Anice C Lowen

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.

76
papers5,001
citations31
h-index70
g-index88
ext. papers6,026
ext. citations8.1
avg, IF6
L-index

#	Paper	IF	Citations
76	Intra- and inter-host evolution of H9N2 influenza A virus in Japanese quail Virus Evolution, 2022, 8, vea	ac <u>9</u> , 9 1	O
75	Timing of exposure is critical in a highly sensitive model of SARS-CoV-2 transmission <i>PLoS Pathogens</i> , 2022 , 18, e1010181	7.6	1
74	Mutation L319Q in the PB1 Polymerase Subunit Improves Attenuation of a Candidate Live-Attenuated Influenza A Virus Vaccine <i>Microbiology Spectrum</i> , 2022 , e0007822	8.9	O
73	Recombinant SARS-CoV-2 genomes are currently circulating at low levels 2021,		16
72	Filamentous viruses prevail under pressure. <i>Nature Microbiology</i> , 2021 , 6, 536-537	26.6	0
71	A quantitative approach to assess influenza A virus fitness and transmission in guinea pigs. <i>Journal of Virology</i> , 2021 ,	6.6	1
70	Host factor Rab11a is critical for efficient assembly of influenza A virus genomic segments. <i>PLoS Pathogens</i> , 2021 , 17, e1009517	7.6	3
69	Animal models for SARS-CoV-2. Current Opinion in Virology, 2021, 48, 73-81	7.5	24
68	Avian Influenza A Viruses Reassort and Diversify Differently in Mallards and Mammals. <i>Viruses</i> , 2021 , 13,	6.2	4
67	Rab11a mediates cell-cell spread and reassortment of influenza A virus genomes via tunneling nanotubes. <i>PLoS Pathogens</i> , 2021 , 17, e1009321	7.6	2
66	Mammalian orthoreovirus reassortment proceeds with little constraint on segment mixing <i>Journal of Virology</i> , 2021 , JVI0183221	6.6	1
65	Collective interactions augment influenza A virus replication in a host-dependent manner. <i>Nature Microbiology</i> , 2020 , 5, 1158-1169	26.6	9
64	Influenza A viruses are transmitted via the air from the nasal respiratory epithelium of ferrets. Nature Communications, 2020, 11, 766	17.4	78
63	A method for the unbiased quantification of reassortment in segmented viruses. <i>Journal of Virological Methods</i> , 2020 , 280, 113878	2.6	2
62	Human OAS1 activation is highly dependent on both RNA sequence and context of activating RNA motifs. <i>Nucleic Acids Research</i> , 2020 , 48, 7520-7531	20.1	6
61	Type I and Type III Interferons Restrict SARS-CoV-2 Infection of Human Airway Epithelial Cultures. <i>Journal of Virology</i> , 2020 , 94,	6.6	152
60	Characterizing Emerging Canine H3 Influenza Viruses. <i>PLoS Pathogens</i> , 2020 , 16, e1008409	7.6	15

Characterizing Emerging Canine H3 Influenza Viruses 2020, 16, e1008409 59 Characterizing Emerging Canine H3 Influenza Viruses **2020**, 16, e1008409 58 Characterizing Emerging Canine H3 Influenza Viruses 2020, 16, e1008409 57 Characterizing Emerging Canine H3 Influenza Viruses 2020, 16, e1008409 56 Characterizing Emerging Canine H3 Influenza Viruses 2020, 16, e1008409 55 Characterizing Emerging Canine H3 Influenza Viruses 2020, 16, e1008409 54 Incomplete influenza A virus genomes occur frequently but are readily complemented during 53 17.4 32 localized viral spread. Nature Communications, 2019, 10, 3526 Dysregulation of M segment gene expression contributes to influenza A virus host restriction. PLoS 7.6 52 10 Pathogens, 2019, 15, e1007892 H5N8 and H7N9 packaging signals constrain HA reassortment with a seasonal H3N2 influenza A 51 12 virus. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4611-46185 Why Are CD8 T Cell Epitopes of Human Influenza A Virus Conserved?. Journal of Virology, 2019, 93, 6.6 16 50 Orally Efficacious Broad-Spectrum Ribonucleoside Analog Inhibitor of Influenza and Respiratory 49 5.9 89 Syncytial Viruses. Antimicrobial Agents and Chemotherapy, 2018, 62, Implications of segment mismatch for influenza A virus evolution. Journal of General Virology, 2018, 48 4.9 45 99, 3-16 Influenza A Virus Reassortment Is Limited by Anatomical Compartmentalization following 6.6 47 23 Coinfection via Distinct Routes. Journal of Virology, 2018, 92, It's in the mix: Reassortment of segmented viral genomes. PLoS Pathogens, 2018, 14, e1007200 46 7.6 27 Constraints, Drivers, and Implications of Influenza A Virus Reassortment. Annual Review of Virology, 14.6 62 45 **2017**, 4, 105-121 Heterologous Packaging Signals on Segment 4, but Not Segment 6 or Segment 8, Limit Influenza A 6.6 20 44 Virus Reassortment. Journal of Virology, 2017, 91, Seasonal H3N2 and 2009 Pandemic H1N1 Influenza A Viruses Reassort Efficiently but Produce 6.6 30 43 Attenuated Progeny. Journal of Virology, 2017, 91, Identification and Characterization of Influenza Virus Entry Inhibitors through Dual Myxovirus 6.6 42 17 High-Throughput Screening. Journal of Virology, 2016, 90, 7368-7387

41	Virology: Host protein clips bird flus wings in mammals. <i>Nature</i> , 2016 , 529, 30-1	50.4	1
40	Droplet digital PCR: A novel method for detection of influenza virus defective interfering particles. <i>Journal of Virological Methods</i> , 2016 , 237, 159-165	2.6	16
39	Competitive fitness of influenza B viruses with neuraminidase inhibitor-resistant substitutions in a coinfection model of the human airway epithelium. <i>Journal of Virology</i> , 2015 , 89, 4575-87	6.6	18
38	Influenza Virus Reassortment Is Enhanced by Semi-infectious Particles but Can Be Suppressed by Defective Interfering Particles. <i>PLoS Pathogens</i> , 2015 , 11, e1005204	7.6	51
37	Influenza A Virus Coinfection through Transmission Can Support High Levels of Reassortment. <i>Journal of Virology</i> , 2015 , 89, 8453-61	6.6	24
36	In memoriamRichard M. Elliott (1954-2015). Journal of General Virology, 2015, 96, 1975-1978	4.9	2
35	The M segment of the 2009 pandemic influenza virus confers increased neuraminidase activity, filamentous morphology, and efficient contact transmissibility to A/Puerto Rico/8/1934-based reassortant viruses. <i>Journal of Virology</i> , 2014 , 88, 3802-14	6.6	71
34	Roles of humidity and temperature in shaping influenza seasonality. Journal of Virology, 2014, 88, 7692-	·5 6.6	268
33	Intrahost dynamics of influenza virus reassortment. <i>Journal of Virology</i> , 2014 , 88, 7485-92	6.6	30
32	Novel H7N9 influenza virus shows low infectious dose, high growth rate, and efficient contact transmission in the guinea pig model. <i>Journal of Virology</i> , 2014 , 88, 1502-12	6.6	43
31	Mutations to PB2 and NP proteins of an avian influenza virus combine to confer efficient growth in primary human respiratory cells. <i>Journal of Virology</i> , 2014 , 88, 13436-46	6.6	23
30	Influenza A virus reassortment. Current Topics in Microbiology and Immunology, 2014 , 385, 377-401	3.3	67
29	Transmission in the guinea pig model. Current Topics in Microbiology and Immunology, 2014, 385, 157-83	3.3	23
28	Residue 41 of the Eurasian avian-like swine influenza a virus matrix protein modulates virion filament length and efficiency of contact transmission. <i>Journal of Virology</i> , 2014 , 88, 7569-77	6.6	22
27	Filament-producing mutants of influenza A/Puerto Rico/8/1934 (H1N1) virus have higher neuraminidase activities than the spherical wild-type. <i>PLoS ONE</i> , 2014 , 9, e112462	3.7	15
26	Spherical influenza viruses have a fitness advantage in embryonated eggs, while filament-producing strains are selected in vivo. <i>Journal of Virology</i> , 2013 , 87, 13343-53	6.6	45
25	Influenza virus reassortment occurs with high frequency in the absence of segment mismatch. <i>PLoS Pathogens</i> , 2013 , 9, e1003421	7.6	116
24	Transmission of a 2009 pandemic influenza virus shows a sensitivity to temperature and humidity similar to that of an H3N2 seasonal strain. <i>Journal of Virology</i> , 2011 , 85, 1400-2	6.6	100

(2004-2011)

23	The M segment of the 2009 new pandemic H1N1 influenza virus is critical for its high transmission efficiency in the guinea pig model. <i>Journal of Virology</i> , 2011 , 85, 11235-41	6.6	111	
22	Virulence-associated substitution D222G in the hemagglutinin of 2009 pandemic influenza A(H1N1) virus affects receptor binding. <i>Journal of Virology</i> , 2010 , 84, 11802-13	6.6	171	
21	Transmission of pandemic H1N1 influenza virus and impact of prior exposure to seasonal strains or interferon treatment. <i>Journal of Virology</i> , 2010 , 84, 21-6	6.6	101	
20	Animal Models for Influenza Virus Pathogenesis and Transmission. <i>Viruses</i> , 2010 , 2, 1530-1563	6.2	247	
19	Blocking interhost transmission of influenza virus by vaccination in the guinea pig model. <i>Journal of Virology</i> , 2009 , 83, 2803-18	6.6	65	
18	Live attenuated influenza viruses containing NS1 truncations as vaccine candidates against H5N1 highly pathogenic avian influenza. <i>Journal of Virology</i> , 2009 , 83, 1742-53	6.6	186	
17	Transmission of influenza virus in a mammalian host is increased by PB2 amino acids 627K or 627E/701N. <i>PLoS Pathogens</i> , 2009 , 5, e1000252	7.6	421	
16	Transmission of influenza virus via aerosols and fomites in the guinea pig model. <i>Journal of Infectious Diseases</i> , 2009 , 199, 858-65	7	148	
15	Transmission of influenza virus in temperate zones is predominantly by aerosol, in the tropics by contact: a hypothesis. <i>PLOS Currents</i> , 2009 , 1, RRN1002		59	
14	High temperature (30 degrees C) blocks aerosol but not contact transmission of influenza virus. <i>Journal of Virology</i> , 2008 , 82, 5650-2	6.6	242	
13	Oseltamivir-resistant influenza A viruses are transmitted efficiently among guinea pigs by direct contact but not by aerosol. <i>Journal of Virology</i> , 2008 , 82, 10052-8	6.6	84	
12	Influenza virus transmission is dependent on relative humidity and temperature. <i>PLoS Pathogens</i> , 2007 , 3, 1470-6	7.6	992	
11	Genetic elements regulating packaging of the Bunyamwera orthobunyavirus genome. <i>Journal of General Virology</i> , 2006 , 87, 177-187	4.9	44	
10	The guinea pig as a transmission model for human influenza viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 9988-92	11.5	270	
9	Mutational analyses of the nonconserved sequences in the Bunyamwera Orthobunyavirus S segment untranslated regions. <i>Journal of Virology</i> , 2005 , 79, 12861-70	6.6	23	
8	Attenuation of bunyavirus replication by rearrangement of viral coding and noncoding sequences. <i>Journal of Virology</i> , 2005 , 79, 6940-6	6.6	35	
7	Complementarity, sequence and structural elements within the 3Sand 5Snon-coding regions of the Bunyamwera orthobunyavirus S segment determine promoter strength. <i>Journal of General Virology</i> , 2004 , 85, 3269-3278	4.9	57	
6	Efficient bunyavirus rescue from cloned cDNA. <i>Virology</i> , 2004 , 330, 493-500	3.6	79	

5	Why Are CD8 T Cell Epitopes of Human Influenza A Virus Conserved?		1
4	Type I and Type III IFN Restrict SARS-CoV-2 Infection of Human Airway Epithelial Cultures		16
3	Incomplete influenza A virus genomes are abundant but readily complemented during spatially structured viral spread		3
2	Collective interactions augment influenza A virus replication in a host-dependent manner		2
1	Recombinant SARS-CoV-2 genomes circulated at low levels over the first year of the pandemic. Virus Evolution 3:	 7	10