

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.	13.7	515
2	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	13.7	323
3	Molecular mapping of Zika spread. <i>Nature</i> , 2017, 546, 355-356.	13.7	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.	5.5	898
5	Modeling mosquito-borne diseases in complex urban environments. <i>Acta Tropica</i> , 2017, 176, 332-334.	0.9	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.	2.5	4
7	Infection via mosquito bite alters Zika virus tissue tropism and replication kinetics in rhesus macaques. <i>Nature Communications</i> , 2017, 8, 2096.	5.8	87
8	Zika virus evolution on the edges of the Pacific ocean. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-3.	3.0	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.	2.6	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.	1.2	9
11	Simple visit behavior unifies complex Zika outbreaks. <i>Heliyon</i> , 2017, 3, e00482.	1.4	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.	1.3	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.	1.3	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.	1.2	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.	0.9	8
16	Genomic Insights into Zika Virus Emergence and Spread. <i>Cell</i> , 2018, 172, 1160-1162.	13.5	56
17	Considering the Potential Application of Whole Genome Sequencing to Gonorrhea Prevention and Control. <i>Sexually Transmitted Diseases</i> , 2018, 45, e29-e32.	0.8	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.	0.7	3

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20	Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques. <i>Nature Communications</i> , 2018, 9, 1624.	5.8	68
21	Biochemistry and Molecular Biology of Flaviviruses. <i>Chemical Reviews</i> , 2018, 118, 4448-4482.	23.0	211
22	Performance of the Trioplex real-time RT-PCR assay for detection of Zika, dengue, and chikungunya viruses. <i>Nature Communications</i> , 2018, 9, 1391.	5.8	134
23	Zika Immunoassay Based on Surface-Enhanced Raman Scattering Nanoprobes. <i>ACS Sensors</i> , 2018, 3, 587-594.	4.0	57
24	What we know and what we don't know about perinatal Zika virus infection: a systematic review. <i>Expert Review of Anti-Infective Therapy</i> , 2018, 16, 243-254.	2.0	13
25	Efficacy of larvicides for the control of dengue, Zika, and chikungunya vectors in an urban cemetery in southern Mexico. <i>Parasitology Research</i> , 2018, 117, 1941-1952.	0.6	10
26	Field-deployable viral diagnostics using CRISPR-Cas13. <i>Science</i> , 2018, 360, 444-448.	6.0	982
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28	Consensus and conflict among ecological forecasts of Zika virus outbreaks in the United States. <i>Scientific Reports</i> , 2018, 8, 4921.	1.6	50
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30	Modeling neuro-immune interactions during Zika virus infection. <i>Human Molecular Genetics</i> , 2018, 27, 41-52.	1.4	50
31	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. <i>Infection, Genetics and Evolution</i> , 2018, 63, 295-306.	1.0	32
32	Disaster Preparedness: Biological Threats and Treatment Options. <i>Pharmacotherapy</i> , 2018, 38, 217-234.	1.2	30
33	Towards a genomics-informed, real-time, global pathogen surveillance system. <i>Nature Reviews Genetics</i> , 2018, 19, 9-20.	7.7	505
34	Screening for Zika virus in deceased organ donors in Florida. <i>American Journal of Transplantation</i> , 2018, 18, 731-736.	2.6	10
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37	Quantifying the risk of local Zika virus transmission in the contiguous US during the 2015-2016 ZIKV epidemic. <i>BMC Medicine</i> , 2018, 16, 195.	2.3	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, .	3.9	85
39	Simple protocol for population (Sanger) sequencing for Zika virus genomic regions. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2018, 113, 38-44.	0.8	5
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41	The influence of phylodynamic model specifications on parameter estimates of the Zika virus epidemic. <i>Virus Evolution</i> , 2018, 4, vex044.	2.2	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.	1.6	20
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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.	2.2	8
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52	MERS-CoV spillover at the camel-human interface. <i>ELife</i> , 2018, 7, .	2.8	172
53	Establishment of <i>Aedes albopictus</i> (Diptera: Culicidae) in the Florida Keys, 2001–2017. <i>Journal of Medical Entomology</i> , 2018, 55, 1607-1612.	0.9	5
54	The epidemiological characteristics and molecular phylogeny of the dengue virus in Guangdong, China, 2015. <i>Scientific Reports</i> , 2018, 8, 9976.	1.6	11
55	Identification of Wild Boar–Habitat Epidemiologic Cycle in African Swine Fever Epizootic. <i>Emerging Infectious Diseases</i> , 2018, 24, 810-812.	2.0	110

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64	Public Health Surveillance for Zika Virus: Data Interpretation and Report Validity. <i>American Journal of Public Health</i> , 2018, 108, 1358-1362.	1.5	12
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66	Downgrading disease transmission risk estimates using terminal importations. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007395.	1.3	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.	1.0	46
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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.	1.5	14
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73	Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. <i>PLoS Pathogens</i> , 2019, 15, e1008042.	2.1	87

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75	Genomic epidemiology supports multiple introductions and cryptic transmission of Zika virus in Colombia. <i>BMC Infectious Diseases</i> , 2019, 19, 963.	1.3	12
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145	Multiple approaches for massively parallel sequencing of SARS-CoV-2 genomes directly from clinical samples. <i>Genome Medicine</i> , 2020, 12, 57.	3.6	104
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161	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	6.0	335
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