7
3	Infectious disease surveillance of apparently healthy horses at a multi-day show using a novel nanoscale real-time PCR panel. Journal of Veterinary Diagnostic Investigation, 2021, 33, 80-86.	1.1	9
4	Draft Genome Sequence of Acholeplasma laidlawii Isolated from the Conjunctiva of a Heifer with Infectious Bovine Keratoconjunctivitis. Microbiology Resource Announcements, 2021, 10, .	0.6	0
5	Genomics accurately predicts antimicrobial resistance in Staphylococcus pseudintermedius collected as part of Vet-LIRN resistance monitoring. Veterinary Microbiology, 2021, 254, 109006.	1.9	11
6	Identification of a SARS-CoV-2 Lineage B1.1.7 Virus in New York following Return Travel from the United Kingdom. Microbiology Resource Announcements, 2021, 10, .	0.6	10
7	Susceptibility of White-Tailed Deer (Odocoileus virginianus) to SARS-CoV-2. Journal of Virology, 2021, 95, .	3.4	192
8	Severe SARS-CoV-2 Infection in a Cat with Hypertrophic Cardiomyopathy. Viruses, 2021, 13, 1510.	3.3	26
9	SALMONELLA ISOLATED FROM CENTRAL NEW YORK WILDLIFE ADMITTED TO A VETERINARY MEDICAL TEACHING HOSPITAL. Journal of Wildlife Diseases, 2021, 57, 743-748.	0.8	2
10	Active surveillance of pathogens from ticks collected in New York State suburban parks and schoolyards. Zoonoses and Public Health, 2020, 67, 684-696.	2.2	19
11	From People to <i>Panthera</i> : Natural SARS-CoV-2 Infection in Tigers and Lions at the Bronx Zoo. MBio, 2020, 11, .	4.1	298
12	Sequence analysis of Salmonella enterica isolates obtained from shelter dogs throughout Texas. Veterinary Medicine and Science, 2020, 6, 975-979.	1.6	8
13	Complete Genome Sequence of SARS-CoV-2 in a Tiger from a U.S. Zoological Collection. Microbiology Resource Announcements, 2020, 9, .	0.6	76
14	Enhancing the one health initiative by using whole genome sequencing to monitor antimicrobial resistance of animal pathogens: Vet-LIRN collaborative project with veterinary diagnostic laboratories in United States and Canada. BMC Veterinary Research, 2019, 15, 130.	1.9	23
15	Reassessing Serosurvey-Based Estimates of the Symptomatic Proportion of Zika Virus Infections. American Journal of Epidemiology, 2019, 188, 206-213.	3.4	28
16	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. Microbial Genomics, 2019, 5, .	2.0	12
17	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. PLoS Pathogens, 2018, 14, e1007438.	4.7	74
18	Genomic Epidemiology of Penicillin-Nonsusceptible Pneumococci with Nonvaccine Serotypes Causing Invasive Disease in the United States. Journal of Clinical Microbiology, 2017, 55, 1104-1115.	3.9	44

#	Article	IF	CITATIONS
19	<i>Notes from the Field</i> : Travel-Associated Melioidosis and Resulting Laboratory Exposures — United States, 2016. Morbidity and Mortality Weekly Report, 2017, 66, 1001-1002.	15.1	8
20	Carriage burden, multiple colonization and antibiotic pressure promote emergence of resistant vaccine escape pneumococci. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140342.	4.0	31
21	Population genomics of post-vaccine changes in pneumococcal epidemiology. Nature Genetics, 2013, 45, 656-663.	21.4	364