

Samantha J Lycett

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

6,536
citations

159525

30
h-index

110317

64
g-index

82
all docs

82
docs citations

82
times ranked

10221
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic analysis of an emergent <i>Mycobacterium bovis</i> outbreak in an area with no previously known wildlife infections. <i>Journal of Applied Ecology</i> , 2022, 59, 210-222.	1.9	19
2	Accessory Gene Products of Influenza A Virus. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021, 11, a038380.	2.9	12
3	Re-emergence of H5N8 highly pathogenic avian influenza virus in wild birds, China. <i>Emerging Microbes and Infections</i> , 2021, 10, 1819-1823.	3.0	17
4	Using machine learning improves predictions of herd-level bovine tuberculosis breakdowns in Great Britain. <i>Scientific Reports</i> , 2021, 11, 2208.	1.6	9
5	Dealing with Highly Pathogenic Avian Influenza: An Impending Crisis. <i>Innovation(China)</i> , 2021, 2, 100084.	5.2	1
6	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	13.5	541
7	Monitoring SARS-CoV-2 Circulation and Diversity through Community Wastewater Sequencing, the Netherlands and Belgium. <i>Emerging Infectious Diseases</i> , 2021, 27, 1405-1415.	2.0	168
8	Phylogenetic Structure and Sequential Dominance of Sub-Lineages of PRRSV Type-2 Lineage 1 in the United States. <i>Vaccines</i> , 2021, 9, 608.	2.1	38
9	Integrating animal movements with phylogeography to model the spread of PRRSV in the USA. <i>Virus Evolution</i> , 2021, 7, veab060.	2.2	14
10	The fall and rise of group B Streptococcus in dairy cattle: reintroduction due to human-to-cattle host jumps?. <i>Microbial Genomics</i> , 2021, 7, .	1.0	12
11	What are SARS-CoV-2 genomes from the WHO Africa region member states telling us?. <i>BMJ Global Health</i> , 2021, 6, e004408.	2.0	9
12	Adaptation, spread and transmission of SARS-CoV-2 in farmed minks and associated humans in the Netherlands. <i>Nature Communications</i> , 2021, 12, 6802.	5.8	81
13	Identification of African swine fever virus-like elements in the soft tick genome provides insights into the virus's evolution. <i>BMC Biology</i> , 2020, 18, 136.	1.7	28
14	Genesis and spread of multiple reassortants during the 2016/2017 H5 avian influenza epidemic in Eurasia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20814-20825.	3.3	63
15	Contribution of Segment 3 to the Acquisition of Virulence in Contemporary H9N2 Avian Influenza Viruses. <i>Journal of Virology</i> , 2020, 94, .	1.5	15
16	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004.	2.2	9
17	Prevalence and risk factors associated with failure of transfer of passive immunity in spring born beef suckler calves in Great Britain. <i>Preventive Veterinary Medicine</i> , 2020, 181, 105059.	0.7	15
18	<i>Mycobacterium bovis</i> genomics reveals transmission of infection between cattle and deer in Ireland. <i>Microbial Genomics</i> , 2020, 6, .	1.0	39

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19	Identifying likely transmissions in Mycobacterium bovis infected populations of cattle and badgers using the Kolmogorov Forward Equations. Scientific Reports, 2020, 10, 21980.	1.6	2
20	Phylogeographic Analysis and Identification of Factors Impacting the Diffusion of Foot-and-Mouth Disease Virus in Africa. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	22
21	Predicting vaccine effectiveness in livestock populations: A theoretical framework applied to PRRS virus infections in pigs. PLoS ONE, 2019, 14, e0220738.	1.1	32
22	A brief history of bird flu. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180257.	1.8	137
23	The evolution and phylodynamics of serotype A and SAT2 foot-and-mouth disease viruses in endemic regions of Africa. Scientific Reports, 2019, 9, 5614.	1.6	17
24	A guide to machine learning for bacterial host attribution using genome sequence data. Microbial Genomics, 2019, 5, .	1.0	26
25	Combining genomics and epidemiology to analyse bi-directional transmission of Mycobacterium bovis in a multi-host system. ELife, 2019, 8, .	2.8	63
26	Gene exchange drives the ecological success of a multi-host bacterial pathogen. Nature Ecology and Evolution, 2018, 2, 1468-1478.	3.4	156
27	Using whole genome sequencing to investigate transmission in a multi-host system: bovine tuberculosis in New Zealand. BMC Genomics, 2017, 18, 180.	1.2	86
28	Analysis of bovine viral diarrhoea virus: Biobank and sequence database to support eradication in Scotland. Veterinary Record, 2017, 180, 447-447.	0.2	10
29	Quantifying predictors for the spatial diffusion of avian influenza virus in China. BMC Evolutionary Biology, 2017, 17, 16.	3.2	31
30	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	3.5	53
31	Assessing the Epidemic Potential of RNA and DNA Viruses. Emerging Infectious Diseases, 2016, 22, 2037-2044.	2.0	72
32	Role of the B Allele of Influenza A Virus Segment 8 in Setting Mammalian Host Range and Pathogenicity. Journal of Virology, 2016, 90, 9263-9284.	1.5	26
33	Role for migratory wild birds in the global spread of avian influenza H5N8. Science, 2016, 354, 213-217.	6.0	362
34	Modelling the impact of co-circulating low pathogenic avian influenza viruses on epidemics of highly pathogenic avian influenza in poultry. Epidemics, 2016, 17, 27-34.	1.5	13
35	A Direct Comparison of Two Densely Sampled HIV Epidemics: The UK and Switzerland. Scientific Reports, 2016, 6, 32251.	1.6	17
36	Broadwick: a framework for computational epidemiology. BMC Bioinformatics, 2016, 17, 65.	1.2	15

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37	Fast Dating Using Least-Squares Criteria and Algorithms. <i>Systematic Biology</i> , 2016, 65, 82-97.	2.7	336
38	Transmission of Non-B HIV Subtypes in the United Kingdom Is Increasingly Driven by Large Non-Heterosexual Transmission Clusters. <i>Journal of Infectious Diseases</i> , 2016, 213, 1410-1418.	1.9	67
39	Use of bacterial whole-genome sequencing to investigate local persistence and spread in bovine tuberculosis. <i>Epidemics</i> , 2016, 14, 26-35.	1.5	70
40	Bones hold the key to virus history and epidemiology. <i>Journal of Clinical Virology</i> , 2015, 70, S81.	1.6	1
41	Bones hold the key to DNA virus history and epidemiology. <i>Scientific Reports</i> , 2015, 5, 17226.	1.6	27
42	Reassortment between Influenza B Lineages and the Emergence of a Coadapted PB1â€“PB2â€“HA Gene Complex. <i>Molecular Biology and Evolution</i> , 2015, 32, 162-172.	3.5	63
43	Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions. <i>Aids</i> , 2014, 28, 1967-1975.	1.0	69
44	Reassortment patterns of avian influenza virus internal segments among different subtypes. <i>BMC Evolutionary Biology</i> , 2014, 14, 16.	3.2	77
45	Supersize me: how whole-genome sequencing and big data are transforming epidemiology. <i>Trends in Microbiology</i> , 2014, 22, 282-291.	3.5	115
46	Determining the Phylogenetic and Phylogeographic Origin of Highly Pathogenic Avian Influenza (H7N3) in Mexico. <i>PLoS ONE</i> , 2014, 9, e107330.	1.1	25
47	The genesis and source of the H7N9 influenza viruses causing human infections in China. <i>Nature</i> , 2013, 502, 241-244.	13.7	429
48	The Effect of the PB2 Mutation 627K on Highly Pathogenic H5N1 Avian Influenza Virus Is Dependent on the Virus Lineage. <i>Journal of Virology</i> , 2013, 87, 9983-9996.	1.5	56
49	Evolutionary interactions between haemagglutinin and neuraminidase in avian influenza. <i>BMC Evolutionary Biology</i> , 2013, 13, 222.	3.2	24
50	Investigation of Influenza Virus Polymerase Activity in Pig Cells. <i>Journal of Virology</i> , 2013, 87, 384-394.	1.5	46
51	The evolutionary dynamics of influenza A virus adaptation to mammalian hosts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120382.	1.8	40
52	Automated analysis of phylogenetic clusters. <i>BMC Bioinformatics</i> , 2013, 14, 317.	1.2	305
53	Estimating the Rate of Intersubtype Recombination in Early HIV-1 Group M Strains. <i>Journal of Virology</i> , 2013, 87, 1967-1973.	1.5	24
54	Real-time characterization of the molecular epidemiology of an influenza pandemic. <i>Biology Letters</i> , 2013, 9, 20130331.	1.0	41

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55	The Short Stalk Length of Highly Pathogenic Avian Influenza H5N1 Virus Neuraminidase Limits Transmission of Pandemic H1N1 Virus in Ferrets. <i>Journal of Virology</i> , 2013, 87, 10539-10551.	1.5	72
56	Estimating reassortment rates in co-circulating Eurasian swine influenza viruses. <i>Journal of General Virology</i> , 2012, 93, 2326-2336.	1.3	42
57	Origin and fate of A/H1N1 influenza in Scotland during 2009. <i>Journal of General Virology</i> , 2012, 93, 1253-1260.	1.3	14
58	Transmission Network Parameters Estimated From HIV Sequences for a Nationwide Epidemic. <i>Journal of Infectious Diseases</i> , 2011, 204, 1463-1469.	1.9	184
59	Detection of Mammalian Virulence Determinants in Highly Pathogenic Avian Influenza H5N1 Viruses: Multivariate Analysis of Published Data. <i>Journal of Virology</i> , 2009, 83, 9901-9910.	1.5	76
60	Molecular Phylodynamics of the Heterosexual HIV Epidemic in the United Kingdom. <i>PLoS Pathogens</i> , 2009, 5, e1000590.	2.1	155
61	Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic. <i>Nature</i> , 2009, 459, 1122-1125.	13.7	1,870
62	An advantage of chaotic neural dynamics. <i>Neural Networks (IJCNN), International Joint Conference on</i> , 2007, , .	0.0	0
63	Influence of segregation in quantum well structures. <i>Journal of Materials Science: Materials in Electronics</i> , 1996, 7, 341.	1.1	2
64	Observation of blue shift in GaAs/InGaP quantum well p-i-n diodes. <i>Materials Science and Engineering B: Solid-State Materials for Advanced Technology</i> , 1994, 28, 323-326.	1.7	1