

Antoinette van Schalkwyk

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

432
citations

840776

11
h-index

794594

19
g-index

25
all docs

25
docs citations

25
times ranked

457
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis and insights into recombination signals in lumpy skin disease virus recovered in the field. PLoS ONE, 2018, 13, e0207480.	2.5	81
2	<i>Ralstonia solanacearum</i> Needs Flp Pili for Virulence on Potato. Molecular Plant-Microbe Interactions, 2012, 25, 546-556.	2.6	45
3	Full-length genome characterization of a novel recombinant vaccine-like lumpy skin disease virus strain detected during the climatic winter in Russia, 2019. Archives of Virology, 2020, 165, 2675-2677.	2.1	43
4	Introduction of the AmpliChip CYP450 Test to a South African cohort: a platform comparative prospective cohort study. BMC Medical Genetics, 2013, 14, 20.	2.1	42
5	Potential link of single nucleotide polymorphisms to virulence of vaccine-associated field strains of lumpy skin disease virus in South Africa. Transboundary and Emerging Diseases, 2020, 67, 2946-2960.	3.0	28
6	An in-depth bioinformatic analysis of the novel recombinant lumpy skin disease virus strains: from unique patterns to established lineage. BMC Genomics, 2022, 23, .	2.8	21
7	Development of three triplex real-time reverse transcription PCR assays for the qualitative molecular typing of the nine serotypes of African horse sickness virus. Journal of Virological Methods, 2015, 223, 69-74.	2.1	20
8	Estimating evolutionary changes between highly passaged and original parental lumpy skin disease virus strains. Transboundary and Emerging Diseases, 2022, 69, .	3.0	20
9	Bin mapping of tomato diversity array (DART) markers to genomic regions of <i>Solanum lycopersicum</i> — <i>Solanum pennellii</i> introgression lines. Theoretical and Applied Genetics, 2012, 124, 947-956.	3.6	18
10	Comparative Analysis of Full Genome Sequences of African Swine Fever Virus Isolates Taken from Wild Boars in Russia in 2019. Pathogens, 2021, 10, 521.	2.8	18
11	A comparative genome analysis of Rift Valley Fever virus isolates from foci of the disease outbreak in South Africa in 2008-2010. PLoS Neglected Tropical Diseases, 2019, 13, e0006576.	3.0	13
12	South African bovine ephemeral fever virus glycoprotein sequences are phylogenetically distinct from those from the rest of the world. Archives of Virology, 2020, 165, 1207-1210.	2.1	10
13	Molecular characterization of a novel recombinant lumpy skin disease virus isolated during an outbreak in Tyumen, Russia, in 2019. Transboundary and Emerging Diseases, 2022, 69, .	3.0	10
14	Genomic Characterization of Rift Valley Fever Virus, South Africa, 2018. Emerging Infectious Diseases, 2019, 25, 1979-1981.	4.3	9
15	Evidence of Intragenic Recombination in African Horse Sickness Virus. Viruses, 2019, 11, 654.	3.3	8
16	The Development of Dual Vaccines against Lumpy Skin Disease (LSD) and Bovine Ephemeral Fever (BEF). Vaccines, 2021, 9, 1215.	4.4	8
17	Vaccination with Rift Valley fever virus live attenuated vaccine strain Smithburn caused meningoencephalitis in alpacas. Journal of Veterinary Diagnostic Investigation, 2021, 33, 777-781.	1.1	7
18	B-cell epitopes of African horse sickness virus serotype 4 recognised by immune horse sera. Onderstepoort Journal of Veterinary Research, 2017, 84, e1-e12.	1.2	6

#	ARTICLE	IF	CITATIONS
19	Epidemiology and Genomic Analysis of Equine Encephalosis Virus Detected in Horses with Clinical Signs in South Africa, 2010–2017. <i>Viruses</i> , 2021, 13, 398.	3.3	6
20	A correlation between capsid protein VP2 and the plaque morphology of African horse sickness virus in cell culture. <i>Virus Genes</i> , 2018, 54, 527-535.	1.6	4
21	Complete Coding Sequences of 23 South African Domestic and Wildlife Rabies Viruses. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
22	Retrospective phylogenetic analyses of formalin-fixed paraffin-embedded samples from the 2011 Rift Valley fever outbreak in South Africa, through sequencing of targeted regions. <i>Journal of Virological Methods</i> , 2021, 287, 114003.	2.1	3
23	Using a new serotype-specific Polymerase Chain Reaction (PCR) and sequencing to differentiate between field and vaccine-derived African Horse Sickness viruses submitted in 2016/2017. <i>Journal of Virological Methods</i> , 2019, 266, 89-94.	2.1	2
24	Complete Genome Sequences of Virus Strains Isolated from Bottle A of the South African Live Attenuated Bluetongue Virus Vaccine. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2