

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 | 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 |
| 2 | A single-dose live-attenuated YF17D-vectored SARS-CoV-2 vaccine candidate. <i>Nature</i> , 2021, 590, 320-325. | 13.7 | 148 |
| 3 | 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 |
| 4 | 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 |
| 5 | Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric Viruses, Including Potential Interspecies Transmitted Viruses. <i>MSphere</i> , 2019, 4, . | 1.3 | 57 |
| 6 | Successional Stages in Infant Gut Microbiota Maturation. <i>MBio</i> , 2021, 12, e0185721. | 1.8 | 48 |
| 7 | 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 |
| 8 | Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. <i>Scientific Reports</i> , 2016, 6, 34209. | 1.6 | 44 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | At Least Seven Distinct Rotavirus Genotype Constellations in Bats with Evidence of Reassortment and Zoonotic Transmissions. <i>MBio</i> , 2021, 12, . | 1.8 | 31 |
| 13 | 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 |
| 14 | 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 |
| 15 | A Previously Undescribed Highly Prevalent Phage Identified in a Danish Enteric Virome Catalog. <i>MSystems</i> , 2021, 6, e0038221. | 1.7 | 22 |
| 16 | Clinical relevance of plasma virome dynamics in liver transplant recipients. <i>EBioMedicine</i> , 2020, 60, 103009. | 2.7 | 21 |
| 17 | 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 |
| 18 | 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 |

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|----|--|-----|-----------|
| 19 | NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. <i>Genes</i> , 2019, 10, 714. | 1.0 | 13 |
| 20 | 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 |
| 21 | NCBI's Virus Discovery Codeathon: Building "The Federated Index of Viral Experiments API Index. <i>Viruses</i> , 2020, 12, 1424. | 1.5 | 3 |
| 22 | 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 |
| 23 | 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 |
| 24 | A45 Genetic diversity of anelloviruses in the blood virome. <i>Virus Evolution</i> , 2019, 5, . | 2.2 | 1 |