

Thomas P Peacock

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.

48
papers

1,051
citations

18
h-index

31
g-index

58
ext. papers

2,079
ext. citations

12.8
avg, IF

4.59
L-index

#	Paper	IF	Citations
48	Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway.. <i>Cell Reports</i> , 2022 , 110344	10.6	10
47	Tracking SARS-CoV-2 mutations and variants through the COG-UK-Mutation Explorer.. <i>Virus Evolution</i> , 2022 , 8, veac023	3.7	1
46	The ChAdOx1 vectored vaccine, AZD2816, induces strong immunogenicity against SARS-CoV-2 beta (B.1.351) and other variants of concern in preclinical studies.. <i>EBioMedicine</i> , 2022 , 77, 103902	8.8	5
45	SARS-CoV-2 variants of concern alpha, beta, gamma and delta have extended ACE2 receptor host ranges.. <i>Journal of General Virology</i> , 2022 , 103,	4.9	2
44	Where is the next SARS-CoV-2 variant of concern?. <i>Lancet, The</i> , 2022 , 399, 1938-1939	4.0	1
43	Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination. <i>PLoS Pathogens</i> , 2021 , 17, e1010022	7.6	35
42	PA-X is an avian virulence factor in H9N2 avian influenza virus. <i>Journal of General Virology</i> , 2021 , 102,	4.9	1
41	The furin cleavage site in the SARS-CoV-2 spike protein is required for transmission in ferrets. <i>Nature Microbiology</i> , 2021 , 6, 899-909	26.6	206
40	SARS-CoV-2 one year on: evidence for ongoing viral adaptation. <i>Journal of General Virology</i> , 2021 , 102,	4.9	63
39	A natural variant in ANP32B impairs influenza virus replication in human cells. <i>Journal of General Virology</i> , 2021 , 102,	4.9	3
38	Adsorptive mutation and N-linked glycosylation modulate influenza virus antigenicity and fitness. <i>Emerging Microbes and Infections</i> , 2020 , 9, 2622-2631	18.9	3
37	Swine ANP32A Supports Avian Influenza Virus Polymerase. <i>Journal of Virology</i> , 2020 , 94,	6.6	11
36	Disrupting HIV-1 capsid formation causes cGAS sensing of viral DNA. <i>EMBO Journal</i> , 2020 , 39, e103958	13	25
35	Contribution of Segment 3 to the Acquisition of Virulence in Contemporary H9N2 Avian Influenza Viruses. <i>Journal of Virology</i> , 2020 , 94,	6.6	5
34	Genetic determinants of receptor-binding preference and zoonotic potential of H9N2 avian influenza viruses. <i>Journal of Virology</i> , 2020 ,	6.6	6
33	ANP32 Proteins Are Essential for Influenza Virus Replication in Human Cells. <i>Journal of Virology</i> , 2019 , 93,	6.6	32
32	Host Determinants of Influenza RNA Synthesis. <i>Annual Review of Virology</i> , 2019 , 6, 215-233	14.6	16

31	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses. <i>Emerging Microbes and Infections</i> , 2018 , 7, 176	18.9	15
30	Association of Increased Receptor-Binding Avidity of Influenza A(H9N2) Viruses with Escape from Antibody-Based Immunity and Enhanced Zoonotic Potential. <i>Emerging Infectious Diseases</i> , 2018 , 25, 63-72	10.2	23
29	Immune Escape Variants of H9N2 Influenza Viruses Containing Deletions at the Hemagglutinin Receptor Binding Site Retain Fitness and Display Enhanced Zoonotic Characteristics. <i>Journal of Virology</i> , 2017 , 91,	6.6	28
28	Variability in H9N2 haemagglutinin receptor-binding preference and the pH of fusion. <i>Emerging Microbes and Infections</i> , 2017 , 6, e11	18.9	31
27	Affimer proteins are versatile and renewable affinity reagents. <i>ELife</i> , 2017 , 6,	8.9	103
26	Antigenic mapping of an H9N2 avian influenza virus reveals two discrete antigenic sites and a novel mechanism of immune escape. <i>Scientific Reports</i> , 2016 , 6, 18745	4.9	36
25	Prevalence and diversity of H9N2 avian influenza in chickens of Northern Vietnam, 2014. <i>Infection, Genetics and Evolution</i> , 2016 , 44, 530-540	4.5	32
24	Vinculin Interacts with the Chlamydia Effector TarP Via a Tripartite Vinculin Binding Domain to Mediate Actin Recruitment and Assembly at the Plasma Membrane. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015 , 5, 88	5.9	20
23	Neutralising antibody activity against SARS-CoV-2 variants, including Omicron, in an elderly cohort vaccinated with BNT162b2		6
22	SARS-CoV-2 variants of concern Alpha, Beta, Gamma and Delta have extended ACE2 receptor host-ranges		3
21	The SARS-CoV-2 variant, Omicron, shows rapid replication in human primary nasal epithelial cultures and efficiently uses the endosomal route of entry		55
20	A Global Perspective on H9N2 Avian Influenza Virus		12
19	The molecular basis of antigenic variation among A(H9N2) avian influenza viruses		1
18	Swine ANP32A supports avian influenza virus polymerase		3
17	A rare variant in ANP32B impairs influenza virus replication in human cells		2
16	PA-X is an avian virulence factor in H9N2 avian influenza virus		1
15	Mammalian ANP32A and ANP32B proteins drive alternative avian influenza virus polymerase adaptations		3
14	The furin cleavage site of SARS-CoV-2 spike protein is a key determinant for transmission due to enhanced replication in airway cells		43

13	Resistance of endothelial cells to SARS-CoV-2 infection in vitro		15
12	Disrupting HIV-1 capsid formation causes cGAS sensing of viral DNA		4
11	A common TMPRSS2 variant protects against severe COVID-19		2
10	The SARS-CoV-2 variants associated with infections in India, B.1.617, show enhanced spike cleavage by furin		40
9	Reduced neutralisation of the Delta (B.1.617.2) SARS-CoV-2 variant of concern following vaccination		24
8	The ChAdOx1 vectored vaccine, AZD2816, induces strong immunogenicity against SARS-CoV-2 Beta (B.1.351) and other variants of concern in preclinical studies		8
7	A Common TMPRSS2 Variant Protects Against Severe COVID-19. <i>SSRN Electronic Journal</i> ,	1	1
6	Increased transmission of SARS-CoV-2 lineage B.1.1.7 (VOC 2020212/01) is not accounted for by a replicative advantage in primary airway cells or antibody escape		45
5	Mutations that adapt SARS-CoV-2 to mustelid hosts do not increase fitness in the human airway		2
4	Identification of a Novel SARS-CoV-2 Delta-Omicron Recombinant Virus in the United States		5
3	The origins and molecular evolution of SARS-CoV-2 lineage B.1.1.7 in the UK		2
2	Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages		7
1	An early warning system for emerging SARS-CoV-2 variants. <i>Nature Medicine</i> ,	50.5	2