

# Nuno Rodrigues Faria

## List of Publications by Year in descending order

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Version: 2024-02-01

134  
papers

17,863  
citations

30070

54  
h-index

18647

119  
g-index

182  
all docs

182  
docs citations

182  
times ranked

24954  
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding the Potential Impact of Different Drug Properties on Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Transmission and Disease Burden: A Modelling Analysis. <i>Clinical Infectious Diseases</i> , 2022, 75, e224-e233.	5.8	10
2	Epidemiology of COVID-19 after Emergence of SARS-CoV-2 Gamma Variant, Brazilian Amazon, 2020â€“2021. <i>Emerging Infectious Diseases</i> , 2022, 28, .	4.3	17
3	Mapping environmental suitability of <i>Haemagogus</i> and <i>Sabethes</i> spp. mosquitoes to understand sylvatic transmission risk of yellow fever virus in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010019.	3.0	19
4	Tracking the emergence of disparities in the subnational spread of COVID-19 in Brazil using an online application for real-time data visualisation: A longitudinal analysis. <i>The Lancet Regional Health Americas</i> , 2022, 5, 100119.	2.6	7
5	Reinfection by the SARS-CoV-2 Gamma variant in blood donors in Manaus, Brazil. <i>BMC Infectious Diseases</i> , 2022, 22, 127.	2.9	15
6	Association between inflammatory cytokines and anti-SARS-CoV-2 antibodies in hospitalized patients with COVID-19. <i>Immunity and Ageing</i> , 2022, 19, 12.	4.2	23
7	Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. <i>Nature Medicine</i> , 2022, 28, 1476-1485.	30.7	24
8	Understanding SabiÃ¡ virus infections (Brazilian mammarenavirus). <i>Travel Medicine and Infectious Disease</i> , 2022, 48, 102351.	3.0	7
9	Clearance of Persistent SARS-CoV-2 RNA Detection in a NFÎ²B-Deficient Patient in Association with the Ingestion of Human Breast Milk: A Case Report. <i>Viruses</i> , 2022, 14, 1042.	3.3	1
10	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017â€“2019. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010255.	3.0	9
11	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , 2021, 73, e2436-e2443.	5.8	40
12	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021, 371, 288-292.	12.6	412
13	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 1608-1613.	8.9	79
14	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
15	Relax, Keep Walking â€” A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	8.9	31
16	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet, The</i> , 2021, 397, 452-455.	13.7	720
17	Early Transmission Dynamics, Spread, and Genomic Characterization of SARS-CoV-2 in Panama. <i>Emerging Infectious Diseases</i> , 2021, 27, 612-615.	4.3	24
18	Dataset on SARS-CoV-2 non-pharmaceutical interventions in Brazilian municipalities. <i>Scientific Data</i> , 2021, 8, 73.	5.3	29

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19	Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 970-972.	4.3	54
20	Higher risk of death from COVID-19 in low-income and non-White populations of São Paulo, Brazil. <i>BMJ Global Health</i> , 2021, 6, e004959.	4.7	55
21	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	12.6	1,125
22	Interacting Epidemics in Amazonian Brazil: Prior Dengue Infection Associated With Increased Coronavirus Disease 2019 (COVID-19) Risk in a Population-Based Cohort Study. <i>Clinical Infectious Diseases</i> , 2021, 73, 2045-2054.	5.8	18
23	Epidemic Spread of SARS-CoV-2 Lineage B.1.1.7 in Brazil. <i>Viruses</i> , 2021, 13, 984.	3.3	14
24	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	115
25	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021, 19, e3001236.	5.6	200
26	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051.	4.9	14
27	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104785.	2.3	5
28	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	12.6	142
29	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. <i>Wellcome Open Research</i> , 2021, 6, 121.	1.8	129
30	Altered demographic profile of hospitalizations during the second COVID-19 wave in Amazonas, Brazil. <i>The Lancet Regional Health Americas</i> , 2021, 2, 100064.	2.6	0
31	Neutralisation of SARS-CoV-2 lineage P.1 by antibodies elicited through natural SARS-CoV-2 infection or vaccination with an inactivated SARS-CoV-2 vaccine: an immunological study. <i>Lancet Microbe</i> , The, 2021, 2, e527-e535.	7.3	92
32	Paramyxoviruses from neotropical bats suggest a novel genus and nephrotropism. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105041.	2.3	10
33	SARS-CoV-2 reinfection caused by the P.1 lineage in Araraquara city, Sao Paulo State, Brazil. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2021, 63, e36.	1.1	37
34	Respiratory Viral Shedding in Healthcare Workers Reinfected with SARS-CoV-2, Brazil, 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 1737-1740.	4.3	16
35	Mortality risk of COVID-19 in elderly males with comorbidities: a multi-country study. <i>Aging</i> , 2021, 13, 27-60.	3.1	49
36	Clusters of SARS-CoV-2 Lineage B.1.1.7 Infection after Vaccination with Adenovirus-Vectored and Inactivated Vaccines. <i>Viruses</i> , 2021, 13, 2127.	3.3	6

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37	Track Omicron™s spread with molecular data. <i>Science</i> , 2021, 374, 1454-1455.	12.6	103
38	Return of the founder Chikungunya virus to its place of introduction into Brazil is revealed by genomic characterization of exanthematic disease cases. <i>Emerging Microbes and Infections</i> , 2020, 9, 53-57.	6.5	11
39	Antibody seroconversion in asymptomatic and symptomatic patients infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). <i>Clinical and Translational Immunology</i> , 2020, 9, e1182.	3.8	65
40	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	4.7	39
41	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	12.6	454
42	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020, 4, 856-865.	12.0	281
43	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	3.0	17
44	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
45	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.	7.1	68
46	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	12.6	253
47	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , 2020, 27, .	3.0	119
48	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	12.6	2,168
49	First report of <i>Aedes albopictus</i> infected by Dengue and Zika virus in a rural outbreak in Brazil. <i>PLoS ONE</i> , 2020, 15, e0229847.	2.5	25
50	Genomic evidence of yellow fever virus in <i>Aedes scapularis</i> , southeastern Brazil, 2016. <i>Acta Tropica</i> , 2020, 205, 105390.	2.0	13
51	Characterisation of HIV-1 Molecular Epidemiology in Nigeria: Origin, Diversity, Demography and Geographic Spread. <i>Scientific Reports</i> , 2020, 10, 3468.	3.3	14
52	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
53	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	13.3	114
54	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , 2020, 15, e0226098.	2.5	7

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55	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020, 94, .	3.4	17
56	Pan-genomics of virus and its applications. , 2020, , 237-250.		0
57	Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2020, 115, e190423.	1.6	30
58	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2020, 62, e30.	1.1	80
59	Title is missing!. , 2020, 15, e0226098.		0
60	Title is missing!. , 2020, 15, e0226098.		0
61	Title is missing!. , 2020, 15, e0226098.		0
62	Title is missing!. , 2020, 15, e0226098.		0
63	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , 2019, 7, .	3.0	14
64	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016â€“2019. <i>Journal of Virology</i> , 2019, 94, .	3.4	62
65	A32â€fGenomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
66	A38â€fGenomic epidemiology quantifies gaps in Aedes-borne virus transmission in the Americas. <i>Virus Evolution</i> , 2019, 5, .	4.9	0
67	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases, The</i> , 2019, 19, 1138-1147.	9.1	63
68	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019, 14, e0217871.	2.5	31
69	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007231.	3.0	44
70	<sc>MVSE</sc>: An Râ€package that estimates a climateâ€driven mosquitoâ€borne viral suitability index. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1357-1370.	5.2	35
71	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 784-787.	4.3	36
72	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	3.0	75

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73	Past and future spread of the arbovirus vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> . <i>Nature Microbiology</i> , 2019, 4, 854-863.	13.3	699
74	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019, 9, 5151.	3.3	89
75	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019, 93, .	3.4	13
76	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , 2019, 220, 233-243.	4.0	23
77	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	4.7	37
78	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2019, 147, e34.	2.1	29
79	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 155-163.	1.1	7
80	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	28.9	56
81	Molecular epidemiology reveals the role of war in the spread of HIV in Ukraine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1051-1056.	7.1	65
82	Challenges in dengue research: A computational perspective. <i>Evolutionary Applications</i> , 2018, 11, 516-533.	3.1	22
83	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of LÄ¼beck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180991.	2.6	21
84	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , 2018, 23, 855-864.e7.	11.0	82
85	Opsoclonus-myoclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , 2018, 75, 11-14.	3.3	13
86	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	12.6	279
87	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	12.8	59
88	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018, 10, .	1.4	43
89	HIV-2, Phylogeographic Insights into the Origins and Epidemic History. , 2018, , 970-978.		0
90	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346

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91	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
92	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515
93	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.	12.0	898
94	Spread of yellow fever virus outbreak in Angola and the Democratic Republic of the Congo 2015-16: a modelling study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 330-338.	9.1	185
95	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017, 7, 15216.	3.3	40
96	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , 2017, 34, 2563-2571.	8.9	64
97	The evolution and molecular epidemiology of epidemic GII.17 noroviruses. <i>Virus Evolution</i> , 2017, 3, .	4.9	0
98	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017, 23, 1742-1744.	4.3	69
99	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005694.	3.0	86
100	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017, 6, .	6.0	80
101	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	4.3	45
102	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016, 22, 2104-2112.	4.3	33
103	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016, 8, 97.	8.2	182
104	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016, 41, 142-145.	2.3	24
105	HIV Maintains an Evolving and Dispersed Population in Multiple Tissues during Suppressive Combined Antiretroviral Therapy in Individuals with Cancer. <i>Journal of Virology</i> , 2016, 90, 8984-8993.	3.4	47
106	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	4.9	105
107	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , 2016, 214, 556-564.	4.0	61
108	Phylodynamics of influenza A(H3N2) in South America, 1999-2012. <i>Infection, Genetics and Evolution</i> , 2016, 43, 312-320.	2.3	3

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109	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016, 32, 3204-3206.	4.1	124
110	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	12.6	877
111	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016, 8, .	1.4	64
112	Dispersion of the HIV-1 Epidemic in Men Who Have Sex with Men in the Netherlands: A Combined Mathematical Model and Phylogenetic Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001898.	8.4	69
113	Longitudinal Genetic Characterization Reveals That Cell Proliferation Maintains a Persistent HIV Type 1 DNA Pool During Effective HIV Therapy. <i>Journal of Infectious Diseases</i> , 2015, 212, 596-607.	4.0	138
114	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	2.0	90
115	Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , 2015, 13, 102.	5.5	369
116	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015, 63, 38-41.	3.1	7
117	Air Travel Is Associated with Intracontinental Spread of Dengue Virus Serotypes 1&2 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2769.	3.0	91
118	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	4.7	330
119	HIV Type 1 Transmission Networks Among Men Having Sex with Men and Heterosexuals in Kenya. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 118-126.	1.1	34
120	The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014, 346, 56-61.	12.6	515
121	Phylogeography of foot-and-mouth disease virus serotype O in Ecuador. <i>Infection, Genetics and Evolution</i> , 2013, 13, 76-88.	2.3	10
122	The HIV-1 reservoir in eight patients on long-term suppressive antiretroviral therapy is stable with few genetic changes over time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4987-96.	7.1	260
123	Improving Bayesian Population Dynamics Inference: A Coalescent-Based Model for Multiple Loci. <i>Molecular Biology and Evolution</i> , 2013, 30, 713-724.	8.9	449
124	Automated subtyping of HIV-1 genetic sequences for clinical and surveillance purposes: Performance evaluation of the new REGA version 3 and seven other tools. <i>Infection, Genetics and Evolution</i> , 2013, 19, 337-348.	2.3	313
125	Single Cell Analysis of Lymph Node Tissue from HIV-1 Infected Patients Reveals that the Majority of CD4+ T-cells Contain One HIV-1 DNA Molecule. <i>PLoS Pathogens</i> , 2013, 9, e1003432.	4.7	110
126	Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120196.	4.0	141



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127	Phylogeographic Insights into the Origins and Epidemic History of the Human Immunodeficiency Virus Type 2. , 2013, , 1-9.		0
128	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. Journal of General Virology, 2012, 93, 889-899.	2.9	56
129	Phylogeography of Dengue Virus Serotype 4, Brazil, 2010â€“2011. Emerging Infectious Diseases, 2012, 18, 1858-1864.	4.3	68
130	Phylodynamics of the HIV-1 CRF02_AG clade in Cameroon. Infection, Genetics and Evolution, 2012, 12, 453-460.	2.3	52
131	Toward a quantitative understanding of viral phylogeography. Current Opinion in Virology, 2011, 1, 423-429.	5.4	74
132	A Sensitive Assay for Virus Discovery in Respiratory Clinical Samples. PLoS ONE, 2011, 6, e16118.	2.5	80
133	Rooting human parechovirus evolution in time. BMC Evolutionary Biology, 2009, 9, 164.	3.2	36
134	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. Wellcome Open Research, 0, 6, 241.	1.8	10