

## 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.

41 papers	917 citations	15 h-index	30 g-index
51 ext. papers	1,302 ext. citations	8.4 avg, IF	4.24 L-index

#	Paper	IF	Citations
41	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , <b>2017</b> , 544, 309-315	50.4	238
40	Rapid outbreak sequencing of Ebola virus in Sierra Leone identifies transmission chains linked to sporadic cases. <i>Virus Evolution</i> , <b>2016</b> , 2, vew016	3.7	89
39	A64 Viral sequence classification using deep learning algorithms. <i>Virus Evolution</i> , <b>2019</b> , 5,	3.7	78
38	Deep sequencing of norovirus genomes defines evolutionary patterns in an urban tropical setting. <i>Journal of Virology</i> , <b>2014</b> , 88, 11056-69	6.6	57
37	A prospective multi-center observational study of children hospitalized with diarrhea in Ho Chi Minh City, Vietnam. <i>American Journal of Tropical Medicine and Hygiene</i> , <b>2015</b> , 92, 1045-52	3.2	41
36	Emergence and spread of a SARS-CoV-2 lineage A variant (A.23.1) with altered spike protein in Uganda. <i>Nature Microbiology</i> , <b>2021</b> , 6, 1094-1101	26.6	39
35	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , <b>2021</b> , 374, 423-431	33.3	35
34	Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation of multiple groups of rotaviruses and a putative zoonotic infection. <i>Virus Evolution</i> , <b>2016</b> , 2, vew027	3.7	35
33	Identification and characterization of Coronaviridae genomes from Vietnamese bats and rats based on conserved protein domains. <i>Virus Evolution</i> , <b>2018</b> , 4, vey035	3.7	35
32	Whole-Genome Next-Generation Sequencing to Study Within-Host Evolution of Norovirus (NoV) Among Immunocompromised Patients With Chronic NoV Infection. <i>Journal of Infectious Diseases</i> , <b>2017</b> , 216, 1513-1524	7	26
31	Characterization of Norovirus and Other Human Enteric Viruses in Sewage and Stool Samples Through Next-Generation Sequencing. <i>Food and Environmental Virology</i> , <b>2019</b> , 11, 400-409	4	22
30	Virus Metagenomics in Farm Animals: A Systematic Review. <i>Viruses</i> , <b>2020</b> , 12,	6.2	21
29	The impact of environmental and climatic variation on the spatiotemporal trends of hospitalized pediatric diarrhea in Ho Chi Minh City, Vietnam. <i>Health and Place</i> , <b>2015</b> , 35, 147-54	4.6	20
28	Characterization of Posa and Posa-like virus genomes in fecal samples from humans, pigs, rats, and bats collected from a single location in Vietnam. <i>Virus Evolution</i> , <b>2017</b> , 3, vex022	3.7	17
27	A Novel Astrovirus-Like RNA Virus Detected in Human Stool. <i>Virus Evolution</i> , <b>2016</b> , 2, vew005	3.7	16
26	Metavirome Sequencing to Evaluate Norovirus Diversity in Sewage and Related Bioaccumulated Oysters. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2394	5.7	15
25	Setting a baseline for global urban virome surveillance in sewage. <i>Scientific Reports</i> , <b>2020</b> , 10, 13748	4.9	15

24	Notes from The Field: Ebola Virus Disease Cluster - Northern Sierra Leone, January 2016. <i>Morbidity and Mortality Weekly Report</i> , <b>2016</b> , 65, 681-2	31.7	14
23	Spike protein cleavage-activation mediated by the SARS-CoV-2 P681R mutation: a case-study from its first appearance in variant of interest (VOI) A.23.1 identified in Uganda <b>2021</b> ,		14
22	Severe acute respiratory infection caused by swine influenza virus in a child necessitating extracorporeal membrane oxygenation (ECMO), the Netherlands, October 2016. <i>Eurosurveillance</i> , <b>2016</b> , 21,	19.8	13
21	Genomic analysis of respiratory syncytial virus infections in households and utility in inferring who infects the infant. <i>Scientific Reports</i> , <b>2019</b> , 9, 10076	4.9	12
20	Nosocomial outbreak of the Middle East Respiratory Syndrome coronavirus: A phylogenetic, epidemiological, clinical and infection control analysis. <i>Travel Medicine and Infectious Disease</i> , <b>2020</b> , 37, 101807	8.4	10
19	Complete Genome Sequences of Dengue Virus Type 2 Strains from Kilifi, Kenya. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	9
18	Alternate primers for whole-genome SARS-CoV-2 sequencing. <i>Virus Evolution</i> , <b>2021</b> , 7, veab006	3.7	8
17	Genomic sequence of yellow fever virus from a Dutch traveller returning from the Gambia-Senegal region, the Netherlands, November 2018. <i>Eurosurveillance</i> , <b>2019</b> , 24,	19.8	6
16	Complete Genome Sequences of Six Measles Virus Strains. <i>Genome Announcements</i> , <b>2018</b> , 6,		5
15	Increased resolution of African swine fever virus genome patterns based on profile HMMs of protein domains. <i>Virus Evolution</i> , <b>2020</b> , 6, veaa044	3.7	4
14	Norovirus outbreak in a natural playground: A One Health approach. <i>Zoonoses and Public Health</i> , <b>2020</b> , 67, 453-459	2.9	2
13	SARS-CoV-2 Variants, South Sudan, January-March 2021. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 3133-3136.2	36.2	2
12	Alternate primers for whole-genome SARS-CoV-2 sequencing		2
11	No Evidence Known Viruses Play a Role in the Pathogenesis of Onchocerciasis-Associated Epilepsy. An Explorative Metagenomic Case-Control Study. <i>Pathogens</i> , <b>2021</b> , 10,	4.5	2
10	Complete Genome Characterization of Two Wild-Type Measles Viruses from Vietnamese Infants during the 2014 Outbreak. <i>Genome Announcements</i> , <b>2016</b> , 4,		2
9	Genome Sequences of a Novel Vietnamese Bat Bunyavirus. <i>Genome Announcements</i> , <b>2016</b> , 4,		2
8	Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. <i>Virus Evolution</i> , <b>2021</b> , 7, veab063.7	37.7	2
7	The Utility of Data Transformation for Alignment, De Novo Assembly and Classification of Short Read Virus Sequences. <i>Viruses</i> , <b>2019</b> , 11,	6.2	1

6	Shedding of Yellow Fever Virus From an Imported Case in the Netherlands After Travel to Brazil. <i>Open Forum Infectious Diseases</i> , <b>2020</b> , 7, ofaa020	1	1
5	Genome Sequences of Seven Strains from Chickens in The Netherlands. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1,3	1
4	Increased resolution of African Swine Fever Virus genome patterns based on profile HMM protein domains		1
3	Whole genome sequencing and phylogenetic analysis of human metapneumovirus strains from Kenya and Zambia. <i>BMC Genomics</i> , <b>2020</b> , 21, 5	4,5	1
2	Genomic surveillance reveals the spread patterns of SARS-CoV-2 in coastal Kenya during the first two waves		1
1	Automated download and clean-up of family-specific databases for kmer-based virus identification. <i>Bioinformatics</i> , <b>2021</b> , 37, 705-710	7,2	1