

Michael R Wiley

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,002
citations

361045

20
h-index

360668

35
g-index

38
all docs

38
docs citations

38
times ranked

4368
citing authors

#	ARTICLE	IF	CITATIONS
1	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	13.7	346
2	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	13.7	298
3	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310.	0.9	157
4	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	153
5	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
6	A Multicomponent Animal Virus Isolated from Mosquitoes. <i>Cell Host and Microbe</i> , 2016, 20, 357-367.	5.1	123
7	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. <i>MBio</i> , 2014, 5, e01360-14.	1.8	89
8	Evolution and Spread of Ebola Virus in Liberia, 2014–2015. <i>Cell Host and Microbe</i> , 2015, 18, 659-669.	5.1	87
9	Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016, 2, e1600378.	4.7	62
10	Medical countermeasures during the 2018 Ebola virus disease outbreak in the North Kivu and Ituri Provinces of the Democratic Republic of the Congo: a rapid genomic assessment. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 648-657.	4.6	62
11	First report of naturally infected <i>Aedes aegypti</i> with chikungunya virus genotype ECSA in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005630.	1.3	59
12	Isolation of a Novel Fusogenic Orthoreovirus from <i>Eucampsipoda africana</i> Bat Flies in South Africa. <i>Viruses</i> , 2016, 8, 65.	1.5	41
13	Complete Genome Sequences of Five Zika Virus Isolates. <i>Genome Announcements</i> , 2016, 4, .	0.8	40
14	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018, 22, 1159-1168.	2.9	37
15	Lassa virus circulating in Liberia: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 1371-1378.	4.6	30
16	Isolation of a novel orthobunyavirus from bat flies (<i>Eucampsipoda africana</i>). <i>Journal of General Virology</i> , 2017, 98, 935-945.	1.3	29
17	2018 Ebola virus disease outbreak in Équateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 641-647.	4.6	27
18	Characterization of the Punta Toro species complex (genus <i>Phlebovirus</i> , family <i>Bunyaviridae</i>). <i>Journal of General Virology</i> , 2015, 96, 2079-2085.	1.3	23

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19	Shedding of Marburg Virus in Naturally Infected Egyptian Rousette Bats, South Africa, 2017. <i>Emerging Infectious Diseases</i> , 2020, 26, 3051-3055.	2.0	23
20	Active Targeted Surveillance to Identify Sites of Emergence of Hantavirus. <i>Clinical Infectious Diseases</i> , 2020, 70, 464-473.	2.9	22
21	Ribavirin Had Demonstrable Effects on the Crimean-Congo Hemorrhagic Fever Virus (CCHFV) Population and Load in a Patient With CCHF Infection. <i>Journal of Infectious Diseases</i> , 2018, 217, 1952-1956.	1.9	20
22	Functionality of Two Origins of Replication in <i>Vibrio cholerae</i> Strains With a Single Chromosome. <i>Frontiers in Microbiology</i> , 2018, 9, 2932.	1.5	19
23	A small stem-loop structure of the Ebola virus trailer is essential for replication and interacts with heat-shock protein A8. <i>Nucleic Acids Research</i> , 2016, 44, gkw825.	6.5	16
24	Complete Coding Sequences of Eastern Equine Encephalitis Virus and Venezuelan Equine Encephalitis Virus Strains Isolated from Human Cases. <i>Genome Announcements</i> , 2015, 3, .	0.8	15
25	T-705 induces lethal mutagenesis in Ebola and Marburg populations in macaques. <i>Antiviral Research</i> , 2019, 170, 104529.	1.9	14
26	A novel adenovirus isolated from the Egyptian fruit bat in South Africa is closely related to recent isolates from China. <i>Scientific Reports</i> , 2018, 8, 9584.	1.6	13
27	Modeling mosquito-borne and sexual transmission of Zika virus in an enzootic host, the African green monkey. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008107.	1.3	11
28	Genome Sequences of Simian Hemorrhagic Fever Virus Variant NIH LVR42-0/M6941 Isolates (Arteriviridae: Arterivirus). <i>Genome Announcements</i> , 2014, 2, .	0.8	9
29	Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. <i>Frontiers in Microbiology</i> , 2019, 10, 856.	1.5	8
30	Identification and characterization of Highlands J virus from a Mississippi sandhill crane using unbiased next-generation sequencing. <i>Journal of Virological Methods</i> , 2014, 206, 42-45.	1.0	7
31	Beatrice Hill Virus Represents a Novel Species in the Genus Tibrovirus (Mononegavirales :) Tj ETQq1 1 0.784314 rgBT/Overlock 10 Tf	0.8	6
32	First Detection of the West Nile Virus Koutango Lineage in Sandflies in Niger. <i>Pathogens</i> , 2021, 10, 257.	1.2	4
33	Cross-Border Transmission of Ebola Virus as the Cause of a Resurgent Outbreak in Liberia in April 2016. <i>Clinical Infectious Diseases</i> , 2018, 67, 1147-1149.	2.9	3
34	Complete Coding Sequence of Western Equine Encephalitis Virus Strain Fleming, Isolated from a Human Case. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
35	Complete genomic sequences of Venezuelan equine encephalitis virus subtype IIID isolates from mosquitoes. <i>Archives of Virology</i> , 2020, 165, 1715-1717.	0.9	1
36	Reply to "Expanding the Conversation on High-Throughput Virome Sequencing Standards To Include Consideration of Microbial Contamination Sources" <i>MBio</i> , 2014, 5, e02084.	1.8	0