Derek J Smith

List of Publications by Citations

106 papers	11,891 citations	46 h-index	109 g-index
113 ext. papers	13,921 ext. citations	13.1 avg, IF	5.53 L-index

#	Paper	IF	Citations
106	Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. *Science*, **2009**, 325, 197-201	33.3	1844
105	Mapping the antigenic and genetic evolution of influenza virus. *Science*, **2004**, 305, 371-6	33.3	1181
104	Airborne transmission of influenza A/H5N1 virus between ferrets. *Science*, **2012**, 336, 1534-41	33.3	1162
103	Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from black-headed gulls. *Journal of Virology*, **2005**, 79, 2814-22	6.6	1109
102	The global circulation of seasonal influenza A (H3N2) viruses. *Science*, **2008**, 320, 340-6	33.3	515
101	Substitutions near the receptor binding site determine major antigenic change during influenza virus evolution. *Science*, **2013**, 342, 976-9	33.3	379
100	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. *Nature*, **2015**, 523, 217-20	50.4	302
99	Variable efficacy of repeated annual influenza vaccination. *Proceedings of the National Academy of Sciences of the United States of America*, **1999**, 96, 14001-6	11.5	275
98	Antibody landscapes after influenza virus infection or vaccination. *Science*, **2014**, 346, 996-1000	33.3	259
97	The potential for respiratory droplet-transmissible A/H5N1 influenza virus to evolve in a mammalian host. *Science*, **2012**, 336, 1541-7	33.3	231
96	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. *PLoS Pathogens*, **2014**, 10, e1003932	7.6	230
95	Integrating influenza antigenic dynamics with molecular evolution. *ELife*, **2014**, 3, e01914	8.9	213
94	Virulence-associated substitution D222G in the hemagglutinin of 2009 pandemic influenza A(H1N1) virus affects receptor binding. *Journal of Virology*, **2010**, 84, 11802-13	6.6	171
93	Limited airborne transmission of H7N9 influenza A virus between ferrets. *Nature*, **2013**, 501, 560-3	50.4	164
92	Flavivirus-induced antibody cross-reactivity. *Journal of General Virology*, **2011**, 92, 2821-2829	4.9	163
91	Influenza vaccine strain selection and recent studies on the global migration of seasonal influenza viruses. *Vaccine*, **2008**, 26 Suppl 4, D31-4	4.1	163
90	Reemergence of enterovirus 71 in 2008 in taiwan: dynamics of genetic and antigenic evolution from 1998 to 2008. *Journal of Clinical Microbiology*, **2009**, 47, 3653-62	9.7	155

89	Discordant antigenic drift of neuraminidase and hemagglutinin in H1N1 and H3N2 influenza viruses. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 20748-53	11.5	140
88	Dengue viruses cluster antigenically but not as discrete serotypes. *Science*, **2015**, 349, 1338-43	33.3	139
87	Epidemiological, antigenic and genetic characteristics of seasonal influenza A(H1N1), A(H3N2) and B influenza viruses: basis for the WHO recommendation on the composition of influenza vaccines for use in the 2009-2010 northern hemisphere season. *Vaccine*, **2010**, 28, 1156-67	4.1	130
86	Antigenic and genetic evolution of swine influenza A (H3N2) viruses in Europe. *Journal of Virology*, **2007**, 81, 4315-22	6.6	128
85	Prevalence of antibodies against seasonal influenza A and B viruses in children in Netherlands. *Vaccine Journal*, **2011**, 18, 469-76		125
84	Cochrane re-arranged: support for policies to vaccinate elderly people against influenza. *Vaccine*, **2013**, 31, 6030-3	4.1	117
83	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. *Nature*, **2018**, 557, 418-423	50.4	112
82	Annual revaccination against influenza and mortality risk in community-dwelling elderly persons. *JAMA - Journal of the American Medical Association*, **2004**, 292, 2089-95	27.4	109
81	Recognition of homo- and heterosubtypic variants of influenza A viruses by human CD8+ T lymphocytes. *Journal of Immunology*, **2004**, 172, 2453-60	5.3	104
80	Genomewide analysis of reassortment and evolution of human influenza A(H3N2) viruses circulating between 1968 and 2011. *Journal of Virology*, **2014**, 88, 2844-57	6.6	100
79	Genetic and antigenic characterization of H1 influenza viruses from United States swine from 2008. *Journal of General Virology*, **2011**, 92, 919-30	4.9	99
78	Serial Vaccination and the Antigenic Distance Hypothesis: Effects on Influenza Vaccine Effectiveness During A(H3N2) Epidemics in Canada, 2010-2011 to 2014-2015. *Journal of Infectious Diseases*, **2017**, 215, 1059-1099	7	96
77	Enhancing disease surveillance with novel data streams: challenges and opportunities. *EPJ Data Science*, **2015**, 4,	3.4	96
76	A recommended numbering scheme for influenza A HA subtypes. *PLoS ONE*, **2014**, 9, e112302	3.7	94
75	Quantifying the impact of immune escape on transmission dynamics of influenza. *Science*, **2009**, 326, 726-8	33.3	80
74	WHO recommendations for the viruses used in the 2013-2014 Northern Hemisphere influenza vaccine: Epidemiology, antigenic and genetic characteristics of influenza A(H1N1)pdm09, A(H3N2) and B influenza viruses collected from October 2012 to January 2013. *Vaccine*, **2014**, 32, 4713-25	4.1	74
73	Antigenic and genetic evolution of equine influenza A (H3N8) virus from 1968 to 2007. *Journal of Virology*, **2011**, 85, 12742-9	6.6	71
72	The confounded effects of age and exposure history in response to influenza vaccination. *Vaccine*, **2016**, 34, 540-546	4.1	71

71	Studies needed to address public health challenges of the 2009 H1N1 influenza pandemic: insights from modeling. *PLoS Medicine*, **2010**, 7, e1000275	11.6	69
70	Predictability and preparedness in influenza control. *Science*, **2006**, 312, 392-4	33.3	66
69	Quantifying antigenic relationships among the lyssaviruses. *Journal of Virology*, **2010**, 84, 11841-8	6.6	62
68	Antibody titer has positive predictive value for vaccine protection against challenge with natural antigenic-drift variants of H5N1 high-pathogenicity avian influenza viruses from Indonesia. *Journal of Virology*, **2015**, 89, 3746-62	6.6	59
67	Identification of amino acid substitutions supporting antigenic change of influenza A(H1N1)pdm09 viruses. *Journal of Virology*, **2015**, 89, 3763-75	6.6	59
66	Circulating avian influenza viruses closely related to the 1918 virus have pandemic potential. *Cell Host and Microbe*, **2014**, 15, 692-705	23.4	56
65	Deriving shape space parameters from immunological data. *Journal of Theoretical Biology*, **1997**, 189, 141-50	2.3	54
64	Viridot: An automated virus plaque (immunofocus) counter for the measurement of serological neutralizing responses with application to dengue virus. *PLoS Neglected Tropical Diseases*, **2018**, 12, e0006862	4.8	52
63	WHO recommendations for the viruses to be used in the 2012 Southern Hemisphere Influenza Vaccine: epidemiology, antigenic and genetic characteristics of influenza A(H1N1)pdm09, A(H3N2) and B influenza viruses collected from February to September 2011. *Vaccine*, **2012**, 30, 6461-71	4.1	50
62	Full restoration of viral fitness by multiple compensatory co-mutations in the nucleoprotein of influenza A virus cytotoxic T-lymphocyte escape mutants. *Journal of General Virology*, **2005**, 86, 1801-1805	4.9	50
61	H7 avian influenza virus vaccines protect chickens against challenge with antigenically diverse isolates. *Vaccine*, **2011**, 29, 7424-9	4.1	47
60	Selection of antigenically advanced variants of seasonal influenza viruses. *Nature Microbiology*, **2016**, 1, 16058	26.6	46
59	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	4.9	44
58	Use of antigenic cartography in vaccine seed strain selection. *Avian Diseases*, **2010**, 54, 220-3	1.6	42
57	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. *Science*, **2020**, 369,	33.3	42
56	Evolution of re-emergent virus and its impact on enterovirus 71 epidemics. *Experimental Biology and Medicine*, **2011**, 236, 899-908	3.7	41
55	A review of influenza haemagglutinin receptor binding as it relates to pandemic properties. *Vaccine* , **2012**, 30, 4369-76	4.1	40
54	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 7557-7562	11.5	39

53	Antigenic variation of clade 2.1 H5N1 virus is determined by a few amino acid substitutions immediately adjacent to the receptor binding site. *MBio*, **2014**, 5, e01070-14	7.8	38
52	Avian influenza virus surveillance in wild birds in Georgia: 2009-2011. *PLoS ONE*, **2013**, 8, e58534	3.7	37
51	Circulation of reassortant influenza A(H7N9) viruses in poultry and humans, Guangdong Province, China, 2013. *Emerging Infectious Diseases*, **2014**, 20, 2034-40	10.2	34
50	Excessive production and extreme editing of human metapneumovirus defective interfering RNA is associated with type I IFN induction. *Journal of General Virology*, **2014**, 95, 1625-1633	4.9	31
49	Vaccination against highly pathogenic avian influenza H5N1 virus in zoos using an adjuvanted inactivated H5N2 vaccine. *Vaccine*, **2007**, 25, 3800-8	4.1	30
48	Antigenic Drift of the Influenza A(H1N1)pdm09 Virus Neuraminidase Results in Reduced Effectiveness of A/California/7/2009 (H1N1pdm09)-Specific Antibodies. *MBio*, **2019**, 10,	7.8	28
47	Antigenic variation of foot-and-mouth disease virus serotype A. *Journal of General Virology*, **2014**, 95, 384-392	4.9	28
46	Mapping Enterovirus A71 Antigenic Determinants from Viral Evolution. *Journal of Virology*, **2015**, 89, 11500-6	6.6	25
45	Applications of bioinformatics and computational biology to influenza surveillance and vaccine strain selection. *Vaccine*, **2003**, 21, 1758-61	4.1	22
44	Gain-of-function experiments on H7N9. *Science*, **2013**, 341, 612-3	33.3	18
43	Using lazy evaluation to simulate realistic-size repertoires in models of the immune system. *Bulletin of Mathematical Biology*, **1998**, 60, 647-58	2.1	17
42	Serological evidence for non-lethal exposures of Mongolian wild birds to highly pathogenic avian influenza H5N1 virus. *PLoS ONE*, **2014**, 9, e113569	3.7	17
41	Evaluation of serological trials submitted for annual re-licensure of influenza vaccines to regulatory authorities between 1992 and 2002. *Vaccine*, **2009**, 28, 392-7	4.1	16
40	An amino acid substitution in the influenza A virus hemagglutinin associated with escape from recognition by human virus-specific CD4+ T-cells. *Virus Research*, **2007**, 126, 282-7	6.4	15
39	Characterizing Emerging Canine H3 Influenza Viruses. *PLoS Pathogens*, **2020**, 16, e1008409	7.6	15
38	The Molecular Basis for Antigenic Drift of Human A/H2N2 Influenza Viruses. *Journal of Virology*, **2019**, 93,	6.6	14
37	Antigenic Relationships among Human Pathogenic Orientia tsutsugamushi Isolates from Thailand. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004723	4.8	14
36	Influenza B vaccine lineage selection--an optimized trivalent vaccine. *Vaccine*, **2016**, 34, 1617-1622	4.1	13

35	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains **2021**,		11
34	Factors determining human-to-human transmissibility of zoonotic pathogens via contact. *Current Opinion in Virology*, **2017**, 22, 7-12	7.5	10
33	Characterization of influenza A(H1N1)pdm09 viruses isolated from Nepalese and Indian outbreak patients in early 2015. *Influenza and Other Respiratory Viruses*, **2017**, 11, 399-403	5.6	10
32	Genetic and antigenic characterisation of influenza A(H3N2) viruses isolated in Yokohama during the 2016/17 and 2017/18 influenza seasons. *Eurosurveillance*, **2019**, 24,	19.8	10
31	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains. *Science Translational Medicine*, **2021**, eabm3302	17.5	10
30	Mapping SARS-CoV-2 antigenic relationships and serological responses		8
29	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains. *Science Translational Medicine*, **2022**, 14,	17.5	8
28	Epistatic interactions can moderate the antigenic effect of substitutions in haemagglutinin of influenza H3N2 virus. *Journal of General Virology*, **2019**, 100, 773-777	4.9	7
27	Immunological Memory is Associative* **1999**, 105-114		7
26	Omicron BA.1 and BA.2 are antigenically distinct SARS-CoV-2 variants		7
25	Defining the risk of SARS-CoV-2 variants on immune protection.. *Nature*, **2022**,	50.4	7
24	Antigenic evolution of dengue viruses over 20 years. *Science*, **2021**, 374, 999-1004	33.3	5
23	Modeling the effects of prior infection on vaccine efficacy		4
22	Modeling the effects of updating the influenza vaccine on the efficacy of repeated vaccination. *International Congress Series*, **2001**, 1219, 655-660		4
21	Plasticity of the Influenza Virus H5 HA Protein. *MBio*, **2021**, 12,	7.8	4
20	Correction for Koel et al., Antigenic Variation of Clade 2.1 H5N1 Virus Is Determined by a Few Amino Acid Substitutions Immediately Adjacent to the Receptor Binding Site. *MBio*, **2014**, 5,	7.8	3
19	Mutations, drift, and the influenza archipelago. *Discovery Medicine*, **2004**, 4, 371-7	2.5	3
18	Influenza virus infection history shapes antibody responses to influenza vaccination.. *Nature Medicine*, **2022**,	50.5	3

17	Reply: Letter to the editor, Cochrane rearranged. *Vaccine*, **2015**, 33, 13-4	4.1	2
16	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. *Wellcome Open Research*, **2018**, 3, 44	4.8	2
15	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. *Wellcome Open Research*, **2018**, 3, 44	4.8	2
14	Epistatic interactions can moderate the antigenic effect of substitutions in hemagglutinin of influenza H3N2 virus		2
13	80 questions for UK biological security. *PLoS ONE*, **2021**, 16, e0241190	3.7	2
12	Vaccination with SARS-CoV-2 variants of concern protects mice from challenge with wild-type virus.. *PLoS Biology*, **2021**, 19, e3001384	9.7	2
11	Antigenic Cartography of Human and Swine Influenza A (H3N2) Viruses. *Novartis Foundation Symposium*,32-44		1
10	Beneath the surface: Amino acid variation underlying two decades of dengue virus antigenic dynamics in Bangkok, Thailand.. *PLoS Pathogens*, **2022**, 18, e1010500	7.6	0
9	Applications of quantitative modeling to influenza virus transmission dynamics, antigenic and genetic evolution, and molecular structure **2013**, 434-452		
8	Recognition of influenza virus epitope variants by human CTL. *International Congress Series*, **2004**, 1263, 145-148		
7	Modeling the Effects of Prior Infection on Vaccine Efficacy **1999**, 144-153		
6	Characterizing Emerging Canine H3 Influenza Viruses **2020**, 16, e1008409		
5	Characterizing Emerging Canine H3 Influenza Viruses **2020**, 16, e1008409		
4	Characterizing Emerging Canine H3 Influenza Viruses **2020**, 16, e1008409		
3	Characterizing Emerging Canine H3 Influenza Viruses **2020**, 16, e1008409		
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