

Rebecca A Halpin

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

2,649
citations

172457

29
h-index

197818

49
g-index

52
all docs

52
docs citations

52
times ranked

4259
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , 2016, 48, 195-200.	21.4	182
2	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19359-19364.	7.1	146
3	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. <i>Journal of Virology</i> , 2014, 88, 2844-2857.	3.4	137
4	The soft palate is an important site of adaptation for transmissible influenza viruses. <i>Nature</i> , 2015, 526, 122-125.	27.8	133
5	Deep Sequencing Reveals Mixed Infection with 2009 Pandemic Influenza A (H1N1) Virus Strains and the Emergence of Oseltamivir Resistance. <i>Journal of Infectious Diseases</i> , 2011, 203, 168-174.	4.0	113
6	Deep Sequencing of Influenza A Virus from a Human Challenge Study Reveals a Selective Bottleneck and Only Limited Intra-host Genetic Diversification. <i>Journal of Virology</i> , 2016, 90, 11247-11258.	3.4	97
7	Mixed Infection and the Genesis of Influenza Virus Diversity. <i>Journal of Virology</i> , 2009, 83, 8832-8841.	3.4	95
8	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. <i>Ecology Letters</i> , 2012, 15, 24-33.	6.4	86
9	Universal Influenza B Virus Genomic Amplification Facilitates Sequencing, Diagnostics, and Reverse Genetics. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1330-1337.	3.9	86
10	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	4.7	83
11	Avian Influenza Viruses in Wild Birds: Virus Evolution in a Multihost Ecosystem. <i>Journal of Virology</i> , 2018, 92, .	3.4	83
12	Genomic and Protein Structural Maps of Adaptive Evolution of Human Influenza A Virus to Increased Virulence in the Mouse. <i>PLoS ONE</i> , 2011, 6, e21740.	2.5	79
13	Respiratory Syncytial Virus whole-genome sequencing identifies convergent evolution of sequence duplication in the C-terminus of the G gene. <i>Scientific Reports</i> , 2016, 6, 26311.	3.3	77
14	Nasopharyngeal <i>Lactobacillus</i> is associated with a reduced risk of childhood wheezing illnesses following acute respiratory syncytial virus infection in infancy. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 142, 1447-1456.e9.	2.9	74
15	Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection. <i>Nature Communications</i> , 2020, 11, 2537.	12.8	72
16	North Atlantic Migratory Bird Flyways Provide Routes for Intercontinental Movement of Avian Influenza Viruses. <i>PLoS ONE</i> , 2014, 9, e92075.	2.5	65
17	Sequencing and Analysis of Globally Obtained Human Respiratory Syncytial Virus A and B Genomes. <i>PLoS ONE</i> , 2015, 10, e0120098.	2.5	61
18	Molecular Evolution and Intraclade Recombination of Enterovirus D68 during the 2014 Outbreak in the United States. <i>Journal of Virology</i> , 2016, 90, 1997-2007.	3.4	59

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19	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005693.	3.0	56
20	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012–2013. <i>Clinical Infectious Diseases</i> , 2018, 67, 327-333.	5.8	53
21	Analysis of Recombinant H7N9 Wild-Type and Mutant Viruses in Pigs Shows that the Q226L Mutation in HA Is Important for Transmission. <i>Journal of Virology</i> , 2014, 88, 8153-8165.	3.4	52
22	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	3.4	51
23	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. <i>PLoS Pathogens</i> , 2016, 12, e1005620.	4.7	48
24	Extensive Geographical Mixing of 2009 Human H1N1 Influenza A Virus in a Single University Community. <i>Journal of Virology</i> , 2011, 85, 6923-6929.	3.4	43
25	Whole genome detection of rotavirus mixed infections in human, porcine and bovine samples co-infected with various rotavirus strains collected from sub-Saharan Africa. <i>Infection, Genetics and Evolution</i> , 2015, 31, 321-334.	2.3	42
26	Reversion of Cold-Adapted Live Attenuated Influenza Vaccine into a Pathogenic Virus. <i>Journal of Virology</i> , 2016, 90, 8454-8463.	3.4	42
27	The effective rate of influenza reassortment is limited during human infection. <i>PLoS Pathogens</i> , 2017, 13, e1006203.	4.7	42
28	Whole genome analyses of G1P[8] rotavirus strains from vaccinated and non-vaccinated South African children presenting with diarrhea. <i>Journal of Medical Virology</i> , 2015, 87, 79-101.	5.0	36
29	Evolution of a reassortant North American gull influenza virus lineage: drift, shift and stability. <i>Virology Journal</i> , 2013, 10, 179.	3.4	34
30	Large-Scale Complete-Genome Sequencing and Phylogenetic Analysis of Eastern Equine Encephalitis Virus Reveals Source-Sink Transmission Dynamics in the United States. <i>Journal of Virology</i> , 2018, 92, .	3.4	31
31	Multiple Introductions and Antigenic Mismatch with Vaccines May Contribute to Increased Predominance of G12P[8] Rotaviruses in the United States. <i>Journal of Virology</i> , 2019, 93, .	3.4	31
32	Whole-genome analyses of DS-1-like human G2P[4] and G8P[4] rotavirus strains from Eastern, Western and Southern Africa. <i>Virus Genes</i> , 2014, 49, 196-207.	1.6	29
33	Phylogeography of Influenza A(H3N2) Virus in Peru, 2010–2012. <i>Emerging Infectious Diseases</i> , 2015, 21, 1330-1338.	4.3	29
34	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. <i>Journal of Virology</i> , 2015, 89, 2442-2447.	3.4	29
35	Spread and Persistence of Influenza A Viruses in Waterfowl Hosts in the North American Mississippi Migratory Flyway. <i>Journal of Virology</i> , 2015, 89, 5371-5381.	3.4	29
36	Multiplex Reverse Transcription-PCR for Simultaneous Surveillance of Influenza A and B Viruses. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3492-3501.	3.9	29

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37	Whole-genome sequencing and analyses identify high genetic heterogeneity, diversity and endemicity of rotavirus genotype P[6] strains circulating in Africa. <i>Infection, Genetics and Evolution</i> , 2018, 63, 79-88.	2.3	26
38	Genomic analysis of 16 Colorado human NL63 coronaviruses identifies a new genotype, high sequence diversity in the N-terminal domain of the spike gene and evidence of recombination. <i>Journal of General Virology</i> , 2012, 93, 2387-2398.	2.9	25
39	Influenza A virus evolution and spatio-temporal dynamics in Eurasian wild birds: a phylogenetic and phylogeographical study of whole-genome sequence data. <i>Journal of General Virology</i> , 2015, 96, 2050-2060.	2.9	23
40	The emergence and evolution of influenza A (H1N1) viruses in swine in Canada and the United States. <i>Journal of General Virology</i> , 2017, 98, 2663-2675.	2.9	23
41	Comparative <i>In Vitro</i> and <i>In Vivo</i> Studies of Porcine Rotavirus G9P[13] and Human Rotavirus Wa G1P[8]. <i>Journal of Virology</i> , 2016, 90, 142-151.	3.4	19
42	Migration and Persistence of Human Influenza A Viruses, Vietnam, 2001–2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 1756-1765.	4.3	16
43	Unseasonal Transmission of H3N2 Influenza A Virus During the Swine-Origin H1N1 Pandemic. <i>Journal of Virology</i> , 2010, 84, 5715-5718.	3.4	15
44	Evolutionary dynamics and molecular epidemiology of West Nile virus in New York State: 1999–2015. <i>Virus Evolution</i> , 2019, 5, vez020.	4.9	14
45	H7N9 influenza A virus in turkeys in Minnesota. <i>Journal of General Virology</i> , 2015, 96, 269-276.	2.9	12
46	Molecular characterization of respiratory syncytial viruses circulating in a paediatric cohort in Amman, Jordan. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
47	Complete Genomic Sequence for an Avian Group G Rotavirus from South Africa. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
48	The evolutionary dynamics of influenza A and B viruses in the tropical city of Managua, Nicaragua. <i>Virology</i> , 2014, 462-463, 81-90.	2.4	6
49	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 508-513.	3.4	6
50	Amino Acid Substitutions in Positions 385 and 393 of the Hydrophobic Region of VP4 May Be Associated with Rotavirus Attenuation and Cell Culture Adaptation. <i>Viruses</i> , 2020, 12, 408.	3.3	6