

Gavin J D Smith

List of Publications by Year in descending order

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Version: 2024-02-01

129
papers

17,731
citations

20759

60
h-index

17546

121
g-index

136
all docs

136
docs citations

136
times ranked

17018
citing authors

#	ARTICLE	IF	CITATIONS
1	Serological exposure in Bactrian and dromedary camels in Kazakhstan to a MERS or MERS-like coronavirus. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	2
2	Early induction of functional SARS-CoV-2-specific T cells associates with rapid viral clearance and mild disease in COVID-19 patients. <i>Cell Reports</i> , 2021, 34, 108728.	2.9	568
3	Etiology of febrile respiratory infections in the general adult population in Singapore, 2007–2013. <i>Heliyon</i> , 2021, 7, e06329.	1.4	1
4	Association of SARS-CoV-2 clades with clinical, inflammatory and virologic outcomes: An observational study. <i>EBioMedicine</i> , 2021, 66, 103319.	2.7	21
5	Habitat impacts the abundance and network structure within tick (Acari: Ixodidae) communities on tropical small mammals. <i>Ticks and Tick-borne Diseases</i> , 2021, 12, 101654.	1.1	7
6	Genetic diversity and expanded host range of astroviruses detected in small mammals in Singapore. <i>One Health</i> , 2021, 12, 100218.	1.5	3
7	Host specificity of Hepatocystis infection in short-nosed fruit bats (<i>Cynopterus brachyotis</i>) in Singapore. <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2021, 15, 35-42.	0.6	0
8	Genetic Characterization of Highly Pathogenic Avian Influenza A(H5N8) Virus in Pakistani Live Bird Markets Reveals Rapid Diversification of Clade 2.3.4.4b Viruses. <i>Viruses</i> , 2021, 13, 1633.	1.5	7
9	A mouse model of lethal respiratory dysfunction for SARS-CoV-2 infection. <i>Antiviral Research</i> , 2021, 193, 105138.	1.9	14
10	H5Nx Viruses Emerged during the Suppression of H5N1 Virus Populations in Poultry. <i>Microbiology Spectrum</i> , 2021, 9, e0130921.	1.2	7
11	Genomic Evidence for Sequestration of Influenza A Virus Lineages in Sea Duck Host Species. <i>Viruses</i> , 2021, 13, 172.	1.5	1
12	Ancestral sequence reconstruction pinpoints adaptations that enable avian influenza virus transmission in pigs. <i>Nature Microbiology</i> , 2021, 6, 1455-1465.	5.9	7
13	Robust dengue virus infection in bat cells and limited innate immune responses coupled with positive serology from bats in IndoMalaya and Australasia. <i>Cellular and Molecular Life Sciences</i> , 2020, 77, 1607-1622.	2.4	11
14	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
15	The temporal RNA virome patterns of a lesser dawn bat (<i>Eonycteris spelaea</i>) colony revealed by deep sequencing. <i>Virus Evolution</i> , 2020, 6, veaa017.	2.2	10
16	Co-circulation of both low and highly pathogenic avian influenza H5 viruses in current poultry epidemics in Taiwan. <i>Virus Evolution</i> , 2020, 6, veaa037.	2.2	16
17	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
18	Discovery and Genomic Characterization of a 382-Nucleotide Deletion in ORF7b and ORF8 during the Early Evolution of SARS-CoV-2. <i>MBio</i> , 2020, 11, .	1.8	245

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19	Effects of a major deletion in the SARS-CoV-2 genome on the severity of infection and the inflammatory response: an observational cohort study. <i>Lancet, The</i> , 2020, 396, 603-611.	6.3	394
20	Detection of Recombinant Roussettus Bat Coronavirus GCCDC1 in Lesser Dawn Bats (<i>Eonycteris</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 7	1.5	14
21	Lack of cross-neutralization by SARS patient sera towards SARS-CoV-2. <i>Emerging Microbes and Infections</i> , 2020, 9, 900-902.	3.0	89
22	Ecology of bat flies in Singapore: A study on the diversity, infestation bias and host specificity (Diptera: Nycteribiidae). <i>International Journal for Parasitology: Parasites and Wildlife</i> , 2020, 12, 29-33.	0.6	9
23	Novel Insights for Biosurveillance of Bat-Borne Viruses. <i>Proceedings (mdpi)</i> , 2020, 50, .	0.2	0
24	Characterizing Emerging Canine H3 Influenza Viruses. <i>PLoS Pathogens</i> , 2020, 16, e1008409.	2.1	29
25	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
26	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
27	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
28	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
29	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
30	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
31	Isolation of Highly Pathogenic H5N1 Influenza Viruses in 2009â€“2013 in Vietnam. <i>Frontiers in Microbiology</i> , 2019, 10, 1411.	1.5	5
32	Filovirus-reactive antibodies in humans and bats in Northeast India imply zoonotic spillover. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007733.	1.3	30
33	Discovery and Characterization of Novel Bat Coronavirus Lineages from Kazakhstan. <i>Viruses</i> , 2019, 11, 356.	1.5	11
34	Surveillance and characterisation of influenza viruses among patients with influenza-like illness in Bali, Indonesia, July 2010â€“June 2014. <i>BMC Infectious Diseases</i> , 2019, 19, 231.	1.3	4
35	Diversity and Evolution of Viral Pathogen Community in Cave Nectar Bats (<i>Eonycteris spelaea</i>). <i>Viruses</i> , 2019, 11, 250.	1.5	22
36	Avian influenza viruses in humans: lessons from past outbreaks. <i>British Medical Bulletin</i> , 2019, 132, 81-95.	2.7	85

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37	Seroprevalence and awareness of porcine cysticercosis across different pig production systems in south-central Cambodia. <i>Parasite Epidemiology and Control</i> , 2018, 3, 1-12.	0.6	18
38	High diversity of medically important gastrointestinal rodent-borne helminths in Singapore. <i>Zoonoses and Public Health</i> , 2018, 65, 361-366.	0.9	6
39	Clinical and Molecular Epidemiology of Human Parainfluenza Viruses 4 in Children from Viet Nam. <i>Scientific Reports</i> , 2018, 8, 6833.	1.6	20
40	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
41	Detection and genetic characterization of diverse <i>Bartonella</i> genotypes in the small mammals of Singapore. <i>Zoonoses and Public Health</i> , 2018, 65, e207-e215.	0.9	18
42	Avian Influenza A(H9N2) Virus in Poultry Worker, Pakistan, 2015. <i>Emerging Infectious Diseases</i> , 2018, 25, 136-139.	2.0	28
43	Serologic Evidence of Fruit Bat Exposure to Filoviruses, Singapore, 2011-2016. <i>Emerging Infectious Diseases</i> , 2018, 24, 114-117.	2.0	44
44	Influenza. <i>Nature Reviews Disease Primers</i> , 2018, 4, 3.	18.1	880
45	Prevalence and Phylogenetics of H9N2 in Backyard and Commercial Poultry in Pakistan. <i>Avian Diseases</i> , 2018, 62, 416.	0.4	13
46	Influence of age and body condition on astrovirus infection of bats in Singapore: An evolutionary and epidemiological analysis. <i>One Health</i> , 2017, 4, 27-33.	1.5	18
47	The ecology and adaptive evolution of influenza A interspecies transmission. <i>Influenza and Other Respiratory Viruses</i> , 2017, 11, 74-84.	1.5	83
48	Identification of a Lineage D Betacoronavirus in Cave Nectar Bats (<i>Eonycteris spelaea</i>) in Singapore and an Overview of Lineage D Reservoir Ecology in SE Asian Bats. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 1790-1800.	1.3	22
49	A Report of Adult Human Adenovirus Infections in a Tertiary Hospital. <i>Open Forum Infectious Diseases</i> , 2017, 4, ofx053.	0.4	7
50	Monitoring of Newcastle disease virus in environmental samples. <i>Archives of Virology</i> , 2017, 162, 2843-2846.	0.9	4
51	The effective rate of influenza reassortment is limited during human infection. <i>PLoS Pathogens</i> , 2017, 13, e1006203.	2.1	42
52	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. <i>PLoS Pathogens</i> , 2016, 12, e1005620.	2.1	48
53	Evidence of canine parvovirus transmission to a civet cat (<i>Paradoxurus musangus</i>) in Singapore. <i>One Health</i> , 2016, 2, 122-125.	1.5	11
54	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.	1.5	97

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55	Quantifying human impact on Earth's microbiome. <i>Nature Microbiology</i> , 2016, 1, 16145.	5.9	19
56	Characteristics of acute febrile illness and determinants of illness recovery among adults presenting to Singapore primary care clinics. <i>BMC Infectious Diseases</i> , 2016, 16, 612.	1.3	6
57	Detection of a novel astrovirus from a black-naped monarch (<i>Hypothymis azurea</i>) in Cambodia. <i>Virology Journal</i> , 2015, 12, 182.	1.4	11
58	RNA Virus Reassortment: An Evolutionary Mechanism for Host Jumps and Immune Evasion. <i>PLoS Pathogens</i> , 2015, 11, e1004902.	2.1	97
59	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. <i>Journal of Virology</i> , 2015, 89, 2442-2447.	1.5	29
60	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015, 89, 9689-9692.	1.5	10
61	Ecological Drivers of Virus Evolution: Astrovirus as a Case Study. <i>Journal of Virology</i> , 2015, 89, 6978-6981.	1.5	47
62	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.	1.3	23
63	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
64	Nomenclature updates resulting from the evolution of avian influenza A(H5) virus clades 2.1.3.2a, 2.2.1, and 2.3.4 during 2013â€“2014. <i>Influenza and Other Respiratory Viruses</i> , 2015, 9, 271-276.	1.5	283
65	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	2.8	166
66	Revised and updated nomenclature for highly pathogenic avian influenza A (H5N1) viruses. <i>Influenza and Other Respiratory Viruses</i> , 2014, 8, 384-388.	1.5	151
67	Multiannual patterns of influenza A transmission in Chinese live bird market systems. <i>Influenza and Other Respiratory Viruses</i> , 2013, 7, 97-107.	1.5	41
68	Multilocus sequence analysis of <i>Treponema denticola</i> strains of diverse origin. <i>BMC Microbiology</i> , 2013, 13, 24.	1.3	13
69	The emergence and diversification of panzootic H5N1 influenza viruses. <i>Virus Research</i> , 2013, 178, 35-43.	1.1	107
70	Antigenic and Molecular Characterization of Avian Influenza A(H9N2) Viruses, Bangladesh. <i>Emerging Infectious Diseases</i> , 2013, 19, .	2.0	70
71	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	2.1	83
72	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

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73	Evidence for Antigenic Seniority in Influenza A (H3N2) Antibody Responses in Southern China. PLoS Pathogens, 2012, 8, e1002802.	2.1	184
74	No evidence for intra-segment recombination of 2009 H1N1 influenza virus in swine. Gene, 2012, 494, 242-245.	1.0	16
75	Genetic evolution of the neuraminidase of influenza A (H3N2) viruses from 1968 to 2009 and its correspondence to haemagglutinin evolution. Journal of General Virology, 2012, 93, 1996-2007.	1.3	57
76	Genetic Analysis. Methods in Molecular Biology, 2012, 865, 207-227.	0.4	2
77	Continued evolution of highly pathogenic avian influenza A (H5N1): updated nomenclature. Influenza and Other Respiratory Viruses, 2012, 6, 1-5.	1.5	214
78	Emergence and epidemic occurrence of enterovirus 68 respiratory infections in The Netherlands in 2010. Virology, 2012, 423, 49-57.	1.1	152
79	Feasibility of reconstructed ancestral H5N1 influenza viruses for cross-clade protective vaccine development. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 349-354.	3.3	52
80	Ancient origins determine global biogeography of hot and cold desert cyanobacteria. Nature Communications, 2011, 2, 163.	5.8	203
81	Long-term evolution and transmission dynamics of swine influenza A virus. Nature, 2011, 473, 519-522.	13.7	219
82	Genetic Status of Asiatic Black Bear (Ursus thibetanus) Reintroduced into South Korea Based on Mitochondrial DNA and Microsatellite Loci Analysis. Journal of Heredity, 2011, 102, 165-174.	1.0	63
83	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 19359-19364.	3.3	146
84	Location-specific patterns of exposure to recent pre-pandemic strains of influenza A in southern China. Nature Communications, 2011, 2, 423.	5.8	36
85	The emergence of pandemic influenza viruses. Protein and Cell, 2010, 1, 9-13.	4.8	140
86	Establishment of an H6N2 Influenza Virus Lineage in Domestic Ducks in Southern China. Journal of Virology, 2010, 84, 6978-6986.	1.5	83
87	Reassortment of Pandemic H1N1/2009 Influenza A Virus in Swine. Science, 2010, 328, 1529-1529.	6.0	339
88	Detection of novel astroviruses in urban brown rats and previously known astroviruses in humans. Journal of General Virology, 2010, 91, 2457-2462.	1.3	91
89	Detection of diverse astroviruses from bats in China. Journal of General Virology, 2009, 90, 883-887.	1.3	91
90	Dating the emergence of pandemic influenza viruses. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11709-11712.	3.3	387

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91	Nuclear Factor 90 Negatively Regulates Influenza Virus Replication by Interacting with Viral Nucleoprotein. <i>Journal of Virology</i> , 2009, 83, 7850-7861.	1.5	62
92	Characterization of Avian Influenza Viruses A (H5N1) from Wild Birds, Hong Kong, 2004-2008. <i>Emerging Infectious Diseases</i> , 2009, 15, 402-407.	2.0	94
93	Serologic Survey of Pandemic (H1N1) 2009 Virus, Guangxi Province, China. <i>Emerging Infectious Diseases</i> , 2009, 15, 1849-1850.	2.0	77
94	Analysis of H5N1 avian influenza infections from wild bird surveillance in Hong Kong from January 2006 to October 2007. <i>Avian Pathology</i> , 2009, 38, 107-119.	0.8	24
95	Gene flow and competitive exclusion of avian influenza A virus in natural reservoir hosts. <i>Virology</i> , 2009, 390, 289-297.	1.1	108
96	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	13.7	1,870
97	Continuing progress towards a unified nomenclature for the highly pathogenic H5N1 avian influenza viruses: divergence of clade 2A.2 viruses. <i>Influenza and Other Respiratory Viruses</i> , 2009, 3, 59-62.	1.5	102
98	Molecular Detection of a Novel Human Influenza (H1N1) of Pandemic Potential by Conventional and Real-Time Quantitative RT-PCR Assays. <i>Clinical Chemistry</i> , 2009, 55, 1555-1558.	1.5	110
99	Phylogeny of the basal angiosperm genus <i>Pseuduvaria</i> (Annonaceae) inferred from five chloroplast DNA regions, with interpretation of morphological character evolution. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 188-206.	1.2	51
100	The development and genetic diversity of H5N1 influenza virus in China, 1996-2006. <i>Virology</i> , 2008, 380, 243-254.	1.1	140
101	Antigenic Profile of Avian H5N1 Viruses in Asia from 2002 to 2007. <i>Journal of Virology</i> , 2008, 82, 1798-1807.	1.5	100
102	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
103	Evolutionary Dynamics and Emergence of Panzootic H5N1 Influenza Viruses. <i>PLoS Pathogens</i> , 2008, 4, e1000161.	2.1	143
104	Detection and Phylogenetic Analysis of Group 1 Coronaviruses in South American Bats. <i>Emerging Infectious Diseases</i> , 2008, 14, 1890-1893.	2.0	66
105	Multiple Sublineages of Influenza A Virus (H5N1), Vietnam, 2005-2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 632-636.	2.0	91
106	Avian Influenza A Virus (H5N1) Outbreaks, Kuwait, 2007. <i>Emerging Infectious Diseases</i> , 2008, 14, 958-961.	2.0	20
107	Molecular analysis of avian H7 influenza viruses circulating in Eurasia in 1999-2005: detection of multiple reassortant virus genotypes. <i>Journal of General Virology</i> , 2008, 89, 48-59.	1.3	44
108	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

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109	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
110	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
111	Evolution and Molecular Epidemiology of H9N2 Influenza A Viruses from Quail in Southern China, 2000 to 2005. <i>Journal of Virology</i> , 2007, 81, 2635-2645.	1.5	163
112	Evolutionary Insights into the Ecology of Coronaviruses. <i>Journal of Virology</i> , 2007, 81, 4012-4020.	1.5	240
113	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
114	Avian influenza A (H5N1) infection in a patient in China, 2006. <i>Influenza and Other Respiratory Viruses</i> , 2007, 1, 207-213.	1.5	7
115	Establishment of multiple sublineages of H5N1 influenza virus in Asia: Implications for pandemic control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2845-2850.	3.3	557
116	Distribution of Amantadine-resistant H5N1 Avian Influenza Variants in Asia. <i>Journal of Infectious Diseases</i> , 2006, 193, 1626-1629.	1.9	243
117	H5N1 Influenza Viruses in Lao People's Democratic Republic. <i>Emerging Infectious Diseases</i> , 2006, 12, 1593-1595.	2.0	20
118	Fatal outcome of human influenza A (H5N1) is associated with high viral load and hypercytokinemia. <i>Nature Medicine</i> , 2006, 12, 1203-1207.	15.2	1,645
119	Evolution and adaptation of H5N1 influenza virus in avian and human hosts in Indonesia and Vietnam. <i>Virology</i> , 2006, 350, 258-268.	1.1	212
120	Avian influenza H5N1 in viverrids: implications for wildlife health and conservation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1729-1732.	1.2	80
121	Prevalence and Genetic Diversity of Coronaviruses in Bats from China. <i>Journal of Virology</i> , 2006, 80, 7481-7490.	1.5	301
122	Emergence and predominance of an H5N1 influenza variant in China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16936-16941.	3.3	279
123	H5N1 virus outbreak in migratory waterfowl. <i>Nature</i> , 2005, 436, 191-192.	13.7	708
124	Screening of basidiomycetes and xylariaceous fungi for lignin peroxidase and laccase gene-specific sequences. <i>Mycological Research</i> , 2005, 109, 115-124.	2.5	69
125	Human Infection with an Avian H9N2 Influenza A Virus in Hong Kong in 2003. <i>Journal of Clinical Microbiology</i> , 2005, 43, 5760-5767.	1.8	561
126	Community structure of free-floating filamentous cyanobacterial mats from the Wonder Lake geothermal springs in the Philippines. <i>Canadian Journal of Microbiology</i> , 2005, 51, 583-589.	0.8	15

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127	Oseltamivir Resistance during Treatment of Influenza A (H5N1) Infection. New England Journal of Medicine, 2005, 353, 2667-2672.	13.9	823
128	Genesis of a highly pathogenic and potentially pandemic H5N1 influenza virus in eastern Asia. Nature, 2004, 430, 209-213.	13.7	1,147
129	A Look inside the Replication Dynamics of SARS-CoV-2 in Blyth's Horseshoe Bat (<i>Rhinolophus</i>) Tj ETQq1 1 0,784314 rgBT /Ov	1.2	2