

Dhanasekaran Vijaykrishna

List of Publications by Year in descending order

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98
papers

9,829
citations

43973

48
h-index

38300

95
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all docs

110
docs citations

110
times ranked

10211
citing authors

#	ARTICLE	IF	CITATIONS
1	Monitoring International Travelers Arriving in Hong Kong for Genomic Surveillance of SARS-CoV-2. <i>Emerging Infectious Diseases</i> , 2022, 28, 247-250.	2.0	8
2	Genomic epidemiology of SARS-CoV-2 under an elimination strategy in Hong Kong. <i>Nature Communications</i> , 2022, 13, 736.	5.8	26
3	Human seasonal influenza under COVID-19 and the potential consequences of influenza lineage elimination. <i>Nature Communications</i> , 2022, 13, 1721.	5.8	116
4	Off-season RSV epidemics in Australia after easing of COVID-19 restrictions. <i>Nature Communications</i> , 2022, 13, .	5.8	135
5	Genomic epidemiology of seasonal influenza circulation in China during prolonged border closure from 2020 to 2021. <i>Virus Evolution</i> , 2022, 8, .	2.2	1
6	Detection of Tioman Virus in <i>Pteropus vampyrus</i> Near Flores, Indonesia. <i>Viruses</i> , 2021, 13, 563.	1.5	3
7	Reassortment and Persistence of Influenza A Viruses from Diverse Geographic Origins within Australian Wild Birds: Evidence from a Small, Isolated Population of Ruddy Turnstones. <i>Journal of Virology</i> , 2021, 95, .	1.5	6
8	Lineage-specific protection and immune imprinting shape the age distributions of influenza B cases. <i>Nature Communications</i> , 2021, 12, 4313.	5.8	17
9	Genetic and Antigenic Characterization of an Influenza A(H3N2) Outbreak in Cambodia and the Greater Mekong Subregion during the COVID-19 Pandemic, 2020. <i>Journal of Virology</i> , 2021, 95, e0126721.	1.5	15
10	Air travel-related outbreak of multiple SARS-CoV-2 variants. <i>Journal of Travel Medicine</i> , 2021, 28, .	1.4	14
11	Genetic Diversity of SARS-CoV-2 among Travelers Arriving in Hong Kong. <i>Emerging Infectious Diseases</i> , 2021, 27, 2666-2668.	2.0	8
12	Factors Associated With Fatality Due to Avian Influenza A(H7N9) Infection in China. <i>Clinical Infectious Diseases</i> , 2020, 71, 128-132.	2.9	18
13	Genetic diversity of respiratory enteroviruses and rhinoviruses in febrile adults, Singapore, 2007-2013. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 67-71.	1.5	9
14	Locally Acquired Human Infection with Swine-Origin Influenza A(H3N2) Variant Virus, Australia, 2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 143-147.	2.0	14
15	Divergent evolutionary trajectories of influenza B viruses underlie their contemporaneous epidemic activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 619-628.	3.3	80
16	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. <i>Molecular Biology and Evolution</i> , 2020, 37, 3363-3379.	3.5	81
17	CD4+ T Cells Recognize Conserved Influenza A Epitopes through Shared Patterns of V-Gene Usage and Complementary Biochemical Features. <i>Cell Reports</i> , 2020, 32, 107885.	2.9	11
18	Global Transmission, Spatial Segregation, and Recombination Determine the Long-Term Evolution and Epidemiology of Bovine Coronaviruses. <i>Viruses</i> , 2020, 12, 534.	1.5	21

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19	Positive epistasis between viral polymerase and the 3' untranslated region of its genome reveals the epidemiologic fitness of dengue virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11038-11047.	3.3	22
20	Epidemiological trends in notified influenza cases in Australia's Northern Territory, 2007-2016. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 541-550.	1.5	9
21	Genome-Scale Phylogeny and Evolutionary Analysis of Ross River Virus Reveals Periodic Sweeps of Lineage Dominance in Western Australia, 1977-2014. <i>Journal of Virology</i> , 2020, 94, .	1.5	14
22	Influenza A-associated severe pneumonia in hospitalized patients: Risk factors and NAI treatments. <i>International Journal of Infectious Diseases</i> , 2020, 92, 208-213.	1.5	35
23	Forensic genomics of a novel <i>Klebsiella quasipneumoniae</i> type from a neonatal intensive care unit in China reveals patterns of colonization, evolution and epidemiology. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
24	A rapid pyrosequencing assay for the molecular detection of influenza viruses with reduced baloxavir susceptibility due to PA/138X amino acid substitutions. <i>Influenza and Other Respiratory Viruses</i> , 2020, 14, 460-464.	1.5	12
25	Locally Acquired Human Infection with Swine-Origin Influenza A(H3N2) Variant Virus, Australia, 2018. <i>Emerging Infectious Diseases</i> , 2020, 26, .	2.0	0
26	Clinical characteristics and outcomes during a severe influenza season in China during 2017-2018. <i>BMC Infectious Diseases</i> , 2019, 19, 668.	1.3	16
27	A T164S mutation in the dengue virus NS1 protein is associated with greater disease severity in mice. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	32
28	Phylogenetic analysis revealed the co-circulation of four dengue virus serotypes in Southern Thailand. <i>PLoS ONE</i> , 2019, 14, e0221179.	1.1	31
29	Emergence of Influenza A(H7N4) Virus, Cambodia. <i>Emerging Infectious Diseases</i> , 2019, 25, 1988-1991.	2.0	10
30	Antarctic Penguins as Reservoirs of Diversity for Avian Avulaviruses. <i>Journal of Virology</i> , 2019, 93, .	1.5	19
31	Baloxavir marboxil susceptibility of influenza viruses from the Asia-Pacific, 2012-2018. <i>Antiviral Research</i> , 2019, 164, 91-96.	1.9	51
32	Human CD8+ T cell cross-reactivity across influenza A, B and C viruses. <i>Nature Immunology</i> , 2019, 20, 613-625.	7.0	180
33	Divergent Barmah Forest Virus from Papua New Guinea. <i>Emerging Infectious Diseases</i> , 2019, 25, 2266-2269.	2.0	11
34	Diversity of A(H5N1) clade 2.3.2.1c avian influenza viruses with evidence of reassortment in Cambodia, 2014-2016. <i>PLoS ONE</i> , 2019, 14, e0226108.	1.1	10
35	The evolution and genetic diversity of avian influenza A(H9N2) viruses in Cambodia, 2015 -2016. <i>PLoS ONE</i> , 2019, 14, e0225428.	1.1	10
36	Intense interseasonal influenza outbreaks, Australia, 2018/19. <i>Eurosurveillance</i> , 2019, 24, .	3.9	27

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37	Evidence for Viral Interference and Cross-reactive Protective Immunity Between Influenza B Virus Lineages. <i>Journal of Infectious Diseases</i> , 2018, 217, 548-559.	1.9	49
38	Adaptive evolution during the establishment of European avian-like H1N1 influenza A virus in swine. <i>Evolutionary Applications</i> , 2018, 11, 534-546.	1.5	12
39	FusC, a member of the M16 protease family acquired by bacteria for iron piracy against plants. <i>PLoS Biology</i> , 2018, 16, e2006026.	2.6	17
40	Divergent Human-Origin Influenza Viruses Detected in Australian Swine Populations. <i>Journal of Virology</i> , 2018, 92, .	1.5	16
41	Evolution and Spatiotemporal Dynamics of Enterovirus A71 Subgenogroups in Vietnam. <i>Journal of Infectious Diseases</i> , 2017, 216, 1371-1379.	1.9	19
42	The ecology and adaptive evolution of influenza A interspecies transmission. <i>Influenza and Other Respiratory Viruses</i> , 2017, 11, 74-84.	1.5	83
43	The Broad Host Range and Genetic Diversity of Mammalian and Avian Astroviruses. <i>Viruses</i> , 2017, 9, 102.	1.5	118
44	Extended Evaluation of Virological, Immunological and Pharmacokinetic Endpoints of CELADEN: A Randomized, Placebo-Controlled Trial of Celgosivir in Dengue Fever Patients. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004851.	1.3	53
45	Genetic characterization of Enterovirus 71 strains circulating in Vietnam in 2012. <i>Virology</i> , 2016, 495, 1-9.	1.1	25
46	Evidence for the Introduction, Reassortment, and Persistence of Diverse Influenza A Viruses in Antarctica. <i>Journal of Virology</i> , 2016, 90, 9674-9682.	1.5	61
47	A Role of Influenza Virus Exposure History in Determining Pandemic Susceptibility and CD8 ⁺ T Cell Responses. <i>Journal of Virology</i> , 2016, 90, 6936-6947.	1.5	23
48	Differential age susceptibility to influenza B/Victoria lineage viruses in the 2015 Australian influenza season. <i>Eurosurveillance</i> , 2016, 21, .	3.9	37
49	RNA Virus Reassortment: An Evolutionary Mechanism for Host Jumps and Immune Evasion. <i>PLoS Pathogens</i> , 2015, 11, e1004902.	2.1	97
50	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. <i>Journal of Virology</i> , 2015, 89, 2442-2447.	1.5	29
51	Ecological Drivers of Virus Evolution: Astrovirus as a Case Study. <i>Journal of Virology</i> , 2015, 89, 6978-6981.	1.5	47
52	Phylodynamics of H1N1/2009 influenza reveals the transition from host adaptation to immune-driven selection. <i>Nature Communications</i> , 2015, 6, 7952.	5.8	107
53	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	2.8	166
54	Molecular Epidemiology of Influenza A(H1N1)pdm09 Virus among Humans and Swine, Sri Lanka. <i>Emerging Infectious Diseases</i> , 2014, 20, 2080-4.	2.0	5

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55	Detection of Evolutionarily Distinct Avian Influenza A Viruses in Antarctica. <i>MBio</i> , 2014, 5, e01098-14.	1.8	86
56	Preexisting CD8 ⁺ T-cell immunity to the H7N9 influenza A virus varies across ethnicities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1049-1054.	3.3	144
57	Identification and molecular characterization of novel and divergent HoBi-like pestiviruses from naturally infected cattle in India. <i>Veterinary Microbiology</i> , 2014, 174, 239-246.	0.8	52
58	Surveillance and characterization of avian influenza viruses from migratory water birds in eastern Hokkaido, the northern part of Japan, 2009–2010. <i>Virus Genes</i> , 2013, 46, 323-329.	0.7	11
59	Inferring patterns of influenza transmission in swine from multiple streams of surveillance data. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20130872.	1.2	14
60	The Recent Establishment of North American H10 Lineage Influenza Viruses in Australian Wild Waterfowl and the Evolution of Australian Avian Influenza Viruses. <i>Journal of Virology</i> , 2013, 87, 10182-10189.	1.5	39
61	Emergence and Diversification of Dengue 2 Cosmopolitan Genotype in Pakistan, 2011. <i>PLoS ONE</i> , 2013, 8, e56391.	1.1	36
62	No evidence for intra-segment recombination of 2009 H1N1 influenza virus in swine. <i>Gene</i> , 2012, 494, 242-245.	1.0	16
63	Genetic Analysis. <i>Methods in Molecular Biology</i> , 2012, 865, 207-227.	0.4	2
64	Feasibility of reconstructed ancestral H5N1 influenza viruses for cross-clade protective vaccine development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 349-354.	3.3	52
65	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. <i>Nature Communications</i> , 2011, 2, 163.	5.8	203
66	Long-term evolution and transmission dynamics of swine influenza A virus. <i>Nature</i> , 2011, 473, 519-522.	13.7	219
67	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.	3.3	146
68	An update of H5N1 viruses: Are they still a threat to Australia?. <i>Microbiology Australia</i> , 2011, 32, 42.	0.1	0
69	The emergence of pandemic influenza viruses. <i>Protein and Cell</i> , 2010, 1, 9-13.	4.8	140
70	Surveillance and Analysis of Avian Influenza Viruses, Australia. <i>Emerging Infectious Diseases</i> , 2010, 16, 1896-1904.	2.0	68
71	Establishment of an H6N2 Influenza Virus Lineage in Domestic Ducks in Southern China. <i>Journal of Virology</i> , 2010, 84, 6978-6986.	1.5	83
72	Rapid Detection of Reassortment of Pandemic H1N1/2009 Influenza Virus. <i>Clinical Chemistry</i> , 2010, 56, 1340-1344.	1.5	26

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73	Reassortment of Pandemic H1N1/2009 Influenza A Virus in Swine. <i>Science</i> , 2010, 328, 1529-1529.	6.0	339
74	Detection of diverse astroviruses from bats in China. <i>Journal of General Virology</i> , 2009, 90, 883-887.	1.3	91
75	Dating the emergence of pandemic influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11709-11712.	3.3	387
76	Characterization of Avian Influenza Viruses A (H5N1) from Wild Birds, Hong Kong, 2004â€“2008. <i>Emerging Infectious Diseases</i> , 2009, 15, 402-407.	2.0	94
77	Gene flow and competitive exclusion of avian influenza A virus in natural reservoir hosts. <i>Virology</i> , 2009, 390, 289-297.	1.1	108
78	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	13.7	1,870
79	Continuing progress towards a unified nomenclature for the highly pathogenic H5N1 avian influenza viruses: divergence of clade 2Âˆ2 viruses. <i>Influenza and Other Respiratory Viruses</i> , 2009, 3, 59-62.	1.5	102
80	The development and genetic diversity of H5N1 influenza virus in China, 1996â€“2006. <i>Virology</i> , 2008, 380, 243-254.	1.1	140
81	Identification of the Progenitors of Indonesian and Vietnamese Avian Influenza A (H5N1) Viruses from Southern China. <i>Journal of Virology</i> , 2008, 82, 3405-3414.	1.5	81
82	Evolutionary Dynamics and Emergence of Panzootic H5N1 Influenza Viruses. <i>PLoS Pathogens</i> , 2008, 4, e1000161.	2.1	143
83	Multiple Sublineages of Influenza A Virus (H5N1), Vietnam, 2005âˆ“2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 632-636.	2.0	91
84	Toward a Unified Nomenclature System for Highly Pathogenic Avian Influenza Virus (H5N1). <i>Emerging Infectious Diseases</i> , 2008, 14, e1-e1.	2.0	273
85	Characterization of Low-Pathogenic H5 Subtype Influenza Viruses from Eurasia: Implications for the Origin of Highly Pathogenic H5N1 Viruses. <i>Journal of Virology</i> , 2007, 81, 7529-7539.	1.5	114
86	Establishment of Influenza A Virus (H6N1) in Minor Poultry Species in Southern China. <i>Journal of Virology</i> , 2007, 81, 10402-10412.	1.5	106
87	Detection of a Novel and Highly Divergent Coronavirus from Asian Leopard Cats and Chinese Ferret Badgers in Southern China. <i>Journal of Virology</i> , 2007, 81, 6920-6926.	1.5	127
88	Evolutionary Insights into the Ecology of Coronaviruses. <i>Journal of Virology</i> , 2007, 81, 4012-4020.	1.5	240
89	The Genesis and Evolution of H9N2 Influenza Viruses in Poultry from Southern China, 2000 to 2005. <i>Journal of Virology</i> , 2007, 81, 10389-10401.	1.5	214
90	A Phylogenetic Evaluation of Whether Endophytes Become Saprotrophs at Host Senescence. <i>Microbial Ecology</i> , 2007, 53, 579-590.	1.4	313

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91	Establishment of multiple sublineages of H5N1 influenza virus in Asia: Implications for pandemic control. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2845-2850.	3.3	557
92	The family Pleosporaceae: intergeneric relationships and phylogenetic perspectives based on sequence analyses of partial 28S rDNA. Mycologia, 2006, 98, 571-583.	0.8	18
93	Evolution and adaptation of H5N1 influenza virus in avian and human hosts in Indonesia and Vietnam. Virology, 2006, 350, 258-268.	1.1	212
94	The family Pleosporaceae: intergeneric relationships and phylogenetic perspectives based on sequence analyses of partial 28S rDNA. Mycologia, 2006, 98, 571-583.	0.8	59
95	Prevalence and Genetic Diversity of Coronaviruses in Bats from China. Journal of Virology, 2006, 80, 7481-7490.	1.5	301
96	Emergence and predominance of an H5N1 influenza variant in China. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16936-16941.	3.3	279
97	Phylogenetics and evolution of nematode-trapping fungi (Orbiliiales) estimated from nuclear and protein coding genes. Mycologia, 2005, 97, 1034-1046.	0.8	60
98	Phylogenetics and evolution of nematode-trapping fungi (Orbiliiales) estimated from nuclear and protein coding genes. Mycologia, 2005, 97, 1034-1046.	0.8	105