## Colin A Russell

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Antigenic and Genetic Characteristics of Swine-Origin 2009 A(H1N1) Influenza Viruses Circulating in Humans. Science, 2009, 325, 197-201.	12.6	2,127
2	The Global Circulation of Seasonal Influenza A (H3N2) Viruses. Science, 2008, 320, 340-346.	12.6	628
3	Substitutions Near the Receptor Binding Site Determine Major Antigenic Change During Influenza Virus Evolution. Science, 2013, 342, 976-979.	12.6	500
4	The evolution of seasonal influenza viruses. Nature Reviews Microbiology, 2018, 16, 47-60.	28.6	483
5	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. Nature, 2015, 523, 217-220.	27.8	445
6	Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. PLoS Pathogens, 2014, 10, e1003932.	4.7	330
7	Integrating influenza antigenic dynamics with molecular evolution. ELife, 2014, 3, e01914.	6.0	299
8	The Evolution and Genetics of Virus Host Shifts. PLoS Pathogens, 2014, 10, e1004395.	4.7	291
9	The Potential for Respiratory Droplet–Transmissible A/H5N1 Influenza Virus to Evolve in a Mammalian Host. Science, 2012, 336, 1541-1547.	12.6	286
10	Influenza vaccine strain selection and recent studies on the global migration of seasonal influenza viruses. Vaccine, 2008, 26, D31-D34.	3.8	208
11	Virulence-Associated Substitution D222G in the Hemagglutinin of 2009 Pandemic Influenza A(H1N1) Virus Affects Receptor Binding. Journal of Virology, 2010, 84, 11802-11813.	3.4	197
12	Dengue viruses cluster antigenically but not as discrete serotypes. Science, 2015, 349, 1338-1343.	12.6	195
13	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, 20748-20753.	7.1	188
14	Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1701-9.	7.1	165
15	Predicting evolution from the shape of genealogical trees. ELife, 2014, 3, .	6.0	159
16	The global antigenic diversity of swine influenza A viruses. ELife, 2016, 5, e12217.	6.0	146
17	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, 1156-1167.	3.8	145
18	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. Journal of Virology, 2014, 88, 2844-2857.	3.4	137

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19	Antigenic and genetic variations in European and North American equine influenza virus strains (H3N8) isolated from 2006 to 2007. Veterinary Microbiology, 2009, 138, 41-52.	1.9	132
20	Genetic and antigenic characterization of H1 influenza viruses from United States swine from 2008. Journal of General Virology, 2011, 92, 919-930.	2.9	123
21	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, 4713-4725.	3.8	102
22	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. Science Immunology, 2019, 4, .	11.9	98
23	Viral factors in influenza pandemic risk assessment. ELife, 2016, 5, .	6.0	82
24	Predictive Spatial Dynamics and Strategic Planning for Raccoon Rabies Emergence in Ohio. PLoS Biology, 2005, 3, e88.	5.6	81
25	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. PLoS Pathogens, 2017, 13, e1006749.	4.7	78
26	Circulating Avian Influenza Viruses Closely Related to the 1918 Virus Have Pandemic Potential. Cell Host and Microbe, 2014, 15, 692-705.	11.0	71
27	A priori prediction of disease invasion dynamics in a novel environment. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 21-25.	2.6	65
28	Selection of antigenically advanced variants of seasonal influenza viruses. Nature Microbiology, 2016, 1, 16058.	13.3	61
29	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, 6461-6471.	3.8	60
30	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.	2.9	57
31	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.	4.1	57
32	Phylogenetic Clustering by Linear Integer Programming (PhyCLIP). Molecular Biology and Evolution, 2019, 36, 1580-1595.	8.9	54
33	Spatial Control of Rabies on Heterogeneous Landscapes. PLoS ONE, 2006, 1, e27.	2.5	53
34	Improving pandemic influenza risk assessment. ELife, 2014, 3, e03883.	6.0	53
35	Yield of Screening for COVID-19 in Asymptomatic Patients Before Elective or Emergency Surgery Using Chest CT and RT-PCR (SCOUT). Annals of Surgery, 2020, 272, 919-924.	4.2	45
36	Avian Influenza Virus Surveillance in Wild Birds in Georgia: 2009–2011. PLoS ONE, 2013, 8, e58534.	2.5	42

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37	Serologic Surveillance and Phylogenetic Analysis of SARS-CoV-2 Infection Among Hospital Health Care Workers. JAMA Network Open, 2021, 4, e2118554.	5.9	36
38	Genetic diversity and host adaptation of avian H5N1 influenza viruses during human infection. Emerging Microbes and Infections, 2019, 8, 262-271.	6.5	27
39	Individual immune selection pressure has limited impact on seasonal influenza virus evolution. Nature Ecology and Evolution, 2019, 3, 302-311.	7.8	25
40	Asynchrony between virus diversity and antibody selection limits influenza virus evolution. ELife, 2020, 9, .	6.0	25
41	Influenza A virus evolution and spatio-temporal dynamics in Eurasian wild birds: a phylogenetic and phylogeographical study of whole-genome sequence data. Journal of General Virology, 2015, 96, 2050-2060.	2.9	23
42	Combined Influence of B-Cell Receptor Rearrangement and Somatic Hypermutation on B-Cell Class-Switch Fate in Health and in Chronic Lymphocytic Leukemia. Frontiers in Immunology, 2018, 9, 1784.	4.8	22
43	Inferring putative transmission clusters with Phydelity. Virus Evolution, 2019, 5, vez039.	4.9	18
44	The impact of climate and antigenic evolution on seasonal influenza virus epidemics in Australia. Nature Communications, 2020, 11, 2741.	12.8	17
45	A single mRNA vaccine dose in COVID-19 patients boosts neutralizing antibodies against SARS-CoV-2 and variants of concern. Cell Reports Medicine, 2022, 3, 100486.	6.5	16
46	Influenza B vaccine lineage selection—An optimized trivalent vaccine. Vaccine, 2016, 34, 1617-1622.	3.8	14
47	The Glycan Hole Area of HIV-1 Envelope Trimers Contributes Prominently to the Induction of Autologous Neutralization. Journal of Virology, 2022, 96, JVI0155221.	3.4	13
48	Hepatitis C Virus Transmission Among Men Who Have Sex With Men in Amsterdam: External Introductions May Complicate Microelimination Efforts. Clinical Infectious Diseases, 2021, 72, e1056-e1063.	5.8	11
49	Quantifying mechanistic traits of influenza viral dynamics using in vitro data. Epidemics, 2020, 33, 100406.	3.0	10
50	Quantifying the Fitness Advantage of Polymerase Substitutions in Influenza A/H7N9 Viruses during Adaptation to Humans. PLoS ONE, 2013, 8, e76047.	2.5	9
51	Partial immunity and SARS-CoV-2 mutations. Science, 2021, 372, 354-354.	12.6	9
52	Sick birds don't fly…or do they?. Science, 2016, 354, 174-175.	12.6	8
53	Phenotypic Effects of Substitutions within the Receptor Binding Site of Highly Pathogenic Avian Influenza H5N1 Virus Observed during Human Infection. Journal of Virology, 2020, 94, .	3.4	8
54	Within-host evolutionary dynamics of seasonal and pandemic human influenza A viruses in young children. ELife, 2021, 10, .	6.0	8

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#	Article	IF	CITATIONS
55	Influenza A Hemagglutinin Passage Bias Sites and Host Specificity Mutations. Cells, 2019, 8, 958.	4.1	6
56	The Geographic Variation of Surveillance and Zoonotic Spillover Potential of Influenza Viruses in Domestic Poultry and Swine. Open Forum Infectious Diseases, 2018, 5, ofy318.	0.9	5
57	Infectious disease management must be evolutionary. Nature Ecology and Evolution, 2017, 1, 1053-1055.	7.8	4
58	Antigenic Cartography of Human and Swine Influenza A (H3N2) Viruses. Novartis Foundation Symposium, 0, , 32-44.	1.1	1