

# Nuno Rodrigues Faria

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/1839622/nuno-rodrigues-faria-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

154  
papers

11,374  
citations

48  
h-index

105  
g-index

182  
ext. papers

15,564  
ext. citations

12.7  
avg, IF

6.25  
L-index

#	Paper	IF	Citations
154	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> , <b>2022</b> , 16, e0010019	4.8	0
153	Reinfection by the SARS-CoV-2 Gamma variant in blood donors in Manaus, Brazil.. <i>BMC Infectious Diseases</i> , <b>2022</b> , 22, 127	4	5
152	Association between inflammatory cytokines and anti-SARS-CoV-2 antibodies in hospitalized patients with COVID-19.. <i>Immunity and Ageing</i> , <b>2022</b> , 19, 12	9.7	2
151	Understanding Sabiá virus infections (Brazilian mammarenavirus).. <i>Travel Medicine and Infectious Disease</i> , <b>2022</b> , 48, 102351	8.4	1
150	Clearance of Persistent SARS-CoV-2 RNA Detection in a NFB-Deficient Patient in Association with the Ingestion of Human Breast Milk: A Case Report. <i>Viruses</i> , <b>2022</b> , 14, 1042	6.2	0
149	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017-2019.. <i>PLoS Neglected Tropical Diseases</i> , <b>2022</b> , 16, e0010255	4.8	1
148	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. <b>2021</b> ,		3
147	Track Omicron <sup>®</sup> spread with molecular data. <i>Science</i> , <b>2021</b> , 374, eabn4543	33.3	44
146	Report 46: Factors driving extensive spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals <b>2021</b> ,		3
145	Clusters of SARS-CoV-2 Lineage B.1.1.7 Infection after Vaccination with Adenovirus-Vectored and Inactivated Vaccines. <i>Viruses</i> , <b>2021</b> , 13,	6.2	1
144	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 73, e2436-e2443	41.6	10
143	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil <b>2021</b> ,		53
142	Dataset on SARS-CoV-2 non-pharmaceutical interventions in Brazilian municipalities. <i>Scientific Data</i> , <b>2021</b> , 8, 73	8.2	16
141	Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 970-972	10.2	39
140	Higher risk of death from COVID-19 in low-income and non-White populations of São Paulo, Brazil. <i>BMJ Global Health</i> , <b>2021</b> , 6,	6.6	15
139	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , <b>2021</b> , 372, 815-821	33.3	603
138	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> , <b>2021</b> , 73, 2045-2054	11.6	6

137	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , <b>2021</b> , 6, 121	4.8	46
136	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , <b>2021</b> , 19, e3001236	9.7	85
135	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , <b>2021</b> , 7, veab051.7	3.7	4
134	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , <b>2021</b> , 91, 104785	4.5	4
133	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , <b>2021</b> , 373, 889-895	33.3	41
132	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , <b>2021</b> , 371, 288-292	33.3	265
131	A Phylodynamic Workflow to Rapidly Gain Insights into the Dispersal History and Dynamics of SARS-CoV-2 Lineages. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 1608-1613	8.3	36
130	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , <b>2021</b> , 371, 708-712	33.3	159
129	PCR assay to enhance global surveillance for SARS-CoV-2 variants of concern <b>2021</b> ,		15
128	Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 3486-3493	8.3	4
127	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet, The</i> , <b>2021</b> , 397, 452-455	40	481
126	Early Transmission Dynamics, Spread, and Genomic Characterization of SARS-CoV-2 in Panama. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 612-615	10.2	13
125	Global disparities in SARS-CoV-2 genomic surveillance <b>2021</b> ,		26
124	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> , <b>2021</b> , 6, 121	4.8	50
123	Understanding the Potential Impact of Different Drug Properties On SARS-CoV-2 Transmission and Disease Burden: A Modelling Analysis. <i>Clinical Infectious Diseases</i> , <b>2021</b> ,	11.6	6
122	Altered demographic profile of hospitalizations during the second COVID-19 wave in Amazonas, Brazil. <i>The Lancet Regional Health Americas</i> , <b>2021</b> , 2, 100064		
121	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, The</i> , <b>2021</b> , 2, e527-e535	22.2	38
120	Paramyxoviruses from neotropical bats suggest a novel genus and nephrotropism. <i>Infection, Genetics and Evolution</i> , <b>2021</b> , 95, 105041	4.5	0

119	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> , <b>2021</b> , 63, e36	2.2	18
118	Respiratory Viral Shedding in Healthcare Workers Reinfected with SARS-CoV-2, Brazil, 2020. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 1737-1740	10.2	10
117	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , <b>2020</b> , 181, 997-1003.e9	56.2	175
116	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> , <b>2020</b> , 117, 12522-12523	11.5	46
115	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , <b>2020</b> , 369, 582-587	33.3	162
114	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , <b>2020</b> , 27,	12.9	79
113	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , <b>2020</b> , 368, 493-497	33.3	1373
112	First report of Aedes albopictus infected by Dengue and Zika virus in a rural outbreak in Brazil. <i>PLoS ONE</i> , <b>2020</b> , 15, e0229847	3.7	12
111	Genomic evidence of yellow fever virus in Aedes scapularis, southeastern Brazil, 2016. <i>Acta Tropica</i> , <b>2020</b> , 205, 105390	3.2	6
110	Characterisation of HIV-1 Molecular Epidemiology in Nigeria: Origin, Diversity, Demography and Geographic Spread. <i>Scientific Reports</i> , <b>2020</b> , 10, 3468	4.9	7
109	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , <b>2020</b> , 30, 2275-2283.e7	10.6	24
108	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , <b>2020</b> , 5, 443-454	26.6	64
107	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , <b>2020</b> , 15, e0226098	3.7	3
106	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	5
105	Pan-genomics of virus and its applications <b>2020</b> , 237-250		
104	Genomic detection of a virus lineage replacement event of dengue virus serotype 2 in Brazil, 2019. <i>Memorias Do Instituto Oswaldo Cruz</i> , <b>2020</b> , 115, e190423	2.6	10
103	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , <b>2020</b> , 62, e30	2.2	50
102	Mortality risk of COVID-19 in elderly males with comorbidities: a multi-country study. <i>Aging</i> , <b>2020</b> , 13, 27-60	5.6	24

101	The effect of human mobility and control measures on the COVID-19 epidemic in China <b>2020</b> ,		26
100	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> , <b>2020</b> , 9, 53-57	18.9	7
99	Antibody seroconversion in asymptomatic and symptomatic patients infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). <i>Clinical and Translational Immunology</i> , <b>2020</b> , 9, e1182	6.8	42
98	Genomic Surveillance of Yellow Fever Virus Epizootic in S̃o Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008699	7.6	18
97	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , <b>2020</b> , 369, 1255-1260	33.3	277
96	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , <b>2020</b> , 4, 856-865	12.8	151
95	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , <b>2020</b> , 14, e0008405	4.8	6
94	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil <b>2020</b> , 15, e0226098		
93	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil <b>2020</b> , 15, e0226098		
92	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil <b>2020</b> , 15, e0226098		
91	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil <b>2020</b> , 15, e0226098		
90	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , <b>2019</b> , 19, 1138-1147	25.5	40
89	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , <b>2019</b> , 14, e0217871	3.7	16
88	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007231	4.8	17
87	MVSE: An R-package that estimates a climate-driven mosquito-borne viral suitability index. <i>Methods in Ecology and Evolution</i> , <b>2019</b> , 10, 1357-1370	7.7	16
86	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , <b>2019</b> , 25, 784-787	10.2	17
85	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , <b>2019</b> , 13, e0007065	4.8	37
84	Past and future spread of the arbovirus vectors <i>Aedes aegypti</i> and <i>Aedes albopictus</i> . <i>Nature Microbiology</i> , <b>2019</b> , 4, 854-863	26.6	319

83	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , <b>2019</b> , 9, 5151	4.9	55
82	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , <b>2019</b> , 93,	6.6	6
81	Tracing the Impact of Public Health Interventions on HIV-1 Transmission in Portugal Using Molecular Epidemiology. <i>Journal of Infectious Diseases</i> , <b>2019</b> , 220, 233-243	7	11
80	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , <b>2019</b> , 7,	8.9	9
79	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016-2019. <i>Journal of Virology</i> , <b>2019</b> , 94,	6.6	29
78	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.7	78
77	A38 Genomic epidemiology quantifies gaps in Aedes-borne virus transmission in the Americas. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.7	78
76	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007976	7.6	25
75	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , <b>2019</b> , 35, 155-163	1.6	0
74	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , <b>2018</b> , 172, 1160-1162	56.2	39
73	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> , <b>2018</b> , 115, 1051-1056	11.5	32
72	Challenges in dengue research: A computational perspective. <i>Evolutionary Applications</i> , <b>2018</b> , 11, 516-533	3.8	15
71	Opsoclonus-myooclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , <b>2018</b> , 75, 11-14	10.5	5
70	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , <b>2018</b> , 361, 894-899	33.3	184
69	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , <b>2018</b> , 9, 2222	17.4	39
68	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , <b>2018</b> , 10,		29
67	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , <b>2018</b> , 147, e34	4.3	22
66	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of LBeck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2018</b> , 285,	4.4	13

65	Genomic Epidemiology Reconstructs the Introduction and Spread of Zika Virus in Central America and Mexico. <i>Cell Host and Microbe</i> , <b>2018</b> , 23, 855-864.e7	23.4	60
64	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , <b>2017</b> , 544, 309-315	50.4	238
63	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , <b>2017</b> , 546, 401-405	50.4	235
62	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , <b>2017</b> , 546, 406-410	50.4	366
61	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , <b>2017</b> , 12, 1261-1276	18.8	529
60	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> , <b>2017</b> , 17, 330-338	25.5	140
59	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , <b>2017</b> , 7, 15216	4.9	33
58	Using Viral Gene Sequences to Compare and Explain the Heterogeneous Spatial Dynamics of Virus Epidemics. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2563-2571	8.3	39
57	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , <b>2017</b> , 23, 1742-1744	10.2	51
56	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , <b>2017</b> , 11, e0005694	4.8	57
55	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , <b>2017</b> , 6,	8.9	55
54	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , <b>2016</b> , 2, vew016	3.7	89
53	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , <b>2016</b> , 214, 556-64	7	50
52	Phylogenetics of influenza A(H3N2) in South America, 1999-2012. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 43, 312-20	4.5	3
51	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , <b>2016</b> , 32, 3204-3206	7.2	73
50	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , <b>2016</b> , 352, 345-349	33.3	703
49	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , <b>2016</b> , 8,		48
48	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 1788-92	10.2	35

47	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , <b>2016</b> , 22, 2104-2112	10.2	22
46	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , <b>2016</b> , 8, 97	14.4	130
45	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , <b>2016</b> , 41, 142-145	4.5	20
44	HIV Maintains an Evolving and Dispersed Population in Multiple Tissues during Suppressive Combined Antiretroviral Therapy in Individuals with Cancer. <i>Journal of Virology</i> , <b>2016</b> , 90, 8984-93	6.6	32
43	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> , <b>2015</b> , 212, 596-607	7	107
42	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , <b>2015</b> , 12, 18	3.6	67
41	Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , <b>2015</b> , 13, 102	11.4	266
40	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , <b>2015</b> , 63, 38-41	14.5	4
39	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> , <b>2015</b> , 12, e1001898; discussion e1001898	11.6	45
38	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , <b>2014</b> , 346, 56-61	33.3	370
37	Air travel is associated with intracontinental spread of dengue virus serotypes 1-3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , <b>2014</b> , 8, e2769	4.8	67
36	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1003932	7.6	230
35	HIV Type 1 transmission networks among men having sex with men and heterosexuals in Kenya. <i>AIDS Research and Human Retroviruses</i> , <b>2014</b> , 30, 118-26	1.6	31
34	Phylogeography of foot-and-mouth disease virus serotype O in Ecuador. <i>Infection, Genetics and Evolution</i> , <b>2013</b> , 13, 76-88	4.5	9
33	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> , <b>2013</b> , 110, E4987-96	11.5	198
32	Improving Bayesian population dynamics inference: a coalescent-based model for multiple loci. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 713-24	8.3	312
31	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> , <b>2013</b> , 19, 337-48	4.5	229
30	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> , <b>2013</b> , 9, e1003432	7.6	84



29	Simultaneously reconstructing viral cross-species transmission history and identifying the underlying constraints. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2013</b> , 368, 20120196	5.8	101
28	Phylogenetics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , <b>2012</b> , 12, 453-60	4.5	45
27	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. <i>Journal of General Virology</i> , <b>2012</b> , 93, 889-899	4.9	46
26	Phylogeography of dengue virus serotype 4, Brazil, 2010-2011. <i>Emerging Infectious Diseases</i> , <b>2012</b> , 18, 1858-64	10.2	60
25	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , <b>2011</b> , 1, 423-97.5		56
24	A sensitive assay for virus discovery in respiratory clinical samples. <i>PLoS ONE</i> , <b>2011</b> , 6, e16118	3.7	72
23	Rooting human parechovirus evolution in time. <i>BMC Evolutionary Biology</i> , <b>2009</b> , 9, 164	3	29
22	MVSE: an R-package that estimates a climate-driven mosquito-borne viral suitability index		1
21	Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China		6
20	Routes for COVID-19 importation in Brazil		5
19	Epidemiological and clinical characteristics of the early phase of the COVID-19 epidemic in Brazil		6
18	Monitoring social distancing and SARS-CoV-2 transmission in Brazil using cell phone mobility data		8
17	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16
16	Subnational analysis of the COVID-19 epidemic in Brazil		12
15	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
14	Early transmission dynamics, spread, and genomic characterization of SARS-CoV-2 in Panama		3
13	COVID-19 herd immunity in the Brazilian Amazon		15
12	Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK		9

11	Social and racial inequalities in COVID-19 risk of hospitalisation and death across S̃ Paulo state, Brazil	1
10	Genomic and epidemiological monitoring of yellow fever virus transmission potential	3
9	Emergence of the Zika virus Asian lineage in Angola	1
8	Genomic Surveillance of Yellow Fever Virus Epizootic in S̃ Paulo, Brazil, 2016–2018	4
7	The evolutionary dynamics of Oropouche Virus (OROV) in South America	1
6	Yellow fever virus spread in Rio de Janeiro and Esp̃ito Santo, 2016-2019: Phylodynamic assessment to improve intervention strategies	1
5	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak	1
4	Reinfection by the SARS-CoV-2 Gamma variant in blood donors in Manaus, Brazil	5
3	SARS-CoV-2 shedding, infectivity and evolution in an immunocompromised adult patient	2
2	Understanding the Potential Impact of Different Drug Properties On SARS-CoV-2 Transmission and Disease Burden: A Modelling Analysis	2
1	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> ,6, 241	4.8 2