Martin M Nyaga

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4797690/publications.pdf

Version: 2024-02-01

35

papers

1,944

citations

623734

14

h-index

377865

34

g-index

35

all docs

35

docs citations

35

times ranked

2668

citing authors

#	Article	IF	Citations
1	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 2022, 603, 679-686.	27.8	1,210
2	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	12.6	144
3	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. Nature, 0, , .	27.8	61
4	Update of Rotavirus Strains Circulating in Africa From 2007 Through 2011. Pediatric Infectious Disease Journal, 2014, 33, S76-S84.	2.0	57
5	Whole genome detection of rotavirus mixed infections in human, porcine and bovine samples co-infected with various rotavirus strains collected from sub-Saharan Africa. Infection, Genetics and Evolution, 2015, 31, 321-334.	2.3	42
6	Rotavirus G and P Types Circulating in the Eastern Region of Kenya. Pediatric Infectious Disease Journal, 2014, 33, S85-S88.	2.0	37
7	Whole genome analyses of G1P[8] rotavirus strains from vaccinated and non-vaccinated South African children presenting with diarrhea. Journal of Medical Virology, 2015, 87, 79-101.	5.0	36
8	Poultry gut health â€“ microbiome functions, environmental impacts, microbiome engineering and advancements in characterization technologies. Journal of Animal Science and Biotechnology, 2021, 12, 119.	5.3	35
9	Novel NSP1 genotype characterised in an African camel G8P[11] rotavirus strain. Infection, Genetics and Evolution, 2014, 21, 58-66.	2.3	34
10	Whole-genome analyses of DS-1-like human G2P[4] and G8P[4] rotavirus strains from Eastern, Western and Southern Africa. Virus Genes, 2014, 49, 196-207.	1.6	29
11	Whole-genome sequencing and analyses identify high genetic heterogeneity, diversity and endemicity of rotavirus genotype P[6] strains circulating in Africa. Infection, Genetics and Evolution, 2018, 63, 79-88.	2.3	26
12	Surveillance for Rotavirus Gastroenteritis in Children Less Than 5 Years of Age in Togo. Pediatric Infectious Disease Journal, 2014, 33, S14-S18.	2.0	24
13	Sequence analysis of the whole genomes of five African human G9 rotavirus strains. Infection, Genetics and Evolution, 2013, 16, 62-77.	2.3	19
14	Whole genome analyses of DS-1-like Rotavirus A strains detected in children with acute diarrhoea in southern Mozambique suggest several reassortment events. Infection, Genetics and Evolution, 2019, 69, 68-75.	2.3	16
15	Whole genomeÂand in-silico analyses of G1P[8] rotavirus strains from pre- and post-vaccination periods in Rwanda. Scientific Reports, 2020, 10, 13460.	3.3	16
16	Molecular Characterisation of a Rare Reassortant Porcine-Like G5P[6] Rotavirus Strain Detected in an Unvaccinated Child in Kasama, Zambia. Pathogens, 2020, 9, 663.	2.8	15
17	Complete genome analyses of the first porcine rotavirus group H identified from a South African pig does not provide evidence for recent interspecies transmission events. Infection, Genetics and Evolution, 2016, 38, 1-7.	2.3	13
18	Rotavirus Genotypes in Hospitalized Children With Acute Gastroenteritis Before and After Rotavirus Vaccine Introduction in Blantyre, Malawi, 1997â€“2019. Journal of Infectious Diseases, 2020, , .	4.0	13

#	ARTICLE	IF	CITATIONS
19	Whole Genome Analysis of Human Rotaviruses Reveals Single Gene Reassortant Rotavirus Strains in Zambia. Viruses, 2021, 13, 1872.	3.3	13
20	Uncovering the First Atypical DS-1-like G1P[8] Rotavirus Strains That Circulated during Pre-Rotavirus Vaccine Introduction Era in South Africa. Pathogens, 2020, 9, 391.	2.8	13
21	Whole-genome characterization of G12 rotavirus strains detected in Mozambique reveals a co-infection with a GXP[14] strain of possible animal origin. Journal of General Virology, 2019, 100, 932-937.	2.9	12
22	Metagenomic Analysis of the Enteric RNA Virome of Infants from the Oukasie Clinic, North West Province, South Africa, Reveals Diverse Eukaryotic Viruses. Viruses, 2020, 12, 1260.	3.3	11
23	Whole-Genome Analyses Identifies Multiple Reassortant Rotavirus Strains in Rwanda Post-Vaccine Introduction. Viruses, 2021, 13, 95.	3.3	11
24	Whole Genome In-Silico Analysis of South African G1P[8] Rotavirus Strains before and after Vaccine Introduction over a Period of 14 Years. Vaccines, 2020, 8, 609.	4.4	9
25	Complete Genomic Sequence for an Avian Group G Rotavirus from South Africa. Genome Announcements, 2015, 3, .	0.8	7
26	Genetic characterization of G12P[6] and G12P[8] rotavirus strains collected in six African countries between 2010 and 2014. BMC Infectious Diseases, 2021, 21, 107.	2.9	7
27	Report of the 1st African Enteric Viruses Genome Initiative (AEVGI) Data and Bioinformatics Workshop on whole-genome analysis of some African rotavirus strains held in Bloemfontein, South Africa. Vaccine, 2020, 38, 5402-5407.	3.8	5
28	Genetic Characterisation of South African and Mozambican Bovine Rotaviruses Reveals a Typical Bovine-like Artiodactyl Constellation Derived through Multiple Reassortment Events. Pathogens, 2021, 10, 1308.	2.8	5
29	Molecular Epidemiology of Rotavirus Strains in Symptomatic and Asymptomatic Children in ManhiÃ§a District, Southern Mozambique 2008â€“2019. Viruses, 2022, 14, 134.	3.3	5
30	Genetic diversity of rotavirus genome segment 6 (encoding VP6) in Pretoria, South Africa. SpringerPlus, 2014, 3, 179.	1.2	4
31	Baseline Data of the Fungal Phytobiome of Three Sorghum (Sorghum bicolor) Cultivars in South Africa using Targeted Environmental Sequencing. Journal of Fungi (Basel, Switzerland), 2021, 7, 978.	3.5	4
32	The Repurposing of Acetylsalicylic Acid as a Photosensitiser to Inactivate the Growth of Cryptococcal Cells. Pharmaceuticals, 2021, 14, 404.	3.8	3
33	A decontamination strategy for resolving SARS-CoV-2 amplicon contamination in a next-generation sequencing laboratory. Archives of Virology, 2022, 167, 1175-1179.	2.1	3
34	Evolutionary changes between pre- and post-vaccine South African group A G2P[4] rotavirus strains, 2003â€“2017. Microbial Genomics, 2022, 8, .	2.0	3
35	Using genomics to improve preparedness and response of future epidemics or pandemics in Africa. Lancet Microbe, The, 2020, 1, e275-e276.	7.3	2