NÃ;dia Conceição-Neto

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7017692/publications.pdf

Version: 2024-02-01

23 papers 1,478 citations

18 h-index 610482 24 g-index

25 all docs

25 docs citations

25 times ranked

2809 citing authors

#	Article	IF	CITATIONS
1	Genetic Variants of the MGAT5 Gene Are Functionally Implicated in the Modulation of T Cells Glycosylation and Plasma IgG Glycome Composition in Ulcerative Colitis. Clinical and Translational Gastroenterology, 2020, 11, e00166.	1.3	20
2	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. MSphere, 2019, 4, .	1.3	57
3	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. Cell, 2019, 177, 1109-1123.e14.	13.5	541
4	Structural and functional similarities in bunyaviruses: Perspectives for panâ€bunya antivirals. Reviews in Medical Virology, 2019, 29, e2039.	3.9	21
5	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. Gut, 2018, 67, 1558-1559.	6.1	46
6	NetoVIR: Modular Approach to Customize Sample Preparation Procedures for Viral Metagenomics. Methods in Molecular Biology, 2018, 1838, 85-95.	0.4	33
7	Viral gut metagenomics of sympatric wild and domestic canids, and monitoring of viruses: Insights from an endangered wolf population. Ecology and Evolution, 2017, 7, 4135-4146.	0.8	28
8	Novel highly divergent sapoviruses detected by metagenomics analysis in straw-colored fruit bats in Cameroon. Emerging Microbes and Infections, 2017, 6, 1-7.	3.0	44
9	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. BMC Genomics, 2017, 18, 249.	1.2	42
10	Identification of an enterovirus recombinant with a torovirus-like gene insertion during a diarrhea outbreak in fattening pigs. Virus Evolution, 2017, 3, vex024.	2.2	30
11	Experimental feline enteric coronavirus infection reveals an aberrant infection pattern and shedding of mutants with impaired infectivity in enterocyte cultures. Scientific Reports, 2016, 6, 20022.	1.6	35
12	A single bat species in Cameroon harbors multiple highly divergent papillomaviruses in stool identified by metagenomics analysis. Virology Reports, 2016, 6, 74-80.	0.4	8
13	Reassortment among picobirnaviruses found in wolves. Archives of Virology, 2016, 161, 2859-2862.	0.9	24
14	Emergence of human G2P[4] rotaviruses containing animal derived gene segments in the post-vaccine era. Scientific Reports, 2016, 6, 36841.	1.6	11
15	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. Scientific Reports, 2016, 6, 34209.	1.6	44
16	Characterization of a genetically heterogeneous porcine rotavirus C, and other viruses present in the fecal virome of a non-diarrheic Belgian piglet. Infection, Genetics and Evolution, 2016, 43, 135-145.	1.0	25
17	Molecular detection of bovine Noroviruses in Argentinean dairy calves: Circulation of a tentative new genotype. Infection, Genetics and Evolution, 2016, 40, 144-150.	1.0	20
18	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. Scientific Reports, 2015, 5, 16532.	1.6	277

#	Article	IF	CITATIONS
19	Fecal virome analysis of three carnivores reveals a novel nodavirus and multiple gemycircularviruses. Virology Journal, 2015, 12, 79.	1.4	29
20	Complete Genome Sequence of a Porcine Epidemic Diarrhea Virus from a Novel Outbreak in Belgium, January 2015. Genome Announcements, 2015 , 3 , .	0.8	70
21	Molecular characterization of equine rotaviruses isolated in Europe in 2013: Implications for vaccination. Veterinary Microbiology, 2015, 176, 179-185.	0.8	16
22	Rotavirus Surveillance in Kisangani, the Democratic Republic of the Congo, Reveals a High Number of Unusual Genotypes and Gene Segments of Animal Origin in Non-Vaccinated Symptomatic Children. PLoS ONE, 2014, 9, e100953.	1.1	43
23	First report of a norovirus outbreak associated with the variant Sydney 2012 in Portugal. Journal of Infection in Developing Countries, 2014, 8, 1350-1352.	0.5	3