

Nuno Rodrigues Faria

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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	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020 , 368, 493-497	33.3	1373
153	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016 , 352, 345-349	33.3	703
152	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021 , 372, 815-821	33.3	603
151	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	18.8	529
150	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet, The</i> , 2021 , 397, 452-455	40	481
149	HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014 , 346, 56-61	33.3	370
148	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017 , 546, 406-410	50.4	366
147	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	26.6	319
146	Improving Bayesian population dynamics inference: a coalescent-based model for multiple loci. <i>Molecular Biology and Evolution</i> , 2013 , 30, 713-24	8.3	312
145	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020 , 369, 1255-1260	33.3	277
144	Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , 2015 , 13, 102	11.4	266
143	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021 , 371, 288-292	33.3	265
142	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
141	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
140	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , 2014 , 10, e1003932	7.6	230
139	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, 337-48	4.5	229
138	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	11.5	198

137	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018 , 361, 894-899	33.3	184
136	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020 , 181, 997-1003.e9	56.2	175
135	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020 , 369, 582-587	33.3	162
134	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021 , 371, 708-712	33.3	159
133	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020 , 4, 856-865	12.8	151
132	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> , 2017 , 17, 330-338	25.5	140
131	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016 , 8, 97	14.4	130
130	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	7	107
129	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	5.8	101
128	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016 , 2, vew016	3.7	89
127	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021 , 19, e3001236	9.7	85
126	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	7.6	84
125	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , 2020 , 27,	12.9	79
124	A32 Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
123	A38 Genomic epidemiology quantifies gaps in Aedes-borne virus transmission in the Americas. <i>Virus Evolution</i> , 2019 , 5,	3.7	78
122	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016 , 32, 3204-3206	7.2	73
121	A sensitive assay for virus discovery in respiratory clinical samples. <i>PLoS ONE</i> , 2011 , 6, e16118	3.7	72
120	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015 , 12, 18	3.6	67

119	Air travel is associated with intracontinental spread of dengue virus serotypes 1-3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e2769	4.8	67
118	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020 , 5, 443-454	26.6	64
117	Phylogeography of dengue virus serotype 4, Brazil, 2010-2011. <i>Emerging Infectious Diseases</i> , 2012 , 18, 1858-64	10.2	60
116	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	23.4	60
115	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005694	4.8	57
114	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011 , 1, 423-97.5		56
113	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019 , 9, 5151	4.9	55
112	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017 , 6,	8.9	55
111	Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil 2021 ,		53
110	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1742-1744	10.2	51
109	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , 2016 , 214, 556-64	7	50
108	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	2.2	50
107	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	4.8	50
106	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016 , 8,		48
105	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	11.5	46
104	Phylogeographical footprint of colonial history in the global dispersal of human immunodeficiency virus type 2 group A. <i>Journal of General Virology</i> , 2012 , 93, 889-899	4.9	46
103	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	4.8	46
102	Phylodynamics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 453-60	4.5	45

101	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; discussion e1001898	11.6	45
100	Track Omicron [®] spread with molecular data. <i>Science</i> , 2021 , 374, eabn4543	33.3	44
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> , 2020 , 9, e1182	6.8	42
98	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021 , 373, 889-895	33.3	41
97	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , 2019 , 19, 1138-1147	25.5	40
96	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018 , 172, 1160-1162	56.2	39
95	Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018 , 9, 2222	17.4	39
94	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	8.3	39
93	Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , 2021 , 27, 970-972	10.2	39
92	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> , 2021 , 2, e527-e535	22.2	38
91	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007065	4.8	37
90	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	8.3	36
89	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1788-92	10.2	35
88	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017 , 7, 15216	4.9	33
87	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	11.5	32
86	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, 8984-93	6.6	32
85	HIV Type 1 transmission networks among men having sex with men and heterosexuals in Kenya. <i>AIDS Research and Human Retroviruses</i> , 2014 , 30, 118-26	1.6	31
84	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016-2019. <i>Journal of Virology</i> , 2019 , 94,	6.6	29

83	Rooting human parechovirus evolution in time. <i>BMC Evolutionary Biology</i> , 2009 , 9, 164	3	29
82	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018 , 10,		29
81	The effect of human mobility and control measures on the COVID-19 epidemic in China 2020 ,		26
80	Global disparities in SARS-CoV-2 genomic surveillance 2021 ,		26
79	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019 , 15, e1007976	7.6	25
78	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020 , 30, 2275-2283.e7	10.6	24
77	Mortality risk of COVID-19 in elderly males with comorbidities: a multi-country study. <i>Aging</i> , 2020 , 13, 27-60	5.6	24
76	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016 , 22, 2104-2112	10.2	22
75	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2018 , 147, e34	4.3	22
74	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016 , 41, 142-145	4.45	20
73	Genomic Surveillance of Yellow Fever Virus Epizootic in Sã Paulo, Brazil, 2016 - 2018. <i>PLoS Pathogens</i> , 2020 , 16, e1008699	7.6	18
72	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	2.2	18
71	A computational method for the identification of Dengue, Zika and Chikungunya virus species and genotypes. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007231	4.8	17
70	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019 , 25, 784-787	10.2	17
69	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019 , 14, e0217871	3.7	16
68	MVSE: An R-package that estimates a climate-driven mosquito-borne viral suitability index. <i>Methods in Ecology and Evolution</i> , 2019 , 10, 1357-1370	7.7	16
67	A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages		16
66	Dataset on SARS-CoV-2 non-pharmaceutical interventions in Brazilian municipalities. <i>Scientific Data</i> , 2021 , 8, 73	8.2	16

65	Challenges in dengue research: A computational perspective. <i>Evolutionary Applications</i> , 2018 , 11, 516-532	3.8	15
64	COVID-19 herd immunity in the Brazilian Amazon		15
63	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,	6.6	15
62	PCR assay to enhance global surveillance for SARS-CoV-2 variants of concern 2021 ,		15
61	Early Transmission Dynamics, Spread, and Genomic Characterization of SARS-CoV-2 in Panama. <i>Emerging Infectious Diseases</i> , 2021 , 27, 612-615	10.2	13
60	Molecular archaeoparasitology identifies cultural changes in the Medieval Hanseatic trading centre of Lübeck. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018 , 285,	4.4	13
59	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	3.7	12
58	Subnational analysis of the COVID-19 epidemic in Brazil		12
57	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	7	11
56	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	2.6	10
55	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , 2021 , 73, e2436-e2443	4.6	10
54	Respiratory Viral Shedding in Healthcare Workers Reinfected with SARS-CoV-2, Brazil, 2020. <i>Emerging Infectious Diseases</i> , 2021 , 27, 1737-1740	10.2	10
53	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , 2019 , 7,	8.9	9
52	Phylogeography of foot-and-mouth disease virus serotype O in Ecuador. <i>Infection, Genetics and Evolution</i> , 2013 , 13, 76-88	4.5	9
51	Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK		9
50	Monitoring social distancing and SARS-CoV-2 transmission in Brazil using cell phone mobility data		8
49	Characterisation of HIV-1 Molecular Epidemiology in Nigeria: Origin, Diversity, Demography and Geographic Spread. <i>Scientific Reports</i> , 2020 , 10, 3468	4.9	7
48	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	18.9	7

47	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019 , 93,	6.6	6
46	Genomic evidence of yellow fever virus in <i>Aedes scapularis</i> , southeastern Brazil, 2016. <i>Acta Tropica</i> , 2020 , 205, 105390	3.2	6
45	Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China		6
44	Epidemiological and clinical characteristics of the early phase of the COVID-19 epidemic in Brazil		6
43	Evolution and epidemic spread of SARS-CoV-2 in Brazil		6
42	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008405	4.8	6
41	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	11.6	6
40	Understanding the Potential Impact of Different Drug Properties On SARS-CoV-2 Transmission and Disease Burden: A Modelling Analysis. <i>Clinical Infectious Diseases</i> , 2021 ,	11.6	6
39	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020 , 94,	6.6	5
38	Opsoclonus-myooclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , 2018 , 75, 11-14	10.5	5
37	Reinfection by the SARS-CoV-2 Gamma variant in blood donors in Manaus, Brazil.. <i>BMC Infectious Diseases</i> , 2022 , 22, 127	4	5
36	Routes for COVID-19 importation in Brazil		5
35	Reinfection by the SARS-CoV-2 Gamma variant in blood donors in Manaus, Brazil		5
34	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015 , 63, 38-41	14.5	4
33	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016-2018		4
32	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021 , 7, veab053.7	3.7	4
31	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , 2021 , 91, 104785	4.5	4
30	Relax, Keep Walking - A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3486-3493	8.3	4

29	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , 2020 , 15, e0226098	3.7	3
28	Phylogenetics of influenza A(H3N2) in South America, 1999-2012. <i>Infection, Genetics and Evolution</i> , 2016 , 43, 312-20	4.5	3
27	Context-specific emergence and growth of the SARS-CoV-2 Delta variant. 2021 ,		3
26	Report 46: Factors driving extensive spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals 2021 ,		3
25	Early transmission dynamics, spread, and genomic characterization of SARS-CoV-2 in Panama		3
24	Genomic and epidemiological monitoring of yellow fever virus transmission potential		3
23	SARS-CoV-2 shedding, infectivity and evolution in an immunocompromised adult patient		2
22	Understanding the Potential Impact of Different Drug Properties On SARS-CoV-2 Transmission and Disease Burden: A Modelling Analysis		2
21	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> , 6 , 241	4.8	2
20	Association between inflammatory cytokines and anti-SARS-CoV-2 antibodies in hospitalized patients with COVID-19.. <i>Immunity and Ageing</i> , 2022 , 19, 12	9.7	2
19	Clusters of SARS-CoV-2 Lineage B.1.1.7 Infection after Vaccination with Adenovirus-Vectored and Inactivated Vaccines. <i>Viruses</i> , 2021 , 13,	6.2	1
18	MVSE: an R-package that estimates a climate-driven mosquito-borne viral suitability index		1
17	Social and racial inequalities in COVID-19 risk of hospitalisation and death across Sã Paulo state, Brazil		1
16	Emergence of the Zika virus Asian lineage in Angola		1
15	The evolutionary dynamics of Oropouche Virus (OROV) in South America		1
14	Yellow fever virus spread in Rio de Janeiro and Espıto Santo, 2016-2019: Phylogenetic assessment to improve intervention strategies		1
13	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak		1
12	Understanding Sabıvirus infections (Brazilian mammarenavirus).. <i>Travel Medicine and Infectious Disease</i> , 2022 , 48, 102351	8.4	1

11	Molecular and genomic investigation of an urban outbreak of dengue virus serotype 2 in Angola, 2017-2019.. <i>PLoS Neglected Tropical Diseases</i> , 2022 , 16, e0010255	4.8	1
10	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	4.8	0
9	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , 2019 , 35, 155-163	1.6	0
8	Paramyxoviruses from neotropical bats suggest a novel genus and nephrotropism. <i>Infection, Genetics and Evolution</i> , 2021 , 95, 105041	4.5	0
7	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> , 2022 , 14, 1042	6.2	0
6	Pan-genomics of virus and its applications 2020 , 237-250		
5	Altered demographic profile of hospitalizations during the second COVID-19 wave in Amazonas, Brazil. <i>The Lancet Regional Health Americas</i> , 2021 , 2, 100064		
4	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
3	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
2	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil 2020 , 15, e0226098		
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