

Ward Deboutte

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4229265/publications.pdf>

Version: 2024-02-01

24
papers

1,095
citations

566801

15
h-index

610482

24
g-index

26
all docs

26
docs citations

26
times ranked

2626
citing authors

#	ARTICLE	IF	CITATIONS
1	Cold case: The disappearance of Egypt bee virus, a fourth distinct master strain of deformed wing virus linked to honeybee mortality in 1970's Egypt. <i>Virology Journal</i> , 2022, 19, 12.	1.4	17
2	The virota and its transkingdom interactions in the healthy infant gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114619119.	3.3	30
3	The Virome of Healthy Honey Bee Colonies: Ubiquitous Occurrence of Known and New Viruses in Bee Populations. <i>MSystems</i> , 2022, 7, e0007222.	1.7	7
4	Whole genome analysis of Aichivirus A, isolated from a child, suffering from gastroenteritis, in Pakistan. <i>Virus Research</i> , 2021, 299, 198437.	1.1	2
5	At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , 2021, 12, .	1.8	31
6	A single-dose live-attenuated YF17D-vectored SARS-CoV-2 vaccine candidate. <i>Nature</i> , 2021, 590, 320-325.	13.7	148
7	A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221.	1.7	22
8	Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721.	1.8	48
9	Clinical relevance of plasma virome dynamics in liver transplant recipients. <i>EBioMedicine</i> , 2020, 60, 103009.	2.7	21
10	NCBI's Virus Discovery Codeathon: Building "FIVE" The Federated Index of Viral Experiments API Index. <i>Viruses</i> , 2020, 12, 1424.	1.5	3
11	Metagenomic Approach with the NetoVIR Enrichment Protocol Reveals Virus Diversity within Ethiopian Honey Bees (<i>Apis mellifera simensis</i>). <i>Viruses</i> , 2020, 12, 1218.	1.5	16
12	Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10511-10519.	3.3	36
13	Signature of natural resistance in NS3 protease revealed by deep sequencing of HCV strains circulating in Iran. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103966.	1.0	2
14	A45 Genetic diversity of anelloviruses in the blood virome. <i>Virus Evolution</i> , 2019, 5, .	2.2	1
15	Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. <i>Microbiome</i> , 2019, 7, 121.	4.9	109
16	NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , 2019, 10, 714.	1.0	13
17	Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, .	1.3	57
18	A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. <i>Genome Biology and Evolution</i> , 2018, 10, 45-55.	1.1	23

#	ARTICLE	IF	CITATIONS
19	Low eukaryotic viral richness is associated with faecal microbiota transplantation success in patients with UC. <i>Gut</i> , 2018, 67, 1558-1559.	6.1	46
20	Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. <i>BMC Genomics</i> , 2018, 19, 617.	1.2	35
21	Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. <i>Scientific Reports</i> , 2018, 8, 9830.	1.6	59
22	Highly diverse population of Picornaviridae and other members of the Picornavirales, in Cameroonian fruit bats. <i>BMC Genomics</i> , 2017, 18, 249.	1.2	42
23	Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209.	1.6	44
24	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015, 5, 16532.	1.6	277