

Nuno Rodrigues Faria

List of Publications by Year in descending order

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Version: 2024-02-01

134
papers

17,863
citations

30047

54
h-index

18633

119
g-index

182
all docs

182
docs citations

182
times ranked

24954
citing authors

#	ARTICLE	IF	CITATIONS
1	The effect of human mobility and control measures on the COVID-19 epidemic in China. <i>Science</i> , 2020, 368, 493-497.	6.0	2,168
2	Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. <i>Science</i> , 2021, 372, 815-821.	6.0	1,125
3	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.	5.5	898
4	Zika virus in the Americas: Early epidemiological and genetic findings. <i>Science</i> , 2016, 352, 345-349.	6.0	877
5	Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. <i>Lancet</i> , The, 2021, 397, 452-455.	6.3	720
6	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.	5.9	699
7	The early spread and epidemic ignition of HIV-1 in human populations. <i>Science</i> , 2014, 346, 56-61.	6.0	515
8	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	13.7	515
9	Evolution and epidemic spread of SARS-CoV-2 in Brazil. <i>Science</i> , 2020, 369, 1255-1260.	6.0	454
10	Improving Bayesian Population Dynamics Inference: A Coalescent-Based Model for Multiple Loci. <i>Molecular Biology and Evolution</i> , 2013, 30, 713-724.	3.5	449
11	Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic. <i>Science</i> , 2021, 371, 288-292.	6.0	412
12	Emergence and potential for spread of Chikungunya virus in Brazil. <i>BMC Medicine</i> , 2015, 13, 102.	2.3	369
13	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
14	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	6.0	335
15	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	2.1	330
16	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.	1.0	313
17	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
18	Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil. <i>Nature Human Behaviour</i> , 2020, 4, 856-865.	6.2	281

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19	Genomic and epidemiological monitoring of yellow fever virus transmission potential. <i>Science</i> , 2018, 361, 894-899.	6.0	279
20	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.	3.3	260
21	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	6.0	253
22	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	13.5	236
23	Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. <i>PLoS Biology</i> , 2021, 19, e3001236.	2.6	200
24	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.	4.6	185
25	Mobile real-time surveillance of Zika virus in Brazil. <i>Genome Medicine</i> , 2016, 8, 97.	3.6	182
26	Spatiotemporal invasion dynamics of SARS-CoV-2 lineage B.1.1.7 emergence. <i>Science</i> , 2021, 373, 889-895.	6.0	142
27	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.	1.8	141
28	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.	1.9	138
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.	0.9	129
30	SERAPHIM: studying environmental rasters and phylogenetically informed movements. <i>Bioinformatics</i> , 2016, 32, 3204-3206.	1.8	124
31	Routes for COVID-19 importation in Brazil. <i>Journal of Travel Medicine</i> , 2020, 27, .	1.4	119
32	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.	0.9	115
33	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	5.9	114
34	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.	2.1	110
35	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , 2016, 2, vew016.	2.2	105
36	Track Omicron™s spread with molecular data. <i>Science</i> , 2021, 374, 1454-1455.	6.0	103

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37	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.	3.4	92
38	Air Travel Is Associated with Intracontinental Spread of Dengue Virus Serotypes 1â€“3 in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2769.	1.3	91
39	An integrated map of HIV genome-wide variation from a population perspective. <i>Retrovirology</i> , 2015, 12, 18.	0.9	90
40	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. <i>Scientific Reports</i> , 2019, 9, 5151.	1.6	89
41	Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005694.	1.3	86
42	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.	5.1	82
43	A Sensitive Assay for Virus Discovery in Respiratory Clinical Samples. <i>PLoS ONE</i> , 2011, 6, e16118.	1.1	80
44	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.	0.5	80
45	Epidemiological and ecological determinants of Zika virus transmission in an urban setting. <i>ELife</i> , 2017, 6, .	2.8	80
46	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.	3.5	79
47	Genomic, epidemiological and digital surveillance of Chikungunya virus in the Brazilian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007065.	1.3	75
48	Toward a quantitative understanding of viral phylogeography. <i>Current Opinion in Virology</i> , 2011, 1, 423-429.	2.6	74
49	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.	3.9	69
50	Spread of Chikungunya Virus East/Central/South African Genotype in Northeast Brazil. <i>Emerging Infectious Diseases</i> , 2017, 23, 1742-1744.	2.0	69
51	Phylogeography of Dengue Virus Serotype 4, Brazil, 2010â€“2011. <i>Emerging Infectious Diseases</i> , 2012, 18, 1858-1864.	2.0	68
52	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.	3.3	68
53	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.	3.3	65
54	Antibody seroconversion in asymptomatic and symptomatic patients infected with severe acute respiratory syndrome coronavirus 2 (SARSâ€“CoVâ€“2). <i>Clinical and Translational Immunology</i> , 2020, 9, e1182.	1.7	65

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55	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.	3.5	64
56	Epidemiology of Chikungunya Virus in Bahia, Brazil, 2014-2015. <i>PLOS Currents</i> , 2016, 8, .	1.4	64
57	Emergence of the Asian lineage of Zika virus in Angola: an outbreak investigation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1138-1147.	4.6	63
58	Yellow Fever Virus Reemergence and Spread in Southeast Brazil, 2016â€“2019. <i>Journal of Virology</i> , 2019, 94, .	1.5	62
59	The Evolution and Transmission of Epidemic GII.17 Noroviruses. <i>Journal of Infectious Diseases</i> , 2016, 214, 556-564.	1.9	61
60	Phylogenetic assessment of intervention strategies for the West African Ebola virus outbreak. <i>Nature Communications</i> , 2018, 9, 2222.	5.8	59
61	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.	1.3	56
62	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	13.5	56
63	Higher risk of death from COVID-19 in low-income and non-White populations of SÃ£o Paulo, Brazil. <i>BMJ Global Health</i> , 2021, 6, e004959.	2.0	55
64	Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 970-972.	2.0	54
65	Phylogenetics of the HIV-1 CRF02_AG clade in Cameroon. <i>Infection, Genetics and Evolution</i> , 2012, 12, 453-460.	1.0	52
66	Mortality risk of COVID-19 in elderly males with comorbidities: a multi-country study. <i>Aging</i> , 2021, 13, 27-60.	1.4	49
67	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.	1.5	47
68	Distinct Zika Virus Lineage in Salvador, Bahia, Brazil. <i>Emerging Infectious Diseases</i> , 2016, 22, 1788-1792.	2.0	45
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.	1.3	44
70	Epidemiology of the Zika Virus Outbreak in the Cabo Verde Islands, West Africa. <i>PLOS Currents</i> , 2018, 10, .	1.4	43
71	Genomic and epidemiological characterisation of a dengue virus outbreak among blood donors in Brazil. <i>Scientific Reports</i> , 2017, 7, 15216.	1.6	40
72	Fatal Outcome of Chikungunya Virus Infection in Brazil. <i>Clinical Infectious Diseases</i> , 2021, 73, e2436-e2443.	2.9	40

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73	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	2.1	39
74	Distinct rates and patterns of spread of the major HIV-1 subtypes in Central and East Africa. <i>PLoS Pathogens</i> , 2019, 15, e1007976.	2.1	37
75	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	2.9	37
76	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.	0.5	37
77	Rooting human parechovirus evolution in time. <i>BMC Evolutionary Biology</i> , 2009, 9, 164.	3.2	36
78	Early Genomic Detection of Cosmopolitan Genotype of Dengue Virus Serotype 2, Angola, 2018. <i>Emerging Infectious Diseases</i> , 2019, 25, 784-787.	2.0	36
79	<scp>MVSE</scp>: An R package that estimates a climate-driven mosquito-borne viral suitability index. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1357-1370.	2.2	35
80	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.	0.5	34
81	Effect of Live Poultry Market Interventions on Influenza A(H7N9) Virus, Guangdong, China. <i>Emerging Infectious Diseases</i> , 2016, 22, 2104-2112.	2.0	33
82	Circulation of chikungunya virus East/Central/South African lineage in Rio de Janeiro, Brazil. <i>PLoS ONE</i> , 2019, 14, e0217871.	1.1	31
83	Relax, Keep Walking – A Practical Guide to Continuous Phylogeographic Inference with BEAST. <i>Molecular Biology and Evolution</i> , 2021, 38, 3486-3493.	3.5	31
84	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.	0.8	30
85	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2019, 147, e34.	1.0	29
86	Dataset on SARS-CoV-2 non-pharmaceutical interventions in Brazilian municipalities. <i>Scientific Data</i> , 2021, 8, 73.	2.4	29
87	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.	1.1	25
88	Zika virus complete genome from Salvador, Bahia, Brazil. <i>Infection, Genetics and Evolution</i> , 2016, 41, 142-145.	1.0	24
89	Early Transmission Dynamics, Spread, and Genomic Characterization of SARS-CoV-2 in Panama. <i>Emerging Infectious Diseases</i> , 2021, 27, 612-615.	2.0	24
90	Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. <i>Nature Medicine</i> , 2022, 28, 1476-1485.	15.2	24

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91	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.	1.9	23
92	Association between inflammatory cytokines and anti-SARS-CoV-2 antibodies in hospitalized patients with COVID-19. <i>Immunity and Ageing</i> , 2022, 19, 12.	1.8	23
93	Challenges in dengue research: A computational perspective. <i>Evolutionary Applications</i> , 2018, 11, 516-533.	1.5	22
94	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, 20180991.	1.2	21
95	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.	1.3	19
96	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.	2.9	18
97	Yellow fever transmission in non-human primates, Bahia, Northeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008405.	1.3	17
98	Evolutionary Dynamics of Oropouche Virus in South America. <i>Journal of Virology</i> , 2020, 94, .	1.5	17
99	Epidemiology of COVID-19 after Emergence of SARS-CoV-2 Gamma Variant, Brazilian Amazon, 2020â€“2021. <i>Emerging Infectious Diseases</i> , 2022, 28, .	2.0	17
100	Respiratory Viral Shedding in Healthcare Workers Reinfected with SARS-CoV-2, Brazil, 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 1737-1740.	2.0	16
101	Reinfection by the SARS-CoV-2 Gamma variant in blood donors in Manaus, Brazil. <i>BMC Infectious Diseases</i> , 2022, 22, 127.	1.3	15
102	Acute Vector-Borne Viral Infection: Zika and MinION Surveillance. <i>Microbiology Spectrum</i> , 2019, 7, .	1.2	14
103	Characterisation of HIV-1 Molecular Epidemiology in Nigeria: Origin, Diversity, Demography and Geographic Spread. <i>Scientific Reports</i> , 2020, 10, 3468.	1.6	14
104	Epidemic Spread of SARS-CoV-2 Lineage B.1.1.7 in Brazil. <i>Viruses</i> , 2021, 13, 984.	1.5	14
105	Genomic epidemiology of SARS-CoV-2 transmission lineages in Ecuador. <i>Virus Evolution</i> , 2021, 7, veab051.	2.2	14
106	Opsoclonus-myoclonus-ataxia syndrome associated with chikungunya and dengue virus co-infection. <i>International Journal of Infectious Diseases</i> , 2018, 75, 11-14.	1.5	13
107	Reconstruction of the Genetic History and the Current Spread of HIV-1 Subtype A in Germany. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
108	Genomic evidence of yellow fever virus in <i>Aedes scapularis</i> , southeastern Brazil, 2016. <i>Acta Tropica</i> , 2020, 205, 105390.	0.9	13

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109	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.	3.0	11
110	Phylogeography of foot-and-mouth disease virus serotype O in Ecuador. <i>Infection, Genetics and Evolution</i> , 2013, 13, 76-88.	1.0	10
111	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> , 0, 6, 241.	0.9	10
112	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.	2.9	10
113	Paramyxoviruses from neotropical bats suggest a novel genus and nephrotropism. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105041.	1.0	10
114	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.	1.3	9
115	Epidemiological history and genomic characterization of non-D1 HBV strains identified in Iran. <i>Journal of Clinical Virology</i> , 2015, 63, 38-41.	1.6	7
116	The Changing Epidemiological Profile of HIV-1 Subtype B Epidemic in Ukraine. <i>AIDS Research and Human Retroviruses</i> , 2019, 35, 155-163.	0.5	7
117	Persistence of chikungunya ECSA genotype and local outbreak in an upper medium class neighborhood in Northeast Brazil. <i>PLoS ONE</i> , 2020, 15, e0226098.	1.1	7
118	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.	1.5	7
119	Understanding Sabiã virus infections (Brazilian mammarenavirus). <i>Travel Medicine and Infectious Disease</i> , 2022, 48, 102351.	1.5	7
120	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.	1.5	6
121	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104785.	1.0	5
122	Phylodynamics of influenza A(H3N2) in South America, 1999-2012. <i>Infection, Genetics and Evolution</i> , 2016, 43, 312-320.	1.0	3
123	Clearance of Persistent SARS-CoV-2 RNA Detection in a NF- κ B-Deficient Patient in Association with the Ingestion of Human Breast Milk: A Case Report. <i>Viruses</i> , 2022, 14, 1042.	1.5	1
124	The evolution and molecular epidemiology of epidemic GII.17 noroviruses. <i>Virus Evolution</i> , 2017, 3, .	2.2	0
125	Genomic surveillance of Zika virus transmission in the Amazonas State, Brazil. <i>Virus Evolution</i> , 2019, 5, .	2.2	0
126	Genomic epidemiology quantifies gaps in Aedes-borne virus transmission in the Americas. <i>Virus Evolution</i> , 2019, 5, .	2.2	0

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127	Pan-genomics of virus and its applications. , 2020, , 237-250.		0
128	Altered demographic profile of hospitalizations during the second COVID-19 wave in Amazonas, Brazil. The Lancet Regional Health Americas, 2021, 2, 100064.	1.5	0
129	Phylogeographic Insights into the Origins and Epidemic History of the Human Immunodeficiency Virus Type 2. , 2013, , 1-9.		0
130	HIV-2, Phylogeographic Insights into the Origins and Epidemic History. , 2018, , 970-978.		0
131	Title is missing!. , 2020, 15, e0226098.		0
132	Title is missing!. , 2020, 15, e0226098.		0
133	Title is missing!. , 2020, 15, e0226098.		0
134	Title is missing!. , 2020, 15, e0226098.		0