

Derek J Smith

List of Publications by Year in descending order

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104
papers

15,385
citations

36303

51
h-index

38395

95
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114
all docs

114
docs citations

114
times ranked

12865
citing authors

#	ARTICLE	IF	CITATIONS
1	Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans. <i>Science</i> , 2009, 325, 197-201.	12.6	2,127
2	Mapping the Antigenic and Genetic Evolution of Influenza Virus. <i>Science</i> , 2004, 305, 371-376.	12.6	1,527
3	Airborne Transmission of Influenza A/H5N1 Virus Between Ferrets. <i>Science</i> , 2012, 336, 1534-1541.	12.6	1,416
4	Characterization of a Novel Influenza A Virus Hemagglutinin Subtype (H16) Obtained from Black-Headed Gulls. <i>Journal of Virology</i> , 2005, 79, 2814-2822.	3.4	1,274
5	The Global Circulation of Seasonal Influenza A (H3N2) Viruses. <i>Science</i> , 2008, 320, 340-346.	12.6	628
6	Substitutions Near the Receptor Binding Site Determine Major Antigenic Change During Influenza Virus Evolution. <i>Science</i> , 2013, 342, 976-979.	12.6	500
7	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , 2015, 523, 217-220.	27.8	445
8	Antibody landscapes after influenza virus infection or vaccination. <i>Science</i> , 2014, 346, 996-1000.	12.6	379
9	Variable efficacy of repeated annual influenza vaccination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 14001-14006.	7.1	347
10	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. <i>PLoS Pathogens</i> , 2014, 10, e1003932.	4.7	330
11	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , 2014, 3, e01914.	6.0	299
12	The Potential for Respiratory Droplet-Transmissible A/H5N1 Influenza Virus to Evolve in a Mammalian Host. <i>Science</i> , 2012, 336, 1541-1547.	12.6	286
13	Flavivirus-induced antibody cross-reactivity. <i>Journal of General Virology</i> , 2011, 92, 2821-2829.	2.9	214
14	Influenza vaccine strain selection and recent studies on the global migration of seasonal influenza viruses. <i>Vaccine</i> , 2008, 26, D31-D34.	3.8	208
15	Virulence-Associated Substitution D222G in the Hemagglutinin of 2009 Pandemic Influenza A(H1N1) Virus Affects Receptor Binding. <i>Journal of Virology</i> , 2010, 84, 11802-11813.	3.4	197
16	Dengue viruses cluster antigenically but not as discrete serotypes. <i>Science</i> , 2015, 349, 1338-1343.	12.6	195
17	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, 20748-20753.	7.1	188
18	Limited airborne transmission of H7N9 influenza A virus between ferrets. <i>Nature</i> , 2013, 501, 560-563.	27.8	182

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19	Antigenic and Genetic Evolution of Swine Influenza A (H3N2) Viruses in Europe. <i>Journal of Virology</i> , 2007, 81, 4315-4322.	3.4	169
20	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, 3653-3662.	3.9	168
21	Prevalence of Antibodies against Seasonal Influenza A and B Viruses in Children in Netherlands. <i>Vaccine Journal</i> , 2011, 18, 469-476.	3.1	155
22	Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018, 557, 418-423.	27.8	155
23	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 2009â€“2010 Northern Hemisphere season. <i>Vaccine</i> , 2010, 28, 1156-1167.	3.8	145
24	Annual Revaccination Against Influenza and Mortality Risk in Community-Dwelling Elderly Persons. <i>JAMA - Journal of the American Medical Association</i> , 2004, 292, 2089.	7.4	140
25	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. <i>Journal of Virology</i> , 2014, 88, 2844-2857.	3.4	137
26	A Recommended Numbering Scheme for Influenza A HA Subtypes. <i>PLoS ONE</i> , 2014, 9, e112302.	2.5	137
27	Cochrane re-arranged: Support for policies to vaccinate elderly people against influenza. <i>Vaccine</i> , 2013, 31, 6030-6033.	3.8	135
28	Serial Vaccination and the Antigenic Distance Hypothesis: Effects on Influenza Vaccine Effectiveness During A(H3N2) Epidemics in Canada, 2010â€“2011 to 2014â€“2015. <i>Journal of Infectious Diseases</i> , 2017, 215, 1059-1099.	4.0	126
29	Genetic and antigenic characterization of H1 influenza viruses from United States swine from 2008. <i>Journal of General Virology</i> , 2011, 92, 919-930.	2.9	123
30	Recognition of Homo- and Heterosubtypic Variants of Influenza A Viruses by Human CD8+ T Lymphocytes. <i>Journal of Immunology</i> , 2004, 172, 2453-2460.	0.8	121
31	Enhancing disease surveillance with novel data streams: challenges and opportunities. <i>EPJ Data Science</i> , 2015, 4, .	2.8	119
32	Defining the risk of SARS-CoV-2 variants on immune protection. <i>Nature</i> , 2022, 605, 640-652.	27.8	117
33	The confounded effects of age and exposure history in response to influenza vaccination. <i>Vaccine</i> , 2016, 34, 540-546.	3.8	109
34	Diverse variola virus (smallpox) strains were widespread in northern Europe in the Viking Age. <i>Science</i> , 2020, 369, .	12.6	108
35	WHO recommendations for the viruses used in the 2013â€“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, 4713-4725.	3.8	102
36	Quantifying the Impact of Immune Escape on Transmission Dynamics of Influenza. <i>Science</i> , 2009, 326, 726-728.	12.6	96

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37	Viridot: An automated virus plaque (immunofocus) counter for the measurement of serological neutralizing responses with application to dengue virus. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006862.	3.0	93
38	Antigenic and Genetic Evolution of Equine Influenza A (H3N8) Virus from 1968 to 2007. <i>Journal of Virology</i> , 2011, 85, 12742-12749.	3.4	89
39	Antigenic cartography of SARS-CoV-2 reveals that Omicron BA.1 and BA.2 are antigenically distinct. <i>Science Immunology</i> , 2022, 7, .	11.9	89
40	Quantifying Antigenic Relationships among the Lyssaviruses. <i>Journal of Virology</i> , 2010, 84, 11841-11848.	3.4	83
41	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. <i>Journal of Virology</i> , 2015, 89, 3746-3762.	3.4	80
42	Studies Needed to Address Public Health Challenges of the 2009 H1N1 Influenza Pandemic: Insights from Modeling. <i>PLoS Medicine</i> , 2010, 7, e1000275.	8.4	75
43	Identification of Amino Acid Substitutions Supporting Antigenic Change of Influenza A(H1N1)pdm09 Viruses. <i>Journal of Virology</i> , 2015, 89, 3763-3775.	3.4	73
44	Circulating Avian Influenza Viruses Closely Related to the 1918 Virus Have Pandemic Potential. <i>Cell Host and Microbe</i> , 2014, 15, 692-705.	11.0	71
45	Predictability and Preparedness in Influenza Control. <i>Science</i> , 2006, 312, 392-394.	12.6	67
46	Deriving Shape Space Parameters from Immunological Data. <i>Journal of Theoretical Biology</i> , 1997, 189, 141-150.	1.7	66
47	Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7557-7562.	7.1	64
48	Selection of antigenically advanced variants of seasonal influenza viruses. <i>Nature Microbiology</i> , 2016, 1, 16058.	13.3	61
49	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, 6461-6471.	3.8	60
50	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.	2.9	57
51	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.	4.1	57
52	Antigenic Drift of the Influenza A(H1N1)pdm09 Virus Neuraminidase Results in Reduced Effectiveness of A/California/7/2009 (H1N1pdm09)-Specific Antibodies. <i>MBio</i> , 2019, 10, .	4.1	57
53	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains. <i>Science Translational Medicine</i> , 2022, 14, .	12.4	55
54	Use of Antigenic Cartography in Vaccine Seed Strain Selection. <i>Avian Diseases</i> , 2010, 54, 220-223.	1.0	54

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55	H7 avian influenza virus vaccines protect chickens against challenge with antigenically diverse isolates. <i>Vaccine</i> , 2011, 29, 7424-7429.	3.8	53
56	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.	2.9	52
57	A review of influenza haemagglutinin receptor binding as it relates to pandemic properties. <i>Vaccine</i> , 2012, 30, 4369-4376.	3.8	51
58	Evolution of re-emergent virus and its impact on enterovirus 71 epidemics. <i>Experimental Biology and Medicine</i> , 2011, 236, 899-908.	2.4	48
59	Antigenic variation of foot-and-mouth disease virus serotype A. <i>Journal of General Virology</i> , 2014, 95, 384-392.	2.9	42
60	Avian Influenza Virus Surveillance in Wild Birds in Georgia: 2009-2011. <i>PLoS ONE</i> , 2013, 8, e58534.	2.5	42
61	Circulation of Reassortant Influenza A(H7N9) Viruses in Poultry and Humans, Guangdong Province, China, 2013. <i>Emerging Infectious Diseases</i> , 2014, 20, 2034-2040.	4.3	41
62	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.	2.9	40
63	Vaccination against highly pathogenic avian influenza H5N1 virus in zoos using an adjuvanted inactivated H5N2 vaccine. <i>Vaccine</i> , 2007, 25, 3800-3808.	3.8	36
64	Antigenic evolution of dengue viruses over 20 years. <i>Science</i> , 2021, 374, 999-1004.	12.6	34
65	Influenza virus infection history shapes antibody responses to influenza vaccination. <i>Nature Medicine</i> , 2022, 28, 363-372.	30.7	30
66	Characterizing Emerging Canine H3 Influenza Viruses. <i>PLoS Pathogens</i> , 2020, 16, e1008409.	4.7	29
67	Immunological Memory is Associative*. , 1999, , 105-114.		29
68	Mapping Enterovirus A71 Antigenic Determinants from Viral Evolution. <i>Journal of Virology</i> , 2015, 89, 11500-11506.	3.4	28
69	Applications of bioinformatics and computational biology to influenza surveillance and vaccine strain selection. <i>Vaccine</i> , 2003, 21, 1758-1761.	3.8	26
70	Influenza Gain-of-Function Experiments: Their Role in Vaccine Virus Recommendation and Pandemic Preparedness. <i>MBio</i> , 2014, 5, .	4.1	26
71	Gain-of-Function Experiments on H7N9. <i>Science</i> , 2013, 341, 612-613.	12.6	24
72	The Molecular Basis for Antigenic Drift of Human A/H2N2 Influenza Viruses. <i>Journal of Virology</i> , 2019, 93, .	3.4	22

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73	Factors determining human-to-human transmissibility of zoonotic pathogens via contact. <i>Current Opinion in Virology</i> , 2017, 22, 7-12.	5.4	21
74	Using Lazy Evaluation to Simulate Realistic-size Repertoires in Models of the Immune System. <i>Bulletin of Mathematical Biology</i> , 1998, 60, 647-658.	1.9	18
75	Antigenic Relationships among Human Pathogenic <i>Orientia tsutsugamushi</i> Isolates from Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004723.	3.0	18
76	Serological Evidence for Non-Lethal Exposures of Mongolian Wild Birds to Highly Pathogenic Avian Influenza H5N1 Virus. <i>PLoS ONE</i> , 2014, 9, e113569.	2.5	18
77	Genetic and antigenic characterisation of influenza A(H3N2) viruses isolated in Yokohama during the 2016/17 and 2017/18 influenza seasons. <i>Eurosurveillance</i> , 2019, 24, .	7.0	18
78	Evaluation of serological trials submitted for annual re-licensure of influenza vaccines to regulatory authorities between 1992 and 2002. <i>Vaccine</i> , 2009, 28, 392-397.	3.8	16
79	Gain-of-Function Experiments on H7N9. <i>Science</i> , 2013, 341, 612-613.	12.6	16
80	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, 282-287.	2.2	15
81	Vaccination with SARS-CoV-2 variants of concern protects mice from challenge with wild-type virus. <i>PLoS Biology</i> , 2021, 19, e3001384.	5.6	15
82	Influenza B vaccine lineage selection—An optimized trivalent vaccine. <i>Vaccine</i> , 2016, 34, 1617-1622.	3.8	14
83	Epistatic interactions can moderate the antigenic effect of substitutions in haemagglutinin of influenza H3N2 virus. <i>Journal of General Virology</i> , 2019, 100, 773-777.	2.9	13
84	Protective activity of mRNA vaccines against ancestral and variant SARS-CoV-2 strains. <i>Science Translational Medicine</i> , 2021, , eabm3302.	12.4	13
85	Characterization of influenza A(H1N1)pdm09 viruses isolated from Nepalese and Indian outbreak patients in early 2015. <i>Influenza and Other Respiratory Viruses</i> , 2017, 11, 399-403.	3.4	11
86	Plasticity of the Influenza Virus H5 HA Protein. <i>MBio</i> , 2021, 12, .	4.1	8
87	80 questions for UK biological security. <i>PLoS ONE</i> , 2021, 16, e0241190.	2.5	8
88	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, .	4.1	6
89	Complete assembly of a dengue virus type 3 genome from a recent genotype III clade by metagenomic sequencing of serum. <i>Wellcome Open Research</i> , 2018, 3, 44.	1.8	6
90	Modeling the effects of prior infection on vaccine efficacy. , 0, , .		5

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91	Modeling the effects of updating the influenza vaccine on the efficacy of repeated vaccination. International Congress Series, 2001, 1219, 655-660.	0.2	5
92	Beneath the surface: Amino acid variation underlying two decades of dengue virus antigenic dynamics in Bangkok, Thailand. PLoS Pathogens, 2022, 18, e1010500.	4.7	5
93	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.	1.8	4
94	Modeling the Effects of Prior Infection on Vaccine Efficacy. , 1999, , 144-153.		4
95	Reply: Letter to the Editor, Cochrane Rearranged. Vaccine, 2015, 33, 13-14.	3.8	3
96	Mutations, drift, and the influenza archipelago. Discovery Medicine, 2004, 4, 371-7.	0.5	3
97	Recognition of influenza virus epitope variants by human CTL. International Congress Series, 2004, 1263, 145-148.	0.2	1
98	Antigenic Cartography of Human and Swine Influenza A (H3N2) Viruses. Novartis Foundation Symposium, 0, , 32-44.	1.1	1
99	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
100	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
101	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
102	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
103	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0
104	Characterizing Emerging Canine H3 Influenza Viruses. , 2020, 16, e1008409.		0