

Michael R Wiley

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35
papers

1,346
citations

17
h-index

36
g-index

38
ext. papers

1,764
ext. citations

12.8
avg, IF

3.2
L-index

#	Paper	IF	Citations
35	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017 , 544, 309-315	50.4	238
34	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017 , 546, 401-405	50.4	235
33	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2283-2294	2.6	111
32	Taxonomy of the family Arenaviridae and the order Bunyvirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2295-2310	2.6	108
31	A Multicomponent Animal Virus Isolated from Mosquitoes. <i>Cell Host and Microbe</i> , 2016 , 20, 357-367	23.4	76
30	Evolution and Spread of Ebola Virus in Liberia, 2014-2015. <i>Cell Host and Microbe</i> , 2015 , 18, 659-69	23.4	66
29	Reduced evolutionary rate in reemerged Ebola virus transmission chains. <i>Science Advances</i> , 2016 , 2, e1600378	14.3	53
28	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	4.8	46
27	Complete Genome Sequences of Five Zika Virus Isolates. <i>Genome Announcements</i> , 2016 , 4,		39
26	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> , 2019 , 19, 648-657	25.5	36
25	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
24	Isolation of a Novel Fusogenic Orthoreovirus from <i>Eucampsipoda africana</i> Bat Flies in South Africa. <i>Viruses</i> , 2016 , 8, 65	6.2	28
23	Active Ebola Virus Replication and Heterogeneous Evolutionary Rates in EVD Survivors. <i>Cell Reports</i> , 2018 , 22, 1159-1168	10.6	27
22	Lassa virus circulating in Liberia: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , 2019 , 19, 1371-1378	25.5	21
21	Isolation of a novel orthobunyavirus from bat flies (<i>Eucampsipoda africana</i>). <i>Journal of General Virology</i> , 2017 , 98, 935-945	4.9	20
20	Characterization of the Punta Toro species complex (genus Phlebovirus, family Bunyviridae). <i>Journal of General Virology</i> , 2015 , 96, 2079-2085	4.9	18
19	2018 Ebola virus disease outbreak in Equateur Province, Democratic Republic of the Congo: a retrospective genomic characterisation. <i>Lancet Infectious Diseases</i> , 2019 , 19, 641-647	25.5	17

18	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, 9831-9846	20.1	15
17	Active Targeted Surveillance to Identify Sites of Emergence of Hantavirus. <i>Clinical Infectious Diseases</i> , 2020 , 70, 464-473	11.6	11
16	T-705 induces lethal mutagenesis in Ebola and Marburg populations in macaques. <i>Antiviral Research</i> , 2019 , 170, 104529	10.8	9
15	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	7.6	9
14	Complete coding sequences of eastern equine encephalitis virus and venezuelan equine encephalitis virus strains isolated from human cases. <i>Genome Announcements</i> , 2015 , 3,		9
13	Genome Sequences of Simian Hemorrhagic Fever Virus Variant NIH LVR42-0/M6941 Isolates (Arteriviridae: Arterivirus). <i>Genome Announcements</i> , 2014 , 2,		8
12	Shedding of Marburg Virus in Naturally Infected Egyptian Rousette Bats, South Africa, 2017. <i>Emerging Infectious Diseases</i> , 2020 , 26, 3051-3055	10.2	8
11	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	4.9	8
10	Functionality of Two Origins of Replication in Strains With a Single Chromosome. <i>Frontiers in Microbiology</i> , 2018 , 9, 2932	5.7	7
9	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	4.8	6
8	Human, Nonhuman Primate, and Bat Cells Are Broadly Susceptible to Tibrovirus Particle Cell Entry. <i>Frontiers in Microbiology</i> , 2019 , 10, 856	5.7	6
7	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, 42-5	2.6	6
6	Beatrice Hill Virus Represents a Novel Species in the Genus Tibrovirus (Mononegavirales: Rhabdoviridae). <i>Genome Announcements</i> , 2017 , 5,		3
5	Complete Coding Sequence of Western Equine Encephalitis Virus Strain Fleming, Isolated from a Human Case. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	2
4	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	11.6	2
3	Complete genomic sequences of Venezuelan equine encephalitis virus subtype IIID isolates from mosquitoes. <i>Archives of Virology</i> , 2020 , 165, 1715-1717	2.6	1
2	First Detection of the West Nile Virus Koutango Lineage in Sandflies in Niger. <i>Pathogens</i> , 2021 , 10,	4.5	1
1	Reply to "Expanding the conversation on high-throughput virome sequencing standards to include consideration of microbial contamination sources". <i>MBio</i> , 2014 , 5, e02084	7.8	

