

Martha I Nelson

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

5,519
citations

117625

34
h-index

128289

60
g-index

65
all docs

65
docs citations

65
times ranked

6323
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomic and epidemiological dynamics of human influenza A virus. <i>Nature</i> , 2008, 453, 615-619.	27.8	824
2	The evolution of epidemic influenza. <i>Nature Reviews Genetics</i> , 2007, 8, 196-205.	16.3	462
3	The emergence of SARS-CoV-2 in Europe and North America. <i>Science</i> , 2020, 370, 564-570.	12.6	331
4	SARS-CoV-2 infection in free-ranging white-tailed deer. <i>Nature</i> , 2022, 602, 481-486.	27.8	269
5	Reassortment in segmented RNA viruses: mechanisms and outcomes. <i>Nature Reviews Microbiology</i> , 2016, 14, 448-460.	28.6	259
6	Multiple Reassortment Events in the Evolutionary History of H1N1 Influenza A Virus Since 1918. <i>PLoS Pathogens</i> , 2008, 4, e1000012.	4.7	243
7	Origins of the 2009 H1N1 influenza pandemic in swine in Mexico. <i>ELife</i> , 2016, 5, .	6.0	237
8	Reverse zoonosis of influenza to swine: new perspectives on the human-animal interface. <i>Trends in Microbiology</i> , 2015, 23, 142-153.	7.7	196
9	Stochastic Processes Are Key Determinants of Short-Term Evolution in Influenza A Virus. <i>PLoS Pathogens</i> , 2006, 2, e125.	4.7	173
10	Global transmission of influenza viruses from humans to swine. <i>Journal of General Virology</i> , 2012, 93, 2195-2203.	2.9	154
11	Phylogenetic Analysis Reveals the Global Migration of Seasonal Influenza A Viruses. <i>PLoS Pathogens</i> , 2007, 3, e131.	4.7	136
12	Population dynamics of cocirculating swine influenza A viruses in the United States from 2009 to 2012. <i>Influenza and Other Respiratory Viruses</i> , 2013, 7, 42-51.	3.4	134
13	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015, 6, 6696.	12.8	128
14	The early diversification of influenza A/H1N1pdm. <i>PLOS Currents</i> , 2009, 1, RRN1126.	1.4	121
15	Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5110.	12.8	118
16	Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine. <i>PLoS Pathogens</i> , 2011, 7, e1002077.	4.7	116
17	The Role of Viral Introductions in Sustaining Community-Based HIV Epidemics in Rural Uganda: Evidence from Spatial Clustering, Phylogenetics, and Egocentric Transmission Models. <i>PLoS Medicine</i> , 2014, 11, e1001610.	8.4	114
18	Evolution of Novel Reassortant A/H3N2 Influenza Viruses in North American Swine and Humans, 2009-2011. <i>Journal of Virology</i> , 2012, 86, 8872-8878.	3.4	108

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19	Continual Reintroduction of Human Pandemic H1N1 Influenza A Viruses into Swine in the United States, 2009 to 2014. <i>Journal of Virology</i> , 2015, 89, 6218-6226.	3.4	104
20	Molecular Epidemiology of A/H3N2 and A/H1N1 Influenza Virus during a Single Epidemic Season in the United States. <i>PLoS Pathogens</i> , 2008, 4, e1000133.	4.7	97
21	The origin and global emergence of adamantane resistant A/H3N2 influenza viruses. <i>Virology</i> , 2009, 388, 270-278.	2.4	96
22	Introductions and Evolution of Human-Origin Seasonal Influenza A Viruses in Multinational Swine Populations. <i>Journal of Virology</i> , 2014, 88, 10110-10119.	3.4	88
23	Human Influenza A Virus Hemagglutinin Glycan Evolution Follows a Temporal Pattern to a Glycan Limit. <i>MBio</i> , 2019, 10, .	4.1	74
24	Genotype patterns of contemporary reassorted H3N2 virus in US swine. <i>Journal of General Virology</i> , 2013, 94, 1236-1241.	2.9	68
25	Sequencing and Analysis of Globally Obtained Human Respiratory Syncytial Virus A and B Genomes. <i>PLoS ONE</i> , 2015, 10, e0120098.	2.5	61
26	Genomic and evolutionary inferences between American and global strains of porcine epidemic diarrhea virus. <i>Preventive Veterinary Medicine</i> , 2016, 123, 175-184.	1.9	60
27	Phylogeography of the Spring and Fall Waves of the H1N1/09 Pandemic Influenza Virus in the United States. <i>Journal of Virology</i> , 2011, 85, 828-834.	3.4	54
28	Whole Genome Sequencing and Evolutionary Analysis of Human Respiratory Syncytial Virus A and B from Milwaukee, WI 1998-2010. <i>PLoS ONE</i> , 2011, 6, e25468.	2.5	53
29	Genotype patterns of contemporary reassorted H3N2 virus in US swine. <i>Journal of General Virology</i> , 2013, 94, 1236-1241.	2.9	52
30	Characterization of co-circulating swine influenza A viruses in North America and the identification of a novel H1 genetic clade with antigenic significance. <i>Virus Research</i> , 2015, 201, 24-31.	2.2	48
31	Influenza A Viruses of Human Origin in Swine, Brazil. <i>Emerging Infectious Diseases</i> , 2015, 21, 1339-1347.	4.3	46
32	Emergence and Evolution of Novel Reassortant Influenza A Viruses in Canines in Southern China. <i>MBio</i> , 2018, 9, .	4.1	41
33	Genomic reassortment of influenza A virus in North American swine, 1998–2011. <i>Journal of General Virology</i> , 2012, 93, 2584-2589.	2.9	40
34	Characterization and evolution of porcine deltacoronavirus in the United States. <i>Preventive Veterinary Medicine</i> , 2016, 123, 168-174.	1.9	40
35	Contrasting the epidemiological and evolutionary dynamics of influenza spatial transmission. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120199.	4.0	38
36	Origins of the 1918 Pandemic: Revisiting the Swine “Mixing Vessel” Hypothesis. <i>American Journal of Epidemiology</i> , 2018, 187, 2498-2502.	3.4	29

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37	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 173-182.	4.0	28
38	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
39	Novel Human-like Influenza A Viruses Circulate in Swine in Mexico and Chile. <i>PLOS Currents</i> , 2015, 7, .	1.4	23
40	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. <i>Journal of Virology</i> , 2016, 90, 10963-10971.	3.4	22
41	Beyond clinical trials: Evolutionary and epidemiological considerations for development of a universal influenza vaccine. <i>PLoS Pathogens</i> , 2020, 16, e1008583.	4.7	22
42	Evolution of rotavirus C in humans and several domestic animal species. <i>Zoonoses and Public Health</i> , 2019, 66, 546-557.	2.2	20
43	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. <i>Emerging Infectious Diseases</i> , 2019, 25, 691-700.	4.3	18
44	Characterization of an influenza A virus in Mexican swine that is related to the A/H1N1/2009 pandemic clade. <i>Virology</i> , 2012, 433, 176-182.	2.4	17
45	Fogarty International Center collaborative networks in infectious disease modeling: Lessons learnt in research and capacity building. <i>Epidemics</i> , 2019, 26, 116-127.	3.0	16
46	When Pigs Fly: Pandemic influenza enters the 21st century. <i>PLoS Pathogens</i> , 2020, 16, e1008259.	4.7	16
47	Genetic Diversity of Noroviruses Circulating in a Pediatric Cohort in Bangladesh. <i>Journal of Infectious Diseases</i> , 2018, 218, 1937-1942.	4.0	13
48	Characterization of swine-origin H1N1 canine influenza viruses. <i>Emerging Microbes and Infections</i> , 2019, 8, 1017-1026.	6.5	13
49	Genome plasticity of triple-reassortant H1N1 influenza A virus during infection of vaccinated pigs. <i>Journal of General Virology</i> , 2015, 96, 2982-2993.	2.9	9
50	Molecular characterization of respiratory syncytial viruses circulating in a paediatric cohort in Amman, Jordan. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
51	A Heterogeneous Swine Show Circuit Drives Zoonotic Transmission of Influenza A Viruses in the United States. <i>Journal of Virology</i> , 2020, 94, .	3.4	7
52	Homotypic protection against influenza in a pediatric cohort in Managua, Nicaragua. <i>Nature Communications</i> , 2022, 13, 1190.	12.8	7
53	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
54	Tracking the UK SARS-CoV-2 outbreak. <i>Science</i> , 2021, 371, 680-681.	12.6	6

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55	Tracing the Source of Influenza A Virus Zoonoses in Interconnected Circuits of Swine Exhibitions. <i>Journal of Infectious Diseases</i> , 2021, 224, 458-468.	4.0	6
56	The challenges of vaccine strain selection. <i>ELife</i> , 2020, 9, .	6.0	5
57	Coordinating SARS-CoV-2 genomic surveillance in the United States. <i>Virus Evolution</i> , 2021, 7, veab053.	4.9	3
58	The Evolutionary Dynamics of Influenza A Viruses Circulating in Mallards in Duck Hunting Preserves in Maryland, USA. <i>Microorganisms</i> , 2021, 9, 40.	3.6	3
59	Birth cohort relative to an influenza A virus's antigenic cluster introduction drives patterns of children's antibody titers. <i>PLoS Pathogens</i> , 2022, 18, e1010317.	4.7	3
60	Evolution of Influenza A Virus in Intensive and Free-Range Swine Farms in Spain. <i>Virus Evolution</i> , 2022, 7, veab099.	4.9	2
61	Human-Origin Influenza A(H3N2) Reassortant Viruses in Swine, Southeast Mexico. <i>Emerging Infectious Diseases</i> , 2019, 25, .	4.3	0
62	100-year-old pandemic flu viruses yield new genomes. <i>Nature</i> , 2022, 607, 244-245.	27.8	0