

# Genomic epidemiology reveals multiple introductions of

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	27.8	515
2	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	27.8	323
3	Molecular mapping of Zika spread. <i>Nature</i> , 2017, 546, 355-356.	27.8	16
4	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
5	Modeling mosquito-borne diseases in complex urban environments. <i>Acta Tropica</i> , 2017, 176, 332-334.	2.0	11
6	Evidence of increasing diversification of Zika virus strains isolated in the American continent. <i>Journal of Medical Virology</i> , 2017, 89, 2059-2063.	5.0	4
7	Infection via mosquito bite alters Zika virus tissue tropism and replication kinetics in rhesus macaques. <i>Nature Communications</i> , 2017, 8, 2096.	12.8	87
8	Zika virus evolution on the edges of the Pacific ocean. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-3.	6.5	16
9	Zika virus infection of first-trimester human placentas: utility of an explant model of replication to evaluate correlates of immune protection ex vivo. <i>Current Opinion in Virology</i> , 2017, 27, 48-56.	5.4	21
10	Impact of Zika virus for infertility specialists: current literature, guidelines, and resources. <i>Journal of Assisted Reproduction and Genetics</i> , 2017, 34, 1237-1250.	2.5	9
11	Simple visit behavior unifies complex Zika outbreaks. <i>Heliyon</i> , 2017, 3, e00482.	3.2	2
12	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.	3.0	48
13	Host outdoor exposure variability affects the transmission and spread of Zika virus: Insights for epidemic control. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005851.	3.0	34
14	Where vectors collide: the importance of mechanisms shaping the realized niche for modeling ranges of invasive <i>Aedes</i> mosquitoes. <i>Biological Invasions</i> , 2018, 20, 1913-1929.	2.4	44
15	Laboratory Evaluation of Commercially Available Platforms to Detect West Nile and Zika Viruses From Honey Cards. <i>Journal of Medical Entomology</i> , 2018, 55, 717-722.	1.8	8
16	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	28.9	56
17	Considering the Potential Application of Whole Genome Sequencing to Gonorrhea Prevention and Control. <i>Sexually Transmitted Diseases</i> , 2018, 45, e29-e32.	1.7	0
19	Accreditation's Role in Bolstering Resilience in the Face of the Zika Virus Outbreak. <i>Journal of Public Health Management and Practice</i> , 2018, 24, S92-S94.	1.4	3

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20	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. Nature Communications, 2018, 9, 1624.	12.8	68
21	Biochemistry and Molecular Biology of Flaviviruses. Chemical Reviews, 2018, 118, 4448-4482.	47.7	211
22	Performance of the Trioplex real-time RT-PCR assay for detection of Zika, dengue, and chikungunya viruses. Nature Communications, 2018, 9, 1391.	12.8	134
23	Zika Immunoassay Based on Surface-Enhanced Raman Scattering Nanoprobes. ACS Sensors, 2018, 3, 587-594.	7.8	57
24	What we know and what we don't know about perinatal Zika virus infection: a systematic review. Expert Review of Anti-Infective Therapy, 2018, 16, 243-254.	4.4	13
25	Efficacy of larvicides for the control of dengue, Zika, and chikungunya vectors in an urban cemetery in southern Mexico. Parasitology Research, 2018, 117, 1941-1952.	1.6	10
26	Field-deployable viral diagnostics using CRISPR-Cas13. Science, 2018, 360, 444-448.	12.6	982
27	Zika Virus Infection Preferentially Counterbalances Human Peripheral Monocyte and/or NK Cell Activity. MSphere, 2018, 3, .	2.9	32
28	Consensus and conflict among ecological forecasts of Zika virus outbreaks in the United States. Scientific Reports, 2018, 8, 4921.	3.3	50
29	Rapid response to an emerging infectious disease " Lessons learned from development of a synthetic DNA vaccine targeting Zika virus. Microbes and Infection, 2018, 20, 676-684.	1.9	25
30	Modeling neuro-immune interactions during Zika virus infection. Human Molecular Genetics, 2018, 27, 41-52.	2.9	50
31	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. Infection, Genetics and Evolution, 2018, 63, 295-306.	2.3	32
32	Disaster Preparedness: Biological Threats and Treatment Options. Pharmacotherapy, 2018, 38, 217-234.	2.6	30
33	Towards a genomics-informed, real-time, global pathogen surveillance system. Nature Reviews Genetics, 2018, 19, 9-20.	16.3	505
34	Screening for Zika virus in deceased organ donors in Florida. American Journal of Transplantation, 2018, 18, 731-736.	4.7	10
35	A Call to Introduce Structured Zika Surveillance in India. Trends in Parasitology, 2018, 34, 92-95.	3.3	3
36	Infectious Disease Threats and Opportunities for Prevention. Journal of Public Health Management and Practice, 2018, 24, 503-505.	1.4	4
37	Quantifying the risk of local Zika virus transmission in the contiguous US during the 2015-2016 ZIKV epidemic. BMC Medicine, 2018, 16, 195.	5.5	11

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38	Assessment of metagenomic Nanopore and Illumina sequencing for recovering whole genome sequences of chikungunya and dengue viruses directly from clinical samples. <i>Eurosurveillance</i> , 2018, 23, .	7.0	85
39	Simple protocol for population (Sanger) sequencing for Zika virus genomic regions. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, 38-44.	1.6	5
40	Construction sites in Miami-Dade County, Florida are highly favorable environments for vector mosquitoes. <i>PLoS ONE</i> , 2018, 13, e0209625.	2.5	12
41	The influence of phylodynamic model specifications on parameter estimates of the Zika virus epidemic. <i>Virus Evolution</i> , 2018, 4, vex044.	4.9	31
42	The Emergence of Chikungunya and Zika Viruses in the Americas. , 2018, , 215-235.		4
43	Whole genome sequencing, variant analysis, phylogenetics, and deep sequencing of Zika virus strains. <i>Scientific Reports</i> , 2018, 8, 15843.	3.3	20
44	Advanced surveillance and preparedness to meet a new era of invasive vectors and emerging vector-borne diseases. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006761.	3.0	11
45	Zika Virus MB16-23 in Mosquitoes, Miami-Dade County, Florida, USA, 2016. <i>Emerging Infectious Diseases</i> , 2018, 24, 808-810.	4.3	15
46	Gainâ€œfunction experiments with bacteriophage lambda uncover residues under diversifying selection in nature. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 2234-2243.	2.3	14
47	Evolutionary history and spatio-temporal dynamics of dengue virus serotypes in an endemic region of Colombia. <i>PLoS ONE</i> , 2018, 13, e0203090.	2.5	19
48	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
49	Private collection: high correlation of sample collection and patient admission date in clinical microbiological testing complicates sharing of phylodynamic metadata. <i>Virus Evolution</i> , 2018, 4, vey005.	4.9	8
50	Network Analysis as a Grand Unifier in Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 153-180.	6.5	32
51	Countering Zika Virus: The USAMRIID Response. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1062, 303-318.	1.6	3
52	MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018, 7, .	6.0	172
53	Establishment of <i>Aedes albopictus</i> (Diptera: Culicidae) in the Florida Keys, 2001â€œ2017. <i>Journal of Medical Entomology</i> , 2018, 55, 1607-1612.	1.8	5
54	The epidemiological characteristics and molecular phylogeny of the dengue virus in Guangdong, China, 2015. <i>Scientific Reports</i> , 2018, 8, 9976.	3.3	11
55	Identification of Wild Boarâ€œHabitat Epidemiologic Cycle in African Swine Fever Epizootic. <i>Emerging Infectious Diseases</i> , 2018, 24, 810-812.	4.3	110

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56	Managing <i>Aedes aegypti</i> populations in the first Zika transmission zones in the continental United States. <i>Acta Tropica</i> , 2018, 187, 108-118.	2.0	28
57	Untold stories of the Zika virus epidemic in Brazil. <i>Reviews in Medical Virology</i> , 2018, 28, e2000.	8.3	4
58	Monitoring and redirecting virus evolution. <i>PLoS Pathogens</i> , 2018, 14, e1006979.	4.7	13
59	Modeling the importation and local transmission of vector-borne diseases in Florida: The case of Zika outbreak in 2016. <i>Journal of Theoretical Biology</i> , 2018, 455, 342-356.	1.7	12
60	Zika in travellers 1947–2017: a systematic review. <i>Journal of Travel Medicine</i> , 2018, 25, .	3.0	63
61	Immigrant Health Care in the Context of an Incredibly Complicated Health Care System. <i>American Journal of Public Health</i> , 2018, 108, 843-844.	2.7	1
62	History of Mosquitoborne Diseases in the United States and Implications for New Pathogens. <i>Emerging Infectious Diseases</i> , 2018, 24, 821-826.	4.3	32
63	Retention of ancestral polymorphism in <i>Culex nigripalpus</i> (Diptera: Culicidae) from São Paulo, Brazil. <i>Infection, Genetics and Evolution</i> , 2018, 65, 333-339.	2.3	7
64	Public Health Surveillance for Zika Virus: Data Interpretation and Report Validity. <i>American Journal of Public Health</i> , 2018, 108, 1358-1362.	2.7	12
65	Biosurveillance of forest insects: part I—integration and application of genomic tools to the surveillance of non-native forest insects. <i>Journal of Pest Science</i> , 2019, 92, 51-70.	3.7	35
66	Downgrading disease transmission risk estimates using terminal importations. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007395.	3.0	6
67	Congenital and perinatal infections. <i>Handbook of Clinical Neurology</i> / Edited By P J Vinken and G W Bruyn, 2019, 162, 133-153.	1.8	46
68	Inter- and intra-lineage genetic diversity of wild-type Zika viruses reveals both common and distinctive nucleotide variants and clusters of genomic diversity. <i>Emerging Microbes and Infections</i> , 2019, 8, 1126-1138.	6.5	20
69	Mosquito Adaptation to the Extreme Habitats of Urban Construction Sites. <i>Trends in Parasitology</i> , 2019, 35, 607-614.	3.3	20
70	Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity. <i>Journal of Infectious Diseases</i> , 2020, 221, S292-S307.	4.0	64
71	Consensus and uncertainty in the geographic range of <i>Aedes aegypti</i> and <i>Aedes albopictus</i> in the contiguous United States: Multi-model assessment and synthesis. <i>PLoS Computational Biology</i> , 2019, 15, e1007369.	3.2	14
72	Manipulating Solid Forms of Contact Insecticides for Infectious Disease Prevention. <i>Journal of the American Chemical Society</i> , 2019, 141, 16858-16864.	13.7	26
73	Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. <i>PLoS Pathogens</i> , 2019, 15, e1008042.	4.7	87

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74	Urbanization creates diverse aquatic habitats for immature mosquitoes in urban areas. Scientific Reports, 2019, 9, 15335.	3.3	88
75	Genomic epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia. BMC Infectious Diseases, 2019, 19, 963.	2.9	12
76	Occupational Exposure to the Ugandan Research Strain (MR766) of Zika Virus. Open Forum Infectious Diseases, 2019, 6, ofz420.	0.9	1
77	Travel Surveillance and Genomics Uncover a Hidden Zika Outbreak during the Waning Epidemic. Cell, 2019, 178, 1057-1071.e11.	28.9	68
78	Applying next-generation sequencing to track falciparum malaria in sub-Saharan Africa. Malaria Journal, 2019, 18, 268.	2.3	41
79	A dynamic neural network model for predicting risk of Zika in real time. BMC Medicine, 2019, 17, 171.	5.5	75
80	Investigating the probability of establishment of Zika virus and detection through mosquito surveillance under different temperature conditions. PLoS ONE, 2019, 14, e0214306.	2.5	10
81	Better surveillance to protect mothers and infants from Zika. Lancet Infectious Diseases, The, 2019, 19, 1047-1048.	9.1	0
82	A systematic review and evaluation of Zika virus forecasting and prediction research during a public health emergency of international concern. PLoS Neglected Tropical Diseases, 2019, 13, e0007451.	3.0	31
83	Vector Competence: What Has Zika Virus Taught Us?. Viruses, 2019, 11, 867.	3.3	45
84	Arbovirus coinfection and co-transmission: A neglected public health concern?. PLoS Biology, 2019, 17, e3000130.	5.6	106
85	A Statewide Survey of Container Aedes Mosquitoes (Diptera: Culicidae) in North Carolina, 2016: A Multiagency Surveillance Response to Zika Using Ovitrap. Journal of Medical Entomology, 2019, 56, 483-490.	1.8	12
86	The Asian Lineage of Zika Virus: Transmission and Evolution in Asia and the Americas. Virologica Sinica, 2019, 34, 1-8.	3.0	30
87	Identification of Molecular Determinants of Resistance to Pyrethroid Insecticides in Aedes aegypti (Diptera: Culicidae) Populations in California, USA. Journal of Medical Entomology, 2019, 56, 1353-1358.	1.8	8
88	Community Composition and Year-round Abundance of Vector Species of Mosquitoes make Miami-Dade County, Florida a Receptive Gateway for Arbovirus entry to the United States. Scientific Reports, 2019, 9, 8732.	3.3	43
89	Impact of population displacement and forced movements on the transmission and outbreaks of Aedes-borne viral diseases: Dengue as a model. Acta Tropica, 2019, 197, 105066.	2.0	16
90	The phylogenetic approach for viral infectious disease evolution and epidemiology: An updating review. Journal of Medical Virology, 2019, 91, 1707-1724.	5.0	16
91	Tire shops in Miami-Dade County, Florida are important producers of vector mosquitoes. PLoS ONE, 2019, 14, e0217177.	2.5	11

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92	What factors explain the geographical range of mammalian parasites?. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190673.	2.6	14
93	Complexity of the relationship between global warming and urbanization “ an obscure future for predicting increases in vector-borne infectious diseases. Current Opinion in Insect Science, 2019, 35, 1-9.	4.4	69
94	Applied shotgun metagenomics approach for the genetic characterization of dengue viruses. Journal of Biotechnology, 2019, 306, 100009.	3.8	6
95	Induction of RNA interference to block Zika virus replication and transmission in the mosquito Aedes aegypti. Insect Biochemistry and Molecular Biology, 2019, 111, 103169.	2.7	19
96	Localized Control of Aedes aegypti (Diptera: Culicidae) in Miami, FL, via Inundative Releases of Wolbachia-Infected Male Mosquitoes. Journal of Medical Entomology, 2019, 56, 1296-1303.	1.8	91
97	Vector-borne transmission and evolution of Zika virus. Nature Ecology and Evolution, 2019, 3, 561-569.	7.8	96
98	Emerging Challenges and Opportunities in Infectious Disease Epidemiology. American Journal of Epidemiology, 2019, 188, 873-882.	3.4	14
99	Past and future spread of the arbovirus vectors Aedes aegypti and Aedes albopictus. Nature Microbiology, 2019, 4, 854-863.	13.3	699
100	Clinical metagenomics. Nature Reviews Genetics, 2019, 20, 341-355.	16.3	793
101	Inter-annual variation in seasonal dengue epidemics driven by multiple interacting factors in Guangzhou, China. Nature Communications, 2019, 10, 1148.	12.8	36
102	Societal Implications of the Internet of Pathogens. Journal of Clinical Microbiology, 2019, 57, .	3.9	7
103	Utilizing general human movement models to predict the spread of emerging infectious diseases in resource poor settings. Scientific Reports, 2019, 9, 5151.	3.3	89
104	Community based serosurvey of naïve population indicate no local circulation of Zika virus in an hyper endemic area of China 2016. Journal of Infection, 2019, 79, 61-74.	3.3	1
105	Assessment of the effectiveness of BG-Sentinel traps baited with CO2 and BG-Lure for the surveillance of vector mosquitoes in Miami-Dade County, Florida. PLoS ONE, 2019, 14, e0212688.	2.5	35
106	Widespread insecticide resistance in Aedes aegypti L. from New Mexico, U.S.A.. PLoS ONE, 2019, 14, e0212693.	2.5	39
107	Precision epidemiology for infectious disease control. Nature Medicine, 2019, 25, 206-211.	30.7	94
109	Comparison of targeted next-generation sequencing for whole-genome sequencing of Hantaan orthohantavirus in Apodemus agrarius lung tissues. Scientific Reports, 2019, 9, 16631.	3.3	23
110	A natural polymorphism in Zika virus NS2A protein responsible of virulence in mice. Scientific Reports, 2019, 9, 19968.	3.3	23

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112	Phylogenetic surveillance of travel-related Zika virus infections through whole-genome sequencing methods. <i>Scientific Reports</i> , 2019, 9, 16433.	3.3	4
113	The role of disease surveillance in precision public health. , 2019, , 257-265.		0
114	Risk assessment and genomic characterization of Zika virus in China and its surrounding areas. <i>Chinese Medical Journal</i> , 2019, 132, 1645-1653.	2.3	0
115	Islands as Hotspots for Emerging Mosquito-Borne Viruses: A One-Health Perspective. <i>Viruses</i> , 2019, 11, 11.	3.3	35
116	Reconstruction and prediction of viral disease epidemics. <i>Epidemiology and Infection</i> , 2019, 147, e34.	2.1	29
117	Molecular epidemiology of dengue, yellow fever, Zika and Chikungunya arboviruses: An update. <i>Acta Tropica</i> , 2019, 190, 99-111.	2.0	52
118	The evolution of Zika virus from Asia to the Americas. <i>Nature Reviews Microbiology</i> , 2019, 17, 131-139.	28.6	103
119	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019, 20, 8.	8.8	712
120	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	13.3	305
121	Social Simulation Models at the Ethical Crossroads. <i>Science and Engineering Ethics</i> , 2019, 25, 143-157.	2.9	6
122	The Global Expansion of Dengue: How <i>Aedes aegypti</i> Mosquitoes Enabled the First Pandemic Arbovirus. <i>Annual Review of Entomology</i> , 2020, 65, 191-208.	11.8	203
123	Genomic Epidemiology as a Public Health Tool to Combat Mosquito-Borne Virus Outbreaks. <i>Journal of Infectious Diseases</i> , 2020, 221, S308-S318.	4.0	15
124	Sequencing of ZIKV genomes directly from <i>Ae. aegypti</i> and <i>Cx. quinquefasciatus</i> mosquitoes collected during the 2015-16 epidemics in Recife. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104180.	2.3	4
125	Geosmin Attracts <i>Aedes aegypti</i> Mosquitoes to Oviposition Sites. <i>Current Biology</i> , 2020, 30, 127-134.e5.	3.9	65
126	Structure and function of cis-acting RNA elements of flavivirus. <i>Reviews in Medical Virology</i> , 2020, 30, e2092.	8.3	21
127	Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1263-1271.	9.1	352
128	Tracking the Genomic Footprints of SARS-CoV-2 Transmission. <i>Trends in Genetics</i> , 2020, 36, 544-546.	6.7	12
129	Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread. <i>Nature Communications</i> , 2020, 11, 5558.	12.8	39



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130	Going back to the roots: Evaluating Bayesian phylogeographic models with discrete trait uncertainty. <i>Infection, Genetics and Evolution</i> , 2020, 85, 104501.	2.3	3
131	Salvia Spp. Essential Oils against the Arboviruses Vector <i>Aedes albopictus</i> (Diptera: Culicidae): Bioactivity, Composition, and Sensorial Profile—Stage 1. <i>Biology</i> , 2020, 9, 206.	2.8	3
132	Development and Clinical Application of a Rapid and Sensitive Loop-Mediated Isothermal Amplification Test for SARS-CoV-2 Infection. <i>MSphere</i> , 2020, 5, .	2.9	54
133	Surveillance of <i>Aedes aegypti</i> populations in the city of Praia, Cape Verde: Zika virus infection, insecticide resistance and genetic diversity. <i>Parasites and Vectors</i> , 2020, 13, 481.	2.5	15
134	Salivary extracellular vesicles inhibit Zika virus but not SARS-CoV-2 infection. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1808281.	12.2	23
135	Mapping the cryptic spread of the 2015–2016 global Zika virus epidemic. <i>BMC Medicine</i> , 2020, 18, 399.	5.5	3
136	Detection and discrimination of multiple strains of Zika virus by reverse transcription-loop-mediated isothermal amplification. <i>Tropical Medicine and Health</i> , 2020, 48, 87.	2.8	2
137	Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China. <i>Cell</i> , 2020, 181, 997-1003.e9.	28.9	236
138	Mosquito-Borne Disease and Human Mobility in Urban Environments. , 2020, , 489-502.		0
139	State by state implementation of Zika virus testing guidance in the United States in 2017 and 2018. <i>Preventive Medicine Reports</i> , 2020, 18, 101097.	1.8	0
140	Vector Competence Analyses on <i>Aedes aegypti</i> Mosquitoes using Zika Virus. <i>Journal of Visualized Experiments</i> , 2020, , .	0.3	1
141	Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California. <i>Science</i> , 2020, 369, 582-587.	12.6	253
142	Comparison of third-generation sequencing approaches to identify viral pathogens under public health emergency conditions. <i>Virus Genes</i> , 2020, 56, 288-297.	1.6	17
143	Comprehensive Profiling of Zika Virus Risk with Natural and Artificial Mitigating Strategies, United States. <i>Emerging Infectious Diseases</i> , 2020, 26, 700-710.	4.3	0
144	Current trends in large-scale viral surveillance methods in mosquitoes. <i>Entomological Research</i> , 2020, 50, 292-308.	1.1	2
145	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57.	8.2	104
146	Spondweni virus causes fetal harm in <i>Ifnar1</i> mice and is transmitted by <i>Aedes aegypti</i> mosquitoes. <i>Virology</i> , 2020, 547, 35-46.	2.4	12
147	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37

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148	Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. <i>Nature Microbiology</i> , 2020, 5, 443-454.	13.3	114
149	Quantifying the risk of Zika virus spread in Asia during the 2015-16 epidemic in Latin America and the Caribbean: A modeling study. <i>Travel Medicine and Infectious Disease</i> , 2020, 33, 101562.	3.0	13
150	Pan-genomics of virus and its applications. , 2020, , 237-250.		0
151	High Rate of Non-Human Feeding by <i>Aedes aegypti</i> Reduces Zika Virus Transmission in South Texas. <i>Viruses</i> , 2020, 12, 453.	3.3	23
152	Infectious Disease Research in the Era of Big Data. <i>Annual Review of Biomedical Data Science</i> , 2020, 3, 43-59.	6.5	10
153	Sociocultural, behavioural and political factors shaping the COVID-19 pandemic: the need for a biocultural approach to understanding pandemics and (re)emerging pathogens. <i>Global Public Health</i> , 2021, 16, 17-35.	2.0	17
154	Warming temperatures could expose more than 1.3Âbillion new people to Zika virus risk by 2050. <i>Global Change Biology</i> , 2021, 27, 84-93.	9.5	57
155	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 from mainland Europe into Scotland. <i>Nature Microbiology</i> , 2021, 6, 112-122.	13.3	88
156	Genomic epidemiology of the early stages of the SARS-CoV-2 outbreak in Russia. <i>Nature Communications</i> , 2021, 12, 649.	12.8	63
157	Yellow fever in Asiaâ€a risk analysis. <i>Journal of Travel Medicine</i> , 2021, 28, .	3.0	10
158	Data-driven prediction and origin identification of epidemics in population networks. <i>Royal Society Open Science</i> , 2021, 8, 200531.	2.4	0
159	Molecular evolution and codon usage bias of Zika virus. , 2021, , 409-418.		0
160	Global health security threats and related risks in Latin America. <i>Global Security: Health, Science and Policy</i> , 2021, 6, 18-25.	1.6	2
161	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	12.6	335
163	Distribution and diversity of mosquitoes and Oropouche-like virus infection rates in an Amazonian rural settlement. <i>PLoS ONE</i> , 2021, 16, e0246932.	2.5	12
164	A review of models applied to the geographic spread of Zika virus. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2021, 115, 956-964.	1.8	4
165	Modelling distributions of <i>Aedes aegypti</i> and <i>Aedes albopictus</i> using climate, host density and interspecies competition. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009063.	3.0	16
166	Prevalence of congenital microcephaly and its risk factors in an area at risk of Zika outbreaks. <i>BMC Pregnancy and Childbirth</i> , 2021, 21, 214.	2.4	7

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167	Frequency of sodium channel genotypes and association with pyrethrum knockdown time in populations of Californian <i>Aedes aegypti</i> . <i>Parasites and Vectors</i> , 2021, 14, 141.	2.5	12
168	Longitudinal virological changes and underlying pathogenesis in hospitalized COVID-19 patients in Guangzhou, China. <i>Science China Life Sciences</i> , 2021, 64, 2129-2143.	4.9	3
169	Repeated introductions and intensive community transmission fueled a mumps virus outbreak in Washington State. <i>ELife</i> , 2021, 10, .	6.0	13
171	Evaluation of Conserved RNA Secondary Structures within and between Geographic Lineages of Zika Virus. <i>Life</i> , 2021, 11, 344.	2.4	1
172	Contributions of Genetic Evolution to Zika Virus Emergence. <i>Frontiers in Microbiology</i> , 2021, 12, 655065.	3.5	7
173	Characterization of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection Clusters Based on Integrated Genomic Surveillance, Outbreak Analysis and Contact Tracing in an Urban Setting. <i>Clinical Infectious Diseases</i> , 2022, 74, 1039-1046.	5.8	21
174	Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages. <i>Molecular Biology and Evolution</i> , 2021, 38, 4346-4361.	8.9	14
175	Epidemiology and evolution of Zika virus in Minas Gerais, Southeast Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104785.	2.3	5
176	The Potential Role of Clinical Metagenomics in Infectious Diseases: Therapeutic Perspectives. <i>Drugs</i> , 2021, 81, 1453-1466.	10.9	18
177	AmplifyCoV: Rapid Whole-Genome Sequencing Using Multiplex PCR Amplification and Real-Time Oxford Nanopore MinION Sequencing Enables Rapid Variant Identification of SARS-CoV-2. <i>Frontiers in Microbiology</i> , 2021, 12, 651151.	3.5	25
179	The impact of long-term non-pharmaceutical interventions on COVID-19 epidemic dynamics and control: the value and limitations of early models. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20210811.	2.6	27
180	VGEA: an RNA viral assembly toolkit. <i>PeerJ</i> , 2021, 9, e12129.	2.0	2
181	Discriminating Clonotypes of Influenza A Virus Genes by Nanopore Sequencing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10069.	4.1	2
182	Assessing the impact of COVID-19 border restrictions on dengue transmission in Yunnan Province, China: an observational epidemiological and phylogenetic analysis. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 14, 100259.	2.9	11
183	Wave-wise comparative genomic study for revealing the complete scenario and dynamic nature of COVID-19 pandemic in Bangladesh. <i>PLoS ONE</i> , 2021, 16, e0258019.	2.5	13
184	Zika Virus Non-Structural Protein 1 Antigen-Capture Immunoassay. <i>Viruses</i> , 2021, 13, 1771.	3.3	5
185	Genetic and evolutionary analysis of SARS-CoV-2 circulating in the region surrounding Islamabad, Pakistan. <i>Infection, Genetics and Evolution</i> , 2021, 94, 105003.	2.3	7
186	Apiaceae essential oils and their constituents as insecticides against mosquitoes – A review. <i>Industrial Crops and Products</i> , 2021, 171, 113892.	5.2	31

#	ARTICLE	IF	CITATIONS
187	Genomic Epidemiology and Active Surveillance to Investigate Outbreaks of Hantaviruses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 532388.	3.9	14
188	Population bottlenecks and founder effects: implications for mosquito-borne arboviral emergence. <i>Nature Reviews Microbiology</i> , 2021, 19, 184-195.	28.6	51
189	Molecular diagnosis of Zika virus infections. <i>Reviews in Medical Microbiology</i> , 2018, 29, 8-16.	0.9	3
209	Detecting Local Zika Virus Transmission in the Continental United States: A Comparison of Surveillance Strategies. <i>PLOS Currents</i> , 2017, 9, .	1.4	11
210	Inferring the risk factors behind the geographical spread and transmission of Zika in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006194.	3.0	67
211	Spatio-temporal coherence of dengue, chikungunya and Zika outbreaks in Merida, Mexico. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006298.	3.0	60
212	Aerial ULV control of <i>Aedes aegypti</i> with naled (Dibrom) inside simulated rural village and urban cryptic habitats. <i>PLoS ONE</i> , 2018, 13, e0191555.	2.5	7
213	New Insights on the Zika Virus Arrival in the Americas and Spatiotemporal Reconstruction of the Epidemic Dynamics in Brazil. <i>Viruses</i> , 2021, 13, 12.	3.3	20
214	Beyond the Surface: Endocytosis of Mosquito-Borne Flaviviruses. <i>Viruses</i> , 2021, 13, 13.	3.3	22
215	Exploring the mechanisms behind the country-specific time of Zika virus importation. <i>Mathematical Biosciences and Engineering</i> , 2019, 16, 3272-3284.	1.9	2
216	Origin of a High-Latitude Population of <i>Aedes aegypti</i> in Washington, DC. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 98, 445-452.	1.4	36
217	Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. <i>PeerJ</i> , 2019, 7, e8013.	2.0	23
219	Microbial Genetics in Mycology. , 2021, , .		0
220	Progress and challenges in virus genomic epidemiology. <i>Trends in Parasitology</i> , 2021, 37, 1038-1049.	3.3	45
221	Imidacloprid Crystal Polymorphs for Disease Vector Control and Pollinator Protection. <i>Journal of the American Chemical Society</i> , 2021, 143, 17144-17152.	13.7	27
222	Finding disease outbreak locations from human mobility data. <i>EPJ Data Science</i> , 2021, 10, 52.	2.8	7
232	A Simple Model to Predict the Potential Abundance of <i>Aedes aegypti</i> Mosquitoes One Month in Advance. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 100, 434-437.	1.4	6
235	Raiders of the lost HARK: a reproducible inference framework for big data science. <i>Palgrave Communications</i> , 2019, 5, .	4.7	5

#	ARTICLE	IF	CITATIONS
237	A Case Study of Applying Metagenomic Sequencing in Precise Epidemiology for the COVID-19 Pandemic â€” Sichuan Province, China, 2020. China CDC Weekly, 2020, 2, 897-901.	2.3	1
239	Population Outbreaks of Mosquitoes After Hurricanes Matthew and Irma and the Control Efforts in St. Johns County, Northeastern Florida. Journal of the American Mosquito Control Association, 2020, 36, 28-34.	0.7	4
240	Genomic epidemiology reveals multiple introductions of SARS-CoV-2 followed by community and nosocomial spread, Germany, February to May 2020. Eurosurveillance, 2021, 26, .	7.0	11
241	Diagnostic assays for COVID-19: a narrative review. Journal of Bio-X Research, 2020, 3, 123-134.	0.2	2
242	Recent Expansion of Mosquito-Borne Pathogens Into Texas. , 2020, , 339-358.		0
243	Next-Generation Sequencing in the Study of Infectious Diseases. , 2020, , 1-22.		0
244	Genomic and Phylogenetic Analysis of Zika Virus Isolates from Asymptomatic Blood Donors in the United States and Puerto Rico, 2016. American Journal of Tropical Medicine and Hygiene, 2020, 102, 880-883.	1.4	2
245	Genomic diversity of SARS-CoV-2 in Oxford during United Kingdomâ€™s first national lockdown. Scientific Reports, 2021, 11, 21484.	3.3	7
246	Dengue outbreaks in Hawai'i After WWII - A Review of Public Health Response and Scientific Literature. Hawai'i Journal of Medicine & Public Health: A Journal of Asia Pacific Medicine & Public Health, 2018, 77, 315-318.	0.4	5
247	Zika Virus: Relevance to the State of Hawai'i. Hawai'i Journal of Medicine & Public Health: A Journal of Asia Pacific Medicine & Public Health, 2019, 78, 123-127.	0.4	1
248	Urbanization favors the proliferation of Aedes aegypti and Culex quinquefasciatus in urban areas of Miami-Dade County, Florida. Scientific Reports, 2021, 11, 22989.	3.3	32
249	Social physics. Physics Reports, 2022, 948, 1-148.	25.6	231
253	Intrinsic variation in the vertically transmitted core virome of the mosquito <i>Aedes aegypti</i>. Molecular Ecology, 2022, 31, 2545-2561.	3.9	18
254	Investigation of crossâ€‘regional spread and evolution of equine influenza H3N8 at US and global scales using Bayesian phylogeography based on balanced subsampling. Transboundary and Emerging Diseases, 2022, 69, .	3.0	2
255	Mosquito surveillance in maritime entry ports in Miami-Dade County, Florida to increase preparedness and allow the early detection of invasive mosquito species. PLoS ONE, 2022, 17, e0267224.	2.5	6
256	Phylogenetic and phylodynamic approaches to understanding and combating the early SARS-CoV-2 pandemic. Nature Reviews Genetics, 2022, 23, 547-562.	16.3	70
258	Culture-Free Phylogenetic Analysis of Legionella pneumophila Using Targeted CRISPR/Cas9 Next-Generation Sequencing. Microbiology Spectrum, 2022, 10, .	3.0	2
260	Ethical Challenges Associated with Pathogen and Host Genetics in Infectious Disease. New Bioethics, 0, , 1-13.	1.1	1

#	ARTICLE	IF	CITATIONS
261	Computational biology and biosensors as surveillance tools for emerging and re-emerging infectious diseases. , 2022, , 419-441.		0
262	Using multiple sampling strategies to estimate SARS-CoV-2 epidemiological parameters from genomic sequencing data. Nature Communications, 2022, 13, .	12.8	10
263	Analysis of Zika Virus Sequence Data Associated with a School Cohort in Haiti. American Journal of Tropical Medicine and Hygiene, 2022, 107, 873-880.	1.4	1
264	Neutralizing Immunity Induced Against the Omicron BA.1 and BA.2 Variants in Vaccine Breakthrough Infections. Journal of Infectious Diseases, 2022, 226, 1688-1698.	4.0	1
265	Real-time digital data of international passengers will shine in the precaution of epidemics. Intelligent Medicine, 2023, 3, 44-45.	3.1	0
266	Tracing the international arrivals of SARS-CoV-2 Omicron variants after Aotearoa New Zealand reopened its border. Nature Communications, 2022, 13, .	12.8	12
267	Repeated Rapid Active Sampling Surveys Demonstrated a Rapidly Changing Zika Seroprevalence among Children in a Rural Dengue-endemic Region in Southwest Guatemala during the Zika Epidemic (2015â€“2016). American Journal of Tropical Medicine and Hygiene, 2022, , .	1.4	0
268	MÃ©todos de aprendizaje automÃ¡tico para predecir el comportamiento epidemiolÃ³gico de enfermedades arbovirales: revisiÃ³n estructurada de literatura. Revista De La Universidad Industrial De Santander Salud, 2022, 55, .	0.2	0
269	Next-Generation Sequencing in the Study of Infectious Diseases. , 2023, , 35-56.		1
270	Using metagenomics to detect West Nile virus in mosquitoes collected in Oklahoma. Bios, 2023, 93, .	0.0	2
271	Spatiotemporal distribution of vector mosquito species and areas at risk for arbovirus transmission in Maricopa County, Arizona. Acta Tropica, 2023, 240, 106833.	2.0	2
272	Diverse pathways toward a cure. IScience, 2023, 26, 106052.	4.1	0
273	Genomic and phenotypic analyses suggest moderate fitness differences among Zika virus lineages. PLoS Neglected Tropical Diseases, 2023, 17, e0011055.	3.0	2
274	Using Multiplex Amplicon PCR Technology to Efficiently and Timely Generate Rift Valley Fever Virus Sequence Data for Genomic Surveillance. Viruses, 2023, 15, 477.	3.3	1
275	Rapid range shifts in African <i>Anopheles</i> mosquitoes over the last century. Biology Letters, 2023, 19, .	2.3	11
276	Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations. Nature Methods, 2023, 20, 512-522.	19.0	111
277	Genomic epidemiology and surveillance of zoonotic viruses using targeted next-generation sequencing. Korean Journal of Veterinary Service, 2023, 46, 93-106.	0.3	1
278	High-throughput sequencing approaches applied to SARS-CoV-2. Wellcome Open Research, 0, 8, 150.	1.8	0

#	ARTICLE	IF	CITATIONS
279	A scoping review of waterborne and water-related disease in the Florida environment from 1999 to 2022. <i>Reviews on Environmental Health</i> , 2023, .	2.4	0
282	Analyses of Early ZIKV Genomes Are Consistent with Viral Spread from Northeast Brazil to the Americas. <i>Viruses</i> , 2023, 15, 1236.	3.3	0
283	Genomic epidemiology of dengue in Shantou, China, 2019. <i>Frontiers in Public Health</i> , 0, 11, .	2.7	0
285	Highly multiplexed targeted sequencing strategy for infectious disease surveillance. <i>BMC Biotechnology</i> , 2023, 23, .	3.3	0
286	Perspective on the spatio-temporal spread of epidemics in metapopulation networks. <i>Europhysics Letters</i> , 2023, 144, 11001.	2.0	0
287	Two invasions at once: update on the introduction of the invasive species <i>Aedes aegypti</i> and <i>Aedes albopictus</i> in Cyprus – a call for action in Europe. <i>Parasite</i> , 2023, 30, 41.	2.0	0
288	A hybridization target enrichment approach for pathogen genomics. <i>MBio</i> , 2023, 14, .	4.1	1
289	Zika virus M protein latches and locks the E protein from transitioning to an immature state after prM cleavage. , 2023, 1, .		3
290	Interactions between climate change, urban infrastructure and mobility are driving dengue emergence in Vietnam. <i>Nature Communications</i> , 2023, 14, .	12.8	0
293	Genomic epidemiology of West Nile virus in Europe. <i>One Health</i> , 2024, 18, 100664.	3.4	1
295	Tracking arboviruses, their transmission vectors and potential hosts by nanopore sequencing of mosquitoes. <i>Microbial Genomics</i> , 2024, 10, .	2.0	0
296	Development of a quantitative NS1 antigen enzyme-linked immunosorbent assay (ELISA) for Zika virus detection using a novel virus-specific mAb. <i>Scientific Reports</i> , 2024, 14, .	3.3	0
297	Zika Virus—A Reemerging Neurotropic Arbovirus Associated with Adverse Pregnancy Outcomes and Neuropathogenesis. <i>Pathogens</i> , 2024, 13, 177.	2.8	0
298	Hybrid-Capture Target Enrichment in Human Pathogens: Identification, Evolution, Biosurveillance, and Genomic Epidemiology. <i>Pathogens</i> , 2024, 13, 275.	2.8	0