

Derek J Smith

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains. <i>Science Translational Medicine</i> , 2022 , 14,	17.5	8
105	Influenza virus infection history shapes antibody responses to influenza vaccination.. <i>Nature Medicine</i> , 2022 ,	50.5	3
104	Defining the risk of SARS-CoV-2 variants on immune protection.. <i>Nature</i> , 2022 ,	50.4	7
103	Beneath the surface: Amino acid variation underlying two decades of dengue virus antigenic dynamics in Bangkok, Thailand.. <i>PLoS Pathogens</i> , 2022 , 18, e1010500	7.6	0
102	Antigenic evolution of dengue viruses over 20 years. <i>Science</i> , 2021 , 374, 999-1004	33.3	5
101	Plasticity of the Influenza Virus H5 HA Protein. <i>MBio</i> , 2021 , 12,	7.8	4
100	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains 2021 ,		11
99	80 questions for UK biological security. <i>PLoS ONE</i> , 2021 , 16, e0241190	3.7	2
98	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains. <i>Science Translational Medicine</i> , 2021 , eabm3302	17.5	10
97	Vaccination with SARS-CoV-2 variants of concern protects mice from challenge with wild-type virus.. <i>PLoS Biology</i> , 2021 , 19, e3001384	9.7	2
96	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. <i>Science</i> , 2020 , 369,	33.3	42
95	Characterizing Emerging Canine H3 Influenza Viruses. <i>PLoS Pathogens</i> , 2020 , 16, e1008409	7.6	15
94	Characterizing Emerging Canine H3 Influenza Viruses 2020 , 16, e1008409		
93	Characterizing Emerging Canine H3 Influenza Viruses 2020 , 16, e1008409		
92	Characterizing Emerging Canine H3 Influenza Viruses 2020 , 16, e1008409		
91	Characterizing Emerging Canine H3 Influenza Viruses 2020 , 16, e1008409		
90	Characterizing Emerging Canine H3 Influenza Viruses 2020 , 16, e1008409		

89 Characterizing Emerging Canine H3 Influenza Viruses **2020**, 16, e1008409

88 The Molecular Basis for Antigenic Drift of Human A/H2N2 Influenza Viruses. *Journal of Virology*, **2019**, 93, 6.6 14

87 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

86 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

85 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

84 Ancient hepatitis B viruses from the Bronze Age to the Medieval period. *Nature*, **2018**, 557, 418-423 50.4 112

83 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

82 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

81 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

80 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

79 Factors determining human-to-human transmissibility of zoonotic pathogens via contact. *Current Opinion in Virology*, **2017**, 22, 7-12 7.5 10

78 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

77 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

76 Selection of antigenically advanced variants of seasonal influenza viruses. *Nature Microbiology*, **2016**, 1, 16058 26.6 46

75 Antigenic Relationships among Human Pathogenic *Orientia tsutsugamushi* Isolates from Thailand. *PLoS Neglected Tropical Diseases*, **2016**, 10, e0004723 4.8 14

74 Influenza B vaccine lineage selection--an optimized trivalent vaccine. *Vaccine*, **2016**, 34, 1617-1622 4.1 13

73 The confounded effects of age and exposure history in response to influenza vaccination. *Vaccine*, **2016**, 34, 540-546 4.1 71

72 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

71	Mapping Enterovirus A71 Antigenic Determinants from Viral Evolution. <i>Journal of Virology</i> , 2015 , 89, 11500-6	6.6	25
70	Dengue viruses cluster antigenically but not as discrete serotypes. <i>Science</i> , 2015 , 349, 1338-43	33.3	139
69	Reply: Letter to the editor, Cochrane rearranged. <i>Vaccine</i> , 2015 , 33, 13-4	4.1	2
68	Enhancing disease surveillance with novel data streams: challenges and opportunities. <i>EPJ Data Science</i> , 2015 , 4,	3.4	96
67	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015 , 523, 217-20	30.4	302
66	Identification of amino acid substitutions supporting antigenic change of influenza A(H1N1)pdm09 viruses. <i>Journal of Virology</i> , 2015 , 89, 3763-75	6.6	59
65	Excessive production and extreme editing of human metapneumovirus defective interfering RNA is associated with type I IFN induction. <i>Journal of General Virology</i> , 2014 , 95, 1625-1633	4.9	31
64	Genomewide analysis of reassortment and evolution of human influenza A(H3N2) viruses circulating between 1968 and 2011. <i>Journal of Virology</i> , 2014 , 88, 2844-57	6.6	100
63	Antibody landscapes after influenza virus infection or vaccination. <i>Science</i> , 2014 , 346, 996-1000	33.3	259
62	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. <i>MBio</i> , 2014 , 5,	7.8	3
61	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. <i>Vaccine</i> , 2014 , 32, 4713-25	4.1	74
60	Circulating avian influenza viruses closely related to the 1918 virus have pandemic potential. <i>Cell Host and Microbe</i> , 2014 , 15, 692-705	23.4	56
59	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014 , 3, e01914	8.9	213
58	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , 2014 , 10, e1003932	7.6	230
57	Circulation of reassortant influenza A(H7N9) viruses in poultry and humans, Guangdong Province, China, 2013. <i>Emerging Infectious Diseases</i> , 2014 , 20, 2034-40	10.2	34
56	Antigenic variation of clade 2.1 H5N1 virus is determined by a few amino acid substitutions immediately adjacent to the receptor binding site. <i>MBio</i> , 2014 , 5, e01070-14	7.8	38
55	Antigenic variation of foot-and-mouth disease virus serotype A. <i>Journal of General Virology</i> , 2014 , 95, 384-392	4.9	28
54	A recommended numbering scheme for influenza A HA subtypes. <i>PLoS ONE</i> , 2014 , 9, e112302	3.7	94

53	Serological evidence for non-lethal exposures of Mongolian wild birds to highly pathogenic avian influenza H5N1 virus. <i>PLoS ONE</i> , 2014 , 9, e113569	3.7	17
52	Limited airborne transmission of H7N9 influenza A virus between ferrets. <i>Nature</i> , 2013 , 501, 560-3	50.4	164
51	Cochrane re-arranged: support for policies to vaccinate elderly people against influenza. <i>Vaccine</i> , 2013 , 31, 6030-3	4.1	117
50	Substitutions near the receptor binding site determine major antigenic change during influenza virus evolution. <i>Science</i> , 2013 , 342, 976-9	33.3	379
49	Applications of quantitative modeling to influenza virus transmission dynamics, antigenic and genetic evolution, and molecular structure 2013 , 434-452		
48	Gain-of-function experiments on H7N9. <i>Science</i> , 2013 , 341, 612-3	33.3	18
47	Avian influenza virus surveillance in wild birds in Georgia: 2009-2011. <i>PLoS ONE</i> , 2013 , 8, e58534	3.7	37
46	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. <i>Vaccine</i> , 2012 , 30, 6461-71	4.1	50
45	A review of influenza haemagglutinin receptor binding as it relates to pandemic properties. <i>Vaccine</i> , 2012 , 30, 4369-76	4.1	40
44	Genetic evolution of the neuraminidase of influenza A (H3N2) viruses from 1968 to 2009 and its correspondence to haemagglutinin evolution. <i>Journal of General Virology</i> , 2012 , 93, 1996-2007	4.9	44
43	Airborne transmission of influenza A/H5N1 virus between ferrets. <i>Science</i> , 2012 , 336, 1534-41	33.3	1162
42	The potential for respiratory droplet-transmissible A/H5N1 influenza virus to evolve in a mammalian host. <i>Science</i> , 2012 , 336, 1541-7	33.3	231
41	H7 avian influenza virus vaccines protect chickens against challenge with antigenically diverse isolates. <i>Vaccine</i> , 2011 , 29, 7424-9	4.1	47
40	Flavivirus-induced antibody cross-reactivity. <i>Journal of General Virology</i> , 2011 , 92, 2821-2829	4.9	163
39	Prevalence of antibodies against seasonal influenza A and B viruses in children in Netherlands. <i>Vaccine Journal</i> , 2011 , 18, 469-76		125
38	Evolution of re-emergent virus and its impact on enterovirus 71 epidemics. <i>Experimental Biology and Medicine</i> , 2011 , 236, 899-908	3.7	41
37	Discordant antigenic drift of neuraminidase and hemagglutinin in H1N1 and H3N2 influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20748-53	11.5	140
36	Antigenic and genetic evolution of equine influenza A (H3N8) virus from 1968 to 2007. <i>Journal of Virology</i> , 2011 , 85, 12742-9	6.6	71

35	Genetic and antigenic characterization of H1 influenza viruses from United States swine from 2008. <i>Journal of General Virology</i> , 2011 , 92, 919-30	4.9	99
34	Virulence-associated substitution D222G in the hemagglutinin of 2009 pandemic influenza A(H1N1) virus affects receptor binding. <i>Journal of Virology</i> , 2010 , 84, 11802-13	6.6	171
33	Quantifying antigenic relationships among the lyssaviruses. <i>Journal of Virology</i> , 2010 , 84, 11841-8	6.6	62
32	Studies needed to address public health challenges of the 2009 H1N1 influenza pandemic: insights from modeling. <i>PLoS Medicine</i> , 2010 , 7, e1000275	11.6	69
31	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. <i>Vaccine</i> , 2010 , 28, 1156-67	4.1	130
30	Use of antigenic cartography in vaccine seed strain selection. <i>Avian Diseases</i> , 2010 , 54, 220-3	1.6	42
29	Quantifying the impact of immune escape on transmission dynamics of influenza. <i>Science</i> , 2009 , 326, 726-8	33.3	80
28	Reemergence of enterovirus 71 in 2008 in taiwan: dynamics of genetic and antigenic evolution from 1998 to 2008. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 3653-62	9.7	155
27	Evaluation of serological trials submitted for annual re-licensure of influenza vaccines to regulatory authorities between 1992 and 2002. <i>Vaccine</i> , 2009 , 28, 392-7	4.1	16
26	Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. <i>Science</i> , 2009 , 325, 197-201	33.3	1844
25	Influenza vaccine strain selection and recent studies on the global migration of seasonal influenza viruses. <i>Vaccine</i> , 2008 , 26 Suppl 4, D31-4	4.1	163
24	The global circulation of seasonal influenza A (H3N2) viruses. <i>Science</i> , 2008 , 320, 340-6	33.3	515
23	Antigenic and genetic evolution of swine influenza A (H3N2) viruses in Europe. <i>Journal of Virology</i> , 2007 , 81, 4315-22	6.6	128
22	An amino acid substitution in the influenza A virus hemagglutinin associated with escape from recognition by human virus-specific CD4+ T-cells. <i>Virus Research</i> , 2007 , 126, 282-7	6.4	15
21	Vaccination against highly pathogenic avian influenza H5N1 virus in zoos using an adjuvanted inactivated H5N2 vaccine. <i>Vaccine</i> , 2007 , 25, 3800-8	4.1	30
20	Predictability and preparedness in influenza control. <i>Science</i> , 2006 , 312, 392-4	33.3	66
19	Full restoration of viral fitness by multiple compensatory co-mutations in the nucleoprotein of influenza A virus cytotoxic T-lymphocyte escape mutants. <i>Journal of General Virology</i> , 2005 , 86, 1801-1805	4.9	50
18	Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from black-headed gulls. <i>Journal of Virology</i> , 2005 , 79, 2814-22	6.6	1109

17	Recognition of homo- and heterosubtypic variants of influenza A viruses by human CD8+ T lymphocytes. <i>Journal of Immunology</i> , 2004 , 172, 2453-60	5.3	104
16	Annual revaccination against influenza and mortality risk in community-dwelling elderly persons. <i>JAMA - Journal of the American Medical Association</i> , 2004 , 292, 2089-95	27.4	109
15	Mapping the antigenic and genetic evolution of influenza virus. <i>Science</i> , 2004 , 305, 371-6	33.3	1181
14	Recognition of influenza virus epitope variants by human CTL. <i>International Congress Series</i> , 2004 , 1263, 145-148		
13	Mutations, drift, and the influenza archipelago. <i>Discovery Medicine</i> , 2004 , 4, 371-7	2.5	3
12	Applications of bioinformatics and computational biology to influenza surveillance and vaccine strain selection. <i>Vaccine</i> , 2003 , 21, 1758-61	4.1	22
11	Modeling the effects of updating the influenza vaccine on the efficacy of repeated vaccination. <i>International Congress Series</i> , 2001 , 1219, 655-660		4
10	Variable efficacy of repeated annual influenza vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 14001-6	11.5	275
9	Immunological Memory is Associative* 1999 , 105-114		7
8	Modeling the Effects of Prior Infection on Vaccine Efficacy 1999 , 144-153		
7	Using lazy evaluation to simulate realistic-size repertoires in models of the immune system. <i>Bulletin of Mathematical Biology</i> , 1998 , 60, 647-58	2.1	17
6	Deriving shape space parameters from immunological data. <i>Journal of Theoretical Biology</i> , 1997 , 189, 141-50	2.3	54
5	Modeling the effects of prior infection on vaccine efficacy		4
4	Mapping SARS-CoV-2 antigenic relationships and serological responses		8
3	Epistatic interactions can moderate the antigenic effect of substitutions in hemagglutinin of influenza H3N2 virus		2
2	Antigenic Cartography of Human and Swine Influenza A (H3N2) Viruses. <i>Novartis Foundation Symposium</i> , 32-44		1
1	Omicron BA.1 and BA.2 are antigenically distinct SARS-CoV-2 variants		7