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List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

1,221
citations

394421

19
h-index

434195

31
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56
all docs

56
docs citations

56
times ranked

2036
citing authors

#	ARTICLE	IF	CITATIONS
1	Independent infections of porcine deltacoronavirus among Haitian children. <i>Nature</i> , 2021, 600, 133-137.	27.8	165
2	Collection of SARS-CoV-2 Virus from the Air of a Clinic within a University Student Health Care Center and Analyses of the Viral Genomic Sequence. <i>Aerosol and Air Quality Research</i> , 2020, 20, 1167-1171.	2.1	88
3	Concurrence of Iridovirus, Polyomavirus, and a Unique Member of a New Group of Fish Papillomaviruses in Lymphocystis Disease-Affected Gilthead Sea Bream. <i>Journal of Virology</i> , 2016, 90, 8768-8779.	3.4	79
4	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	7.1	68
5	Emergence of recombinant Mayaro virus strains from the Amazon basin. <i>Scientific Reports</i> , 2017, 7, 8718.	3.3	66
6	Collection of SARS-CoV-2 Virus from the Air of a Clinic within a University Student Health Care Center and Analyses of the Viral Genomic Sequence. <i>Aerosol and Air Quality Research</i> , 2020, 20, 1167-1171.	2.1	63
7	A minor population of macrophage-tropic HIV-1 variants is identified in recrudescing viremia following analytic treatment interruption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9981-9990.	7.1	51
8	Ranavirus phylogenomics: Signatures of recombination and inversions among bullfrog ranaculture isolates. <i>Virology</i> , 2017, 511, 330-343.	2.4	50
9	The Genome Sequence of the Emerging Common Midwife Toad Virus Identifies an Evolutionary Intermediate within Ranaviruses. <i>Journal of Virology</i> , 2012, 86, 3617-3625.	3.4	48
10	A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis. <i>JMIR Public Health and Surveillance</i> , 2020, 6, e19170.	2.6	44
11	Islands as Hotspots for Emerging Mosquito-Borne Viruses: A One-Health Perspective. <i>Viruses</i> , 2019, 11, 11.	3.3	35
12	Phyldynamic applications in 21st century global infectious disease research. <i>Global Health Research and Policy</i> , 2017, 2, 13.	3.6	34
13	Toxigenic <i>Vibrio cholerae</i> evolution and establishment of reservoirs in aquatic ecosystems. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7897-7904.	7.1	33
14	Mayaro as a Caribbean traveler: Evidence for multiple introductions and transmission of the virus into Haiti. <i>International Journal of Infectious Diseases</i> , 2019, 87, 151-153.	3.3	30
15	Complete Genome Sequence of the European Sheatfish Virus. <i>Journal of Virology</i> , 2012, 86, 6365-6366.	3.4	28
16	The genome sequence of ectromelia virus Naval and Cornell isolates from outbreaks in North America. <i>Virology</i> , 2014, 462-463, 218-226.	2.4	26
17	Detection and phylogenetic characterization of arbovirus dual-infections among persons during a chikungunya fever outbreak, Haiti 2014. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006505.	3.0	26
18	A new "American" subgroup of African-lineage Chikungunya virus detected in and isolated from mosquitoes collected in Haiti, 2016. <i>PLoS ONE</i> , 2018, 13, e0196857.	2.5	24

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19	Emergence of Madariaga virus as a cause of acute febrile illness in children, Haiti, 2015-2016. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0006972.	3.0	23
20	Multiple Recombination Events and Strong Purifying Selection at the Origin of SARS-CoV-2 Spike Glycoprotein Increased Correlated Dynamic Movements. <i>International Journal of Molecular Sciences</i> , 2021, 22, 80.	4.1	21
21	Under-the-Radar Dengue Virus Infections in Natural Populations of <i>Aedes aegypti</i> Mosquitoes. <i>MSphere</i> , 2020, 5, .	2.9	19
22	Employing Molecular Phylodynamic Methods to Identify and Forecast HIV Transmission Clusters in Public Health Settings: A Qualitative Study. <i>Viruses</i> , 2020, 12, 921.	3.3	15
23	Madariaga Virus: Identification of a Lineage III Strain in a Venezuelan Child With Acute Undifferentiated Febrile Illness, in the Setting of a Possible Equine Epizootic. <i>Clinical Infectious Diseases</i> , 2018, 67, 619-621.	5.8	14
24	Distribution and characterization of Shiga toxin converting temperate phages carried by <i>Shigella flexneri</i> in Hispaniola. <i>Infection, Genetics and Evolution</i> , 2018, 65, 321-328.	2.3	13
25	Establishment of a Zebrafish Infection Model for the Study of Wild-Type and Recombinant European Sheatfish Virus. <i>Journal of Virology</i> , 2015, 89, 10702-10706.	3.4	12
26	Rapid Emergence and Spread of Severe Acute Respiratory Syndrome Coronavirus 2 Gamma (P.1) Variant in Haiti. <i>Clinical Infectious Diseases</i> , 2022, 74, 2057-2060.	5.8	12
27	Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDIS) for phylogenetics. <i>Bioinformatics</i> , 2022, 38, 856-860.	4.1	10
28	Comparison of SARS-CoV-2 Receptors Expression in Primary Endothelial Cells and Retinoic Acid-Differentiated Human Neuronal Cells. <i>Viruses</i> , 2021, 13, 2193.	3.3	10
29	Presentation of Cytosolically Stable Peptides by HLA-B27 Is Not Dependent on the Canonic Interactions of N-Terminal Basic Residues in the A Pocket. <i>Journal of Immunology</i> , 2009, 182, 446-455.	0.8	8
30	Isolation of Mayaro Virus from a Venezuelan Patient with Febrile Illness, Arthralgias, and Rash: Further Evidence of Regional Strain Circulation and Possible Long-Term Endemicity. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 101, 1219-1225.	1.4	8
31	Low-frequency variants in mildly symptomatic vaccine breakthrough infections presents a doubled-edged sword. <i>Journal of Medical Virology</i> , 2022, , .	5.0	8
32	Brain tissue transcriptomic analysis of SIV-infected macaques identifies several altered metabolic pathways linked to neuropathogenesis and poly (ADP-ribose) polymerases (PARPs) as potential therapeutic targets. <i>Journal of NeuroVirology</i> , 2021, 27, 101-115.	2.1	6
33	Genome Sequence of WAU86/88-1, a New Variant of Vaccinia Virus Lister Strain from Poland. <i>Genome Announcements</i> , 2014, 2, .	0.8	5
34	Comparative Pathogenesis, Genomics and Phylogeography of Mousepox. <i>Viruses</i> , 2021, 13, 1146.	3.3	4
35	Fatal Systemic Salmonellosis in a Florida Manatee (<i>Trichechus manatus latirostris</i>). <i>Journal of Wildlife Diseases</i> , 2017, 53, 930-933.	0.8	2
36	Analysis of the Origin and Dissemination of HIV-1 Subtype C in Bulgaria. <i>Viruses</i> , 2022, 14, 263.	3.3	2

#	ARTICLE	IF	CITATIONS
37	Integrating Phylodynamic Techniques for Next-generation HIV Surveillance in Florida. Online Journal of Public Health Informatics, 2019, 11, .	0.7	1
38	Authors' Reply to: Errors in Tracing Coronavirus SARS-CoV-2 Transmission Using a Maximum Likelihood Tree. Comment on "A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis" JMIR Public Health and Surveillance, 2020, 6, e24661.	2.6	1
39	Discordance between HIV-1 Population in Plasma at Rebound after Structured Treatment Interruption and Archived Provirus Population in Peripheral Blood Mononuclear Cells. Microbiology Spectrum, 2022, 10, .	3.0	1
40	Molecular Docking-Based Screening for Novel Inhibitors of the Human Immunodeficiency Virus Type 1 Protease that Effectively Reduce the Viral Replication in Human Cells.. Journal of AIDS & Clinical Research, 2021, 12, .	0.5	0