Mikael Berg

List of Publications by Year in descending order

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MIKAEL REDC

#	Article	IF	CITATIONS
1	Updated unified phylogenetic classification system and revised nomenclature for Newcastle disease virus. Infection, Genetics and Evolution, 2019, 74, 103917.	1.0	227
2	Detection and genetic characterisation of porcine circovirus 3 from pigs in Sweden. Virus Genes, 2018, 54, 466-469.	0.7	74
3	Porcine circovirus type 2 replicase binds the capsid protein and an intermediate filament-like protein. Journal of General Virology, 2006, 87, 3215-3223.	1.3	50
4	Discovery of Novel Viruses in Mosquitoes from the Zambezi Valley of Mozambique. PLoS ONE, 2016, 11, e0162751.	1.1	42
5	Viral Metagenomic Analysis Displays the Co-Infection Situation in Healthy and PMWS Affected Pigs. PLoS ONE, 2016, 11, e0166863.	1.1	34
6	The Intestinal Eukaryotic Virome in Healthy and Diarrhoeic Neonatal Piglets. PLoS ONE, 2016, 11, e0151481.	1.1	28
7	History and current status of peste des petits ruminants virus in Tanzania. Infection Ecology and Epidemiology, 2016, 6, 32701.	0.5	24
8	A longitudinal survey of African swine fever in Uganda reveals high apparent disease incidence rates in domestic pigs, but absence of detectable persistent virus infections in blood and serum. BMC Veterinary Research, 2015, 11, 106.	0.7	23
9	Seroprevalence and risk factors for peste des petits ruminants and selected differential diagnosis in sheep and goats in Tanzania. Infection Ecology and Epidemiology, 2017, 7, 1368336.	0.5	22
10	Characterisation of the Virome of Tonsils from Conventional Pigs and from Specific Pathogen-Free Pigs. Viruses, 2018, 10, 382.	1.5	22
11	Development of a real-time RT-PCR assay for improved detection of Borna disease virus. Journal of Virological Methods, 2007, 143, 1-10.	1.0	21
12	Genetic characterization of a novel picorna-like virus in Culex spp. mosquitoes from Mozambique. Virology Journal, 2018, 15, 71.	1.4	21
13	Seroprevalence of Rift Valley fever virus in sheep and goats in Zambézia, Mozambique. Infection Ecology and Epidemiology, 2016, 6, 31343.	0.5	20
14	Viral metagenomics reveals the presence of highly divergent quaranjavirus in <i>Rhipicephalus</i> ticks from Mozambique. Infection Ecology and Epidemiology, 2018, 8, 1478585.	0.5	20
15	Regulator of G protein signalling 16 is a target for a porcine circovirus type 2 protein. Journal of General Virology, 2009, 90, 2425-2436.	1.3	18
16	The X proteins of bornaviruses interfere with type I interferon signalling. Journal of General Virology, 2013, 94, 263-269.	1.3	16
17	Borna disease virus infection in cats. Veterinary Journal, 2014, 201, 142-149.	0.6	15
18	High seroprevalence of Rift Valley fever phlebovirus in domestic ruminants and African Buffaloes in Mozambique shows need for intensified surveillance. Infection Ecology and Epidemiology, 2017, 7, 1416248.	0.5	14

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19	Single primer isothermal amplification (SPIA) combined with next generation sequencing provides complete bovine coronavirus genome coverage and higher sequence depth compared to sequence-independent single primer amplification (SISPA). PLoS ONE, 2017, 12, e0187780.	1.1	14
20	Markers of Borna disease virus infection in cats with staggering disease. Journal of Feline Medicine and Surgery, 2012, 14, 573-582.	0.6	13
21	Novel Viruses Found in Antricola Ticks Collected in Bat Caves in the Western Amazonia of Brazil. Viruses, 2020, 12, 48.	1.5	10
22	Expression of interferon gamma in the brain of cats with natural Borna disease virus infection. Veterinary Immunology and Immunopathology, 2011, 141, 162-167.	0.5	9
23	Application of Viral Metagenomics for Study of Emerging and Reemerging Tick-Borne Viruses. Vector-Borne and Zoonotic Diseases, 2020, 20, 557-565.	0.6	8
24	Molecular and epidemiological studies ofPorcine rubulavirusinfection – an overview. Infection Ecology and Epidemiology, 2015, 5, 29602.	0.5	7
25	First-time detection of bovine viral diarrhoea virus, BVDV-1, in cattle in Botswana. Onderstepoort Journal of Veterinary Research, 2019, 86, e1-e7.	0.6	7
26	The origin of the PB1 segment of swine influenza A virus subtype H1N2 determines viral pathogenicity in mice. Virus Research, 2014, 188, 97-102.	1.1	6
27	Isolation and characterization of low pathogenic H9N2 avian influenza A viruses from a healthy flock and its comparison to other H9N2 isolates. Indian Journal of Virology: an Official Organ of Indian Virological Society, 2013, 24, 342-348.	0.7	5
28	Cloning, expression and characterization of potential immunogenic recombinant hemagglutinin-neuraminidase protein of Porcine rubulavirus. Protein Expression and Purification, 2016, 128, 1-7.	0.6	5
29	Genome Sequence of a Bovine Rhinitis B Virus Identified in Cattle in Sweden. Genome Announcements, 2017, 5, .	0.8	5
30	Field-Adapted Full Genome Sequencing of Peste-Des-Petits-Ruminants Virus Using Nanopore Sequencing. Frontiers in Veterinary Science, 2020, 7, 542724.	0.9	5
31	Genome constellations of rotavirus a isolated from avian species in Brazil, 2008–2015. Brazilian Journal of Microbiology, 2020, 51, 1363-1375.	0.8	4
32	Molecular Diversity of Hard Tick Species from Selected Areas of a Wildlife-Livestock Interface Ecosystem at Mikumi National Park, Morogoro Region, Tanzania. Veterinary Sciences, 2021, 8, 36.	0.6	4
33	Gizzard erosions in broiler chickens in Sweden caused by fowl adenovirus serotype 1 (FAdV-1): investigation of outbreaks, including whole-genome sequencing of an isolate. Avian Pathology, 2022, 51, 257-266.	0.8	4
34	Complete Genome of Avian coronavirus Vaccine Strains Ma5 and BR-I. Genome Announcements, 2017, 5, .	0.8	3
35	Vector-borne viruses and their detection by viral metagenomics. Infection Ecology and Epidemiology, 2018, 8, 1553465.	0.5	3
36	Detection and phylogenetic analysis of parrot bornavirus 4 identified from a Swedish Blue-winged macaw (<i>Primolius maracana</i>) with unusual nonsuppurative myositis. Infection Ecology and Epidemiology, 2019, 9, 1547097.	0.5	3

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37	Crossing the Line: Seroprevalence and Risk Factors for Transboundary Animal Diseases Along the Tanzania-Zambia Border. Frontiers in Veterinary Science, 2022, 9, 809128.	0.9	2
38	Complete Genome Sequence of Avian Coronavirus Strain D274. Microbiology Resource Announcements, 2018, 7, .	0.3	1
39	Genetic Relationship Between Hard Ticks (Ixodidae) Infesting Cattle from Select Areas of a Wildlife–Livestock Interface Ecosystem at Mikumi National Park, Tanzania. Vector-Borne and Zoonotic Diseases, 2021, 21, 191-199.	0.6	1
40	Bornaviruses in naturally infected <i>Psittacus erithacus</i> in Portugal: insights of molecular epidemiology and ecology. Infection Ecology and Epidemiology, 2019, 9, 1685632.	0.5	0
41	Extinction and emergence of genomic haplotypes during the evolution of Avian coronavirus in chicken embryos. Genetics and Molecular Biology, 2020, 43, e20190064.	0.6	0
42	Complete Coding Sequence of a Pasivirus Found in Swedish Pigs. Microbiology Resource Announcements, 2020, 9, .	0.3	0