

Nathan D Grubaugh

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

137
papers

8,103
citations

44
h-index

89
g-index

160
ext. papers

12,053
ext. citations

20.1
avg, IF

6.43
L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 137 | Comparative transmissibility of SARS-CoV-2 variants Delta and Alpha in New England, USA.. <i>Cell Reports Medicine</i> , 2022 , 3, 100583 | 17.5 | 3 |
| 136 | Evaluation of saliva self-collection devices for SARS-CoV-2 diagnostics.. <i>BMC Infectious Diseases</i> , 2022 , 22, 284 | 3.9 | 1 |
| 135 | Assessment of Clinical Effectiveness of BNT162b2 COVID-19 Vaccine in US Adolescents.. <i>JAMA Network Open</i> , 2022 , 5, e220935 | 10.1 | 1 |
| 134 | Rapid emergence of SARS-CoV-2 Omicron variant is associated with an infection advantage over Delta in vaccinated persons.. <i>Med</i> , 2022 , | 30.9 | 7 |
| 133 | Translating virus evolution into epidemiology.. <i>Cell Host and Microbe</i> , 2022 , 30, 444-448 | 22.8 | 0 |
| 132 | A stem-loop RNA RIG-I agonist protects against acute and chronic SARS-CoV-2 infection in mice. <i>Journal of Experimental Medicine</i> , 2022 , 219, | 16.2 | 10 |
| 131 | Sequencing SARS-CoV-2 genomes from saliva.. <i>Virus Evolution</i> , 2022 , 8, veab098 | 3.6 | 0 |
| 130 | Single-cell multi-omics reveals dyssynchrony of the innate and adaptive immune system in progressive COVID-19.. <i>Nature Communications</i> , 2022 , 13, 440 | 16.9 | 9 |
| 129 | Neutralizing antibodies against the SARS-CoV-2 Delta and Omicron variants following heterologous CoronaVac plus BNT162b2 booster vaccination.. <i>Nature Medicine</i> , 2022 , | 49.3 | 41 |
| 128 | Clinical effectiveness of additional primary SARS-CoV-2 vaccine doses for solid organ transplant recipients.. <i>Clinical Transplantation</i> , 2022 , e14601 | 3.7 | |
| 127 | Combining genomic and epidemiological data to compare the transmissibility of SARS-CoV-2 variants Alpha and Iota.. <i>Communications Biology</i> , 2022 , 5, 439 | 6.5 | 0 |
| 126 | Partial ORF1ab Gene Target Failure with Omicron BA.2.12.1.. <i>Journal of Clinical Microbiology</i> , 2022 , e0060022 | 9.2 | 0 |
| 125 | Intrahost speciations and host switches played an important role in the evolution of herpesviruses. <i>Virus Evolution</i> , 2021 , 7, veab025 | 3.6 | 3 |
| 124 | Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021 , 19, e3001236 | 9.4 | 82 |
| 123 | Longitudinal immune profiling of a SARS-CoV-2 reinfection in a solid organ transplant recipient 2021 , | | 1 |
| 122 | MOG-associated encephalitis following SARS-COV-2 infection. <i>Multiple Sclerosis and Related Disorders</i> , 2021 , 50, 102857 | 3.7 | 14 |
| 121 | Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil. <i>Nature Communications</i> , 2021 , 12, 2619 | 16.9 | 8 |

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|-----|--|------|-----|
| 120 | COVID-19 one year into the pandemic: from genetics and genomics to therapy, vaccination, and policy. <i>Human Genomics</i> , 2021 , 15, 27 | 6.5 | 23 |
| 119 | Diverse functional autoantibodies in patients with COVID-19. <i>Nature</i> , 2021 , 595, 283-288 | 47.5 | 175 |
| 118 | A stem-loop RNA RIG-I agonist confers prophylactic and therapeutic protection against acute and chronic SARS-CoV-2 infection in mice 2021 , | | 5 |
| 117 | Combining genomic and epidemiological data to compare the transmissibility of SARS-CoV-2 lineages 2021 , | | 4 |
| 116 | Viral dynamics of acute SARS-CoV-2 infection and applications to diagnostic and public health strategies. <i>PLoS Biology</i> , 2021 , 19, e3001333 | 9.4 | 38 |
| 115 | Global disparities in SARS-CoV-2 genomic surveillance 2021 , | | 22 |
| 114 | COVID-19 vaccines: Keeping pace with SARS-CoV-2 variants. <i>Cell</i> , 2021 , 184, 5077-5081 | 54.5 | 49 |
| 113 | Emergence of an early SARS-CoV-2 epidemic in the United States. <i>Cell</i> , 2021 , 184, 4939-4952.e15 | 54.5 | 2 |
| 112 | Variant abundance estimation for SARS-CoV-2 in wastewater using RNA-Seq quantification 2021 , | | 3 |
| 111 | Reply to: A finding of sex similarities rather than differences in COVID-19 outcomes. <i>Nature</i> , 2021 , 597, E10-E11 | 47.5 | |
| 110 | Asynchronicity of endemic and emerging mosquito-borne disease outbreaks in the Dominican Republic. <i>Nature Communications</i> , 2021 , 12, 151 | 16.9 | 8 |
| 109 | Multiple Transmission Chains within COVID-19 Cluster, Connecticut, USA, 2020. <i>Emerging Infectious Diseases</i> , 2021 , 27, 2669-2672 | 9.9 | 0 |
| 108 | SARS-CoV-2 infection in pregnancy is associated with robust inflammatory response at the maternal-fetal interface 2021 , | | 8 |
| 107 | PCR assay to enhance global surveillance for SARS-CoV-2 variants of concern 2021 , | | 14 |
| 106 | Emergence of an early SARS-CoV-2 epidemic in the United States 2021 , | | 3 |
| 105 | Early introductions and community transmission of SARS-CoV-2 variant B.1.1.7 in the United States 2021 , | | 9 |
| 104 | Evaluation of saliva self-collection devices for SARS-CoV-2 diagnostics 2021 , | | 4 |
| 103 | SalivaDirect: A simplified and flexible platform to enhance SARS-CoV-2 testing capacity. <i>Med</i> , 2021 , 2, 263-280.e6 | 30.9 | 104 |

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| 102 | Public health actions to control new SARS-CoV-2 variants. <i>Cell</i> , 2021 , 184, 1127-1132 | 54.5 | 82 |
| 101 | Tracking smell loss to identify healthcare workers with SARS-CoV-2 infection. <i>PLoS ONE</i> , 2021 , 16, e0248085 | 30.85 | 7 |
| 100 | Case Study: Longitudinal immune profiling of a SARS-CoV-2 reinfection in a solid organ transplant recipient 2021 , | | 2 |
| 99 | Evidence for SARS-CoV-2 Spike Protein in the Urine of COVID-19 Patients.. <i>Kidney360</i> , 2021 , 2, 924-936 | 1.8 | 9 |
| 98 | Maternal respiratory SARS-CoV-2 infection in pregnancy is associated with a robust inflammatory response at the maternal-fetal interface. <i>Med</i> , 2021 , 2, 591-610.e10 | 30.9 | 38 |
| 97 | Divergent and self-reactive immune responses in the CNS of COVID-19 patients with neurological symptoms. <i>Cell Reports Medicine</i> , 2021 , 2, 100288 | 17.5 | 35 |
| 96 | Early introductions and transmission of SARS-CoV-2 variant B.1.1.7 in the United States. <i>Cell</i> , 2021 , 184, 2595-2604.e13 | 54.5 | 51 |
| 95 | Delayed production of neutralizing antibodies correlates with fatal COVID-19. <i>Nature Medicine</i> , 2021 , 27, 1178-1186 | 49.3 | 64 |
| 94 | Diverse Functional Autoantibodies in Patients with COVID-19 2021 , | | 64 |
| 93 | 301. Detection of Pneumococcal Pneumonia During SARS-CoV-2 Infection. <i>Open Forum Infectious Diseases</i> , 2021 , 8, S257-S257 | 0.9 | |
| 92 | 362. Saliva as a Reliable Sample Type for Mass SARS-CoV-2 Testing Strategies. <i>Open Forum Infectious Diseases</i> , 2021 , 8, S284-S284 | 0.9 | |
| 91 | Of variants and vaccines.. <i>Cell</i> , 2021 , 184, 6222-6223 | 54.5 | 3 |
| 90 | Viral Dynamics of SARS-CoV-2 Variants in Vaccinated and Unvaccinated Persons.. <i>New England Journal of Medicine</i> , 2021 , 385, 2489-2491 | 57.2 | 49 |
| 89 | Authors' Response to Peer Reviews of COVID-19 Outcomes and Genomic Characterization of SARS-CoV-2 Isolated From Veterans in New England States: Retrospective Analysis <i>Jmirx Med</i> , 2021 , 2, e35515 | 0.2 | |
| 88 | An outbreak of SARS-CoV-2 on a transplant unit in the early vaccination era.. <i>Transplant Infectious Disease</i> , 2021 , | 2.6 | 1 |
| 87 | Saliva viral load is a dynamic unifying correlate of COVID-19 severity and mortality 2021 , | | 38 |
| 86 | Longitudinal immune profiling of a SARS-CoV-2 reinfection in a solid organ transplant recipient. <i>Journal of Infectious Diseases</i> , 2021 , | 6.8 | 4 |
| 85 | COVID-19 Outcomes and Genomic Characterization of SARS-CoV-2 Isolated From Veterans in New England States: Retrospective Analysis.. <i>Jmirx Med</i> , 2021 , 2, e31503 | 0.2 | 3 |

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|----|--|------|-----|
| 84 | Impact of circulating SARS-CoV-2 variants on mRNA vaccine-induced immunity. <i>Nature</i> , 2021 , | 47.5 | 61 |
| 83 | Comparative transmissibility of SARS-CoV-2 variants Delta and Alpha in New England, USA 2021 , | | 13 |
| 82 | Tracing the Origin, Spread, and Molecular Evolution of Zika Virus in Puerto Rico, 2016-2017. <i>Emerging Infectious Diseases</i> , 2021 , 27, 2971-2973 | 9.9 | 0 |
| 81 | Detection of SARS-CoV-2 RNA by multiplex RT-qPCR. <i>PLoS Biology</i> , 2020 , 18, e3000867 | 9.4 | 29 |
| 80 | Sex differences in immune responses that underlie COVID-19 disease outcomes. <i>Nature</i> , 2020 , 588, 315-320 | 47.5 | 527 |
| 79 | Analytical sensitivity and efficiency comparisons of SARS-CoV-2 RT-qPCR primer-probe sets. <i>Nature Microbiology</i> , 2020 , 5, 1299-1305 | 25.8 | 374 |
| 78 | Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. <i>Nature Communications</i> , 2020 , 11, 5620 | 16.9 | 6 |
| 77 | Longitudinal analyses reveal immunological misfiring in severe COVID-19. <i>Nature</i> , 2020 , 584, 463-469 | 47.5 | 871 |
| 76 | Measurement of SARS-CoV-2 RNA in wastewater tracks community infection dynamics. <i>Nature Biotechnology</i> , 2020 , 38, 1164-1167 | 43.2 | 335 |
| 75 | Real-time public health communication of local SARS-CoV-2 genomic epidemiology. <i>PLoS Biology</i> , 2020 , 18, e3000869 | 9.4 | 12 |
| 74 | Saliva or Nasopharyngeal Swab Specimens for Detection of SARS-CoV-2. <i>New England Journal of Medicine</i> , 2020 , 383, 1283-1286 | 57.2 | 495 |
| 73 | Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , 2020 , 181, 990-996.e5 | 54.5 | 231 |
| 72 | Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12522-12523 | 11.1 | 45 |
| 71 | Why does Japan have so few cases of COVID-19?. <i>EMBO Molecular Medicine</i> , 2020 , 12, e12481 | 11.6 | 78 |
| 70 | Acute encephalopathy with elevated CSF inflammatory markers as the initial presentation of COVID-19. <i>BMC Neurology</i> , 2020 , 20, 248 | 3 | 78 |
| 69 | Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear. <i>Cell</i> , 2020 , 182, 794-795 | 54.5 | 260 |
| 68 | We shouldn't worry when a virus mutates during disease outbreaks. <i>Nature Microbiology</i> , 2020 , 5, 529-530 | 35.8 | 91 |
| 67 | 456. Implementing an At-Home Smell Test for Early Assessment of COVID-19 in High-Risk Healthcare Workers. <i>Open Forum Infectious Diseases</i> , 2020 , 7, S295-S296 | 0.9 | 1 |

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| 66 | Coast-to-coast spread of SARS-CoV-2 in the United States revealed by genomic epidemiology 2020 , | | 17 |
| 65 | Host response-based screening to identify undiagnosed cases of COVID-19 and expand testing capacity 2020 , | | 2 |
| 64 | Sex differences in immune responses to SARS-CoV-2 that underlie disease outcomes 2020 , | | 36 |
| 63 | Simply saliva: stability of SARS-CoV-2 detection negates the need for expensive collection devices 2020 , | | 36 |
| 62 | Pooling saliva to increase SARS-CoV-2 testing capacity 2020 , | | 24 |
| 61 | Exploratory neuroimmune profiling identifies CNS-specific alterations in COVID-19 patients with neurological involvement 2020 , | | 11 |
| 60 | Two Sides of a Coin: a Zika Virus Mutation Selected in Pregnant Rhesus Macaques Promotes Fetal Infection in Mice but at a Cost of Reduced Fitness in Nonpregnant Macaques and Diminished Transmissibility by Vectors. <i>Journal of Virology</i> , 2020 , 94, | 6.3 | 4 |
| 59 | SARS-CoV-2 infection of the placenta. <i>Journal of Clinical Investigation</i> , 2020 , 130, 4947-4953 | 15.3 | 219 |
| 58 | Tracking Smell Loss to Identify Healthcare Workers with SARS-CoV-2 Infection 2020 , | | 2 |
| 57 | Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. <i>PLoS Pathogens</i> , 2019 , 15, e1008042 | 7.4 | 39 |
| 56 | Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. <i>Cell</i> , 2019 , 178, 1057-1071.e11 | 54.5 | 43 |
| 55 | Arbovirus coinfection and co-transmission: A neglected public health concern?. <i>PLoS Biology</i> , 2019 , 17, e3000130 | 9.4 | 59 |
| 54 | Endless Forms: Within-Host Variation in the Structure of the West Nile Virus RNA Genome during Serial Passage in Bird Hosts. <i>MSphere</i> , 2019 , 4, | 4.9 | 1 |
| 53 | Small RNA responses of Culex mosquitoes and cell lines during acute and persistent virus infection. <i>Insect Biochemistry and Molecular Biology</i> , 2019 , 109, 13-23 | 4.3 | 20 |
| 52 | Precision epidemiology for infectious disease control. <i>Nature Medicine</i> , 2019 , 25, 206-211 | 49.3 | 52 |
| 51 | Misperceived Risks of Zika-related Microcephaly in India. <i>Trends in Microbiology</i> , 2019 , 27, 381-383 | 12 | 15 |
| 50 | An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019 , 20, 8 | 17.7 | 293 |
| 49 | Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019 , 4, 10-19 | 25.8 | 175 |

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| 48 | Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018 , 172, 1160-1162 | 54.5 | 38 |
| 47 | Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. <i>Nature Communications</i> , 2018 , 9, 1624 | 16.9 | 50 |
| 46 | Common PIEZO1 Allele in African Populations Causes RBC Dehydration and Attenuates Plasmodium Infection. <i>Cell</i> , 2018 , 173, 443-455.e12 | 54.5 | 104 |
| 45 | Adventitious viruses persistently infect three commonly used mosquito cell lines. <i>Virology</i> , 2018 , 521, 175-180 | 3.5 | 22 |
| 44 | Inferring the risk factors behind the geographical spread and transmission of Zika in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006194 | 4.6 | 45 |
| 43 | Ontogeny of the B- and T-cell response in a primary Zika virus infection of a dengue-naïve individual during the 2016 outbreak in Miami, FL. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0006000 | 4.6 | 30 |
| 42 | Mosquitoes Transmit Unique West Nile Virus Populations during Each Feeding Episode. <i>Cell Reports</i> , 2017 , 19, 709-718 | 10.3 | 53 |
| 41 | Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405 | 47.5 | 233 |
| 40 | Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017 , 546, 411-415 | 47.5 | 251 |
| 39 | Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017 , 12, 1261-1276 | 18.1 | 514 |
| 38 | Experimental Evolution to Study Virus Emergence. <i>Cell</i> , 2017 , 169, 1-3 | 54.5 | 33 |
| 37 | Neutralizing human monoclonal antibodies prevent Zika virus infection in macaques. <i>Science Translational Medicine</i> , 2017 , 9, | 16.9 | 69 |
| 36 | The Use of Xenosurveillance to Detect Human Bacteria, Parasites, and Viruses in Mosquito Bloodmeals. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017 , 97, 324-329 | 3.2 | 15 |
| 35 | Dynamics of West Nile virus evolution in mosquito vectors. <i>Current Opinion in Virology</i> , 2016 , 21, 132-138.1 | 7.1 | 24 |
| 34 | Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. <i>Cell</i> , 2016 , 167, 1088-1098.e6 | 54.5 | 135 |
| 33 | West Nile Virus Population Structure, Injury, and Interferon-Stimulated Gene Expression in the Brain From a Fatal Case of Encephalitis. <i>Open Forum Infectious Diseases</i> , 2016 , 3, ofv182 | 0.9 | 8 |
| 32 | Isolation of a Novel Insect-Specific Flavivirus from <i>Culiseta melanura</i> in the Northeastern United States. <i>Vector-Borne and Zoonotic Diseases</i> , 2016 , 16, 181-90 | 2.3 | 12 |
| 31 | Temporal and Spatial Variability of Entomological Risk Indices for West Nile Virus Infection in Northern Colorado: 2006-2013. <i>Journal of Medical Entomology</i> , 2016 , 53, 425-34 | 2.2 | 10 |

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|----|--|------|----|
| 30 | Transmission bottlenecks and RNAi collectively influence tick-borne flavivirus evolution. <i>Virus Evolution</i> , 2016 , 2, vew033 | 3.6 | 26 |
| 29 | Genetic Drift during Systemic Arbovirus Infection of Mosquito Vectors Leads to Decreased Relative Fitness during Host Switching. <i>Cell Host and Microbe</i> , 2016 , 19, 481-92 | 22.8 | 96 |
| 28 | West African Anopheles gambiae mosquitoes harbor a taxonomically diverse virome including new insect-specific flaviviruses, mononegaviruses, and totiviruses. <i>Virology</i> , 2016 , 498, 288-299 | 3.5 | 76 |
| 27 | Navigating the Zika panic. <i>F1000Research</i> , 2016 , 5, 1914 | 3.5 | 1 |
| 26 | Experimental evolution of an RNA virus in wild birds: evidence for host-dependent impacts on population structure and competitive fitness. <i>PLoS Pathogens</i> , 2015 , 11, e1004874 | 7.4 | 43 |
| 25 | Xenosurveillance: a novel mosquito-based approach for examining the human-pathogen landscape. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003628 | 4.6 | 45 |
| 24 | Sampling host-seeking anthropophilic mosquito vectors in west Africa: comparisons of an active human-baited tent-trap against gold standard methods. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015 , 92, 415-21 | 3.2 | 7 |
| 23 | Evaluation of ivermectin mass drug administration for malaria transmission control across different West African environments. <i>Malaria Journal</i> , 2014 , 13, 417 | 3.5 | 62 |
| 22 | Evaluation of a field-portable DNA microarray platform and nucleic acid amplification strategies for the detection of arboviruses, arthropods, and bloodmeals. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013 , 88, 245-53 | 3.2 | 15 |
| 21 | Isolation and genomic characterization of Chaoyang virus strain ROK144 from <i>Aedes vexans nipponii</i> from the Republic of Korea. <i>Virology</i> , 2013 , 435, 220-4 | 3.5 | 36 |
| 20 | Multi-gene detection and identification of mosquito-borne RNA viruses using an oligonucleotide microarray. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2349 | 4.6 | 11 |
| 19 | Impact of circulating SARS-CoV-2 variants on mRNA vaccine-induced immunity in uninfected and previously infected individuals | | 11 |
| 18 | Multiplexed RT-qPCR to screen for SARS-COV-2 B.1.1.7, B.1.351, and P.1 variants of concern v3 | | 12 |
| 17 | Viral dynamics of SARS-CoV-2 variants in vaccinated and unvaccinated individuals | | 75 |
| 16 | Generation of SARS-COV-2 RNA transcript standards for qRT-PCR detection assays v1 | | 7 |
| 15 | Saliva Collection and RNA Extraction for SARS-CoV-2 Detection v2 | | 4 |
| 14 | Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples | | 6 |
| 13 | Genetic characterization of the Zika virus epidemic in the US Virgin Islands | | 2 |

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| 12 | Analytical sensitivity and efficiency comparisons of SARS-CoV-2 qRT-PCR primer-probe sets | 47 |
| 11 | Saliva is more sensitive for SARS-CoV-2 detection in COVID-19 patients than nasopharyngeal swabs | 87 |
| 10 | Longitudinal immunological analyses reveal inflammatory misfiring in severe COVID-19 patients | 12 |
| 9 | SalivaDirect: A simplified and flexible platform to enhance SARS-CoV-2 testing capacity | 40 |
| 8 | Lying in wait: the resurgence of dengue virus after the Zika epidemic in Brazil | 3 |
| 7 | Viral dynamics of acute SARS-CoV-2 infection | 44 |
| 6 | Long SARS-CoV-2 nucleocapsid sequences in blood monocytes collected soon after hospital admission | 3 |
| 5 | An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar | 6 |
| 4 | International travelers and genomics uncover a hidden Zika outbreak | 1 |
| 3 | Rapid emergence of SARS-CoV-2 Omicron variant is associated with an infection advantage over Delta in vaccinated persons | 3 |
| 2 | Viral dynamics and duration of PCR positivity of the SARS-CoV-2 Omicron variant | 14 |
| 1 | Immunogenicity of heterologous BNT162b2 booster in fully vaccinated individuals with CoronaVac against SARS-CoV-2 variants Delta and Omicron: the Dominican Republic Experience | 10 |