## Colin A Russell

## List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/3407249/colin-a-russell-publications-by-year.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

63
papers
6,459
citations
h-index
72
g-index
72
ext. papers
2,7738
ext. citations
12.4
avg, IF
L-index

#	Paper	IF	Citations
63	A single mRNA vaccine dose in COVID-19 patients boosts neutralizing antibodies against SARS-CoV-2 and variants of concern <i>Cell Reports Medicine</i> , <b>2022</b> , 3, 100486	18	O
62	The glycan hole area of HIV-1 envelope trimers contributes prominently to the induction of autologous neutralization. <i>Journal of Virology</i> , <b>2021</b> , JVI0155221	6.6	2
61	Hepatitis C Virus Transmission Among Men Who Have Sex With Men in Amsterdam: External Introductions May Complicate Microelimination Efforts. <i>Clinical Infectious Diseases</i> , <b>2021</b> , 72, e1056-e10	o <del>63</del> .6	2
60	Partial immunity and SARS-CoV-2 mutations. <i>Science</i> , <b>2021</b> , 372, 354	33.3	5
59	Serologic Surveillance and Phylogenetic Analysis of SARS-CoV-2 Infection Among Hospital Health Care Workers. <i>JAMA Network Open</i> , <b>2021</b> , 4, e2118554	10.4	13
58	Quantifying mechanistic traits of influenza viral dynamics using in vitro data. <i>Epidemics</i> , <b>2020</b> , 33, 10040	)65.1	1
57	Phenotypic Effects of Substitutions within the Receptor Binding Site of Highly Pathogenic Avian Influenza H5N1 Virus Observed during Human Infection. <i>Journal of Virology</i> , <b>2020</b> , 94,	6.6	3
56	The impact of climate and antigenic evolution on seasonal influenza virus epidemics in Australia. <i>Nature Communications</i> , <b>2020</b> , 11, 2741	17.4	4
55	Asynchrony between virus diversity and antibody selection limits influenza virus evolution. <i>ELife</i> , <b>2020</b> , 9,	8.9	12
54	Yield of Screening for COVID-19 in Asymptomatic Patients Before Elective or Emergency Surgery Using Chest CT and RT-PCR (SCOUT): Multicenter Study. <i>Annals of Surgery</i> , <b>2020</b> , 272, 919-924	7.8	30
53	Influenza A Hemagglutinin Passage Bias Sites and Host Specificity Mutations. Cells, 2019, 8,	7.9	2
52	Genetic diversity and host adaptation of avian H5N1 influenza viruses during human infection. <i>Emerging Microbes and Infections</i> , <b>2019</b> , 8, 262-271	18.9	21
51	Phylogenetic Clustering by Linear Integer Programming (PhyCLIP). <i>Molecular Biology and Evolution</i> , <b>2019</b> , 36, 1580-1595	8.3	21
50	Inferring putative transmission clusters with Phydelity. Virus Evolution, 2019, 5, vez039	3.7	6
49	Incomplete genetic reconstitution of B cell pools contributes to prolonged immunosuppression after measles. <i>Science Immunology</i> , <b>2019</b> , 4,	28	54
48	Individual immune selection pressure has limited impact on seasonal influenza virus evolution. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 302-311	12.3	15
47	The evolution of seasonal influenza viruses. <i>Nature Reviews Microbiology</i> , <b>2018</b> , 16, 47-60	22.2	234

46	The Geographic Variation of Surveillance and Zoonotic Spillover Potential of Influenza Viruses in Domestic Poultry and Swine. <i>Open Forum Infectious Diseases</i> , <b>2018</b> , 5, ofy318	1	2
45	Combined Influence of B-Cell Receptor Rearrangement and Somatic Hypermutation on B-Cell Class-Switch Fate in Health and in Chronic Lymphocytic Leukemia. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 178	48.4	14
44	Genome-wide evolutionary dynamics of influenza B viruses on a global scale. <i>PLoS Pathogens</i> , <b>2017</b> , 13, e1006749	7.6	55
43	Infectious disease management must be evolutionary. <i>Nature Ecology and Evolution</i> , <b>2017</b> , 1, 1053-1055	5 12.3	3
42	Sick birds don't flybr do they?. <i>Science</i> , <b>2016</b> , 354, 174-175	33.3	5
41	Selection of antigenically advanced variants of seasonal influenza viruses. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16058	26.6	46
40	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	11.5	116
39	The global antigenic diversity of swine influenza A viruses. <i>ELife</i> , <b>2016</b> , 5, e12217	8.9	106
38	Viral factors in influenza pandemic risk assessment. <i>ELife</i> , <b>2016</b> , 5,	8.9	61
37	Influenza B vaccine lineage selectionan optimized trivalent vaccine. <i>Vaccine</i> , <b>2016</b> , 34, 1617-1622	4.1	13
36	Influenza A virus evolution and spatio-temporal dynamics in Eurasian wild birds: a phylogenetic and phylogeographical study of whole-genome sequence data. <i>Journal of General Virology</i> , <b>2015</b> , 96, 2050-2	20168	22
35	Dengue viruses cluster antigenically but not as discrete serotypes. <i>Science</i> , <b>2015</b> , 349, 1338-43	33.3	139
34	Global circulation patterns of seasonal influenza viruses vary with antigenic drift. <i>Nature</i> , <b>2015</b> , 523, 21	7 <del>5</del> 204	302
33	Genomewide analysis of reassortment and evolution of human influenza A(H3N2) viruses circulating between 1968 and 2011. <i>Journal of Virology</i> , <b>2014</b> , 88, 2844-57	6.6	100
32	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> , <b>2014</b> , 32, 4713-25	4.1	74
31	Circulating avian influenza viruses closely related to the 1918 virus have pandemic potential. <i>Cell Host and Microbe</i> , <b>2014</b> , 15, 692-705	23.4	56
30	Integrating influenza antigenic dynamics with molecular evolution. <i>ELife</i> , <b>2014</b> , 3, e01914	8.9	213

28	Predicting evolution from the shape of genealogical trees. <i>ELife</i> , <b>2014</b> , 3,	8.9	108
27	Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1003932	7.6	230
26	The evolution and genetics of virus host shifts. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1004395	7.6	177
25	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> , <b>2014</b> , 5, e01070-14	7.8	38
24	Author response: Improving pandemic influenza risk assessment 2014,		2
23	Substitutions near the receptor binding site determine major antigenic change during influenza virus evolution. <i>Science</i> , <b>2013</b> , 342, 976-9	33.3	379
22	Quantifying the fitness advantage of polymerase substitutions in Influenza A/H7N9 viruses during adaptation to humans. <i>PLoS ONE</i> , <b>2013</b> , 8, e76047	3.7	9
21	Avian influenza virus surveillance in wild birds in Georgia: 2009-2011. PLoS ONE, <b>2013</b> , 8, e58534	3.7	37
20	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> , <b>2012</b> , 30, 6461-71	4.1	50
19	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> , <b>2012</b> , 93, 1996-2007	4.9	44
18	The potential for respiratory droplet-transmissible A/H5N1 influenza virus to evolve in a mammalian host. <i>Science</i> , <b>2012</b> , 336, 1541-7	33.3	231
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> , <b>2011</b> , 108, 2074	18 <sup>-1</sup> 53	140
16	Genetic and antigenic characterization of H1 influenza viruses from United States swine from 2008. Journal of General Virology, <b>2011</b> , 92, 919-30	4.9	99
15	Virulence-associated substitution D222G in the hemagglutinin of 2009 pandemic influenza A(H1N1) virus affects receptor binding. <i>Journal of Virology</i> , <b>2010</b> , 84, 11802-13	6.6	171
14	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> , <b>2010</b> , 28, 1156-67	4.1	130
13	Antigenic and genetic variations in European and North American equine influenza virus strains (H3N8) isolated from 2006 to 2007. <i>Veterinary Microbiology</i> , <b>2009</b> , 138, 41-52	3.3	114
12	Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. <i>Science</i> , <b>2009</b> , 325, 197-201	33.3	1844
11	Influenza vaccine strain selection and recent studies on the global migration of seasonal influenza viruses. <i>Vaccine</i> , <b>2008</b> , 26 Suppl 4, D31-4	4.1	163

## LIST OF PUBLICATIONS

1	The global circulation of seasonal influenza A (H3N2) viruses. <i>Science</i> , <b>2008</b> , 320, 340-6	33.3	515	
ç	Spatial control of rabies on heterogeneous landscapes. <i>PLoS ONE</i> , <b>2006</b> , 1, e27	3.7	50	
8	Predictive spatial dynamics and strategic planning for raccoon rabies emergence in Ohio. <i>PLoS Biology</i> , <b>2005</b> , 3, e88	9.7	68	
7	A priori prediction of disease invasion dynamics in a novel environment. <i>Proceedings of the Roy Society B: Biological Sciences</i> , <b>2004</b> , 271, 21-5	yal 4·4	50	
$\epsilon$	Inferring putative transmission clusters with Phydelity		2	
5	Disparate evolution of virus populations in upper and lower airways of mechanically ventilated	d patients	3	
4	Asynchrony between virus diversity and antibody selection limits influenza virus evolution		1	
3	N-glycolylneuraminic acid binding of avian H7 influenza A viruses		1	
2	Phylogenetic Clustering by Linear Integer Programming (PhyCLIP)		1	
1	Antigenic Cartography of Human and Swine Influenza A (H3N2) Viruses. <i>Novartis Foundation</i> Symposium,32-44		1	