David E Wentworth

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.

127	5,384	40	69
papers	citations	h-index	g-index
135	6,525	9.2	5.12
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
127	N-glycosylation profiles of the SARS-CoV-2 spike D614G mutant and its ancestral protein characterized by advanced mass spectrometry. *Scientific Reports*, **2021**, 11, 23561	4.9	3
126	Enhanced fitness of SARS-CoV-2 variant of concern Alpha but not Beta.. *Nature*, **2021**,	50.4	12
125	Intranasal powder live attenuated influenza vaccine is thermostable, immunogenic, and protective against homologous challenge in ferrets. *Npj Vaccines*, **2021**, 6, 59	9.5	3
124	Susceptibility of widely diverse influenza a viruses to PB2 polymerase inhibitor pimodivir. *Antiviral Research*, **2021**, 188, 105035	10.8	5
123	Susceptibility to SARS-CoV-2 of Cell Lines and Substrates Commonly Used to Diagnose and Isolate Influenza and Other Viruses. *Emerging Infectious Diseases*, **2021**, 27, 1380-1392	10.2	4
122	SARS-CoV-2 spike D614G change enhances replication and transmission. *Nature*, **2021**, 592, 122-127	50.4	214
121	Replicative Fitness of Seasonal Influenza A Viruses With Decreased Susceptibility to Baloxavir. *Journal of Infectious Diseases*, **2020**, 221, 367-371	7	19
120	Development of an RNA Strand-Specific Hybridization Assay To Differentiate Replicating versus Nonreplicating Influenza A Viruses. *Journal of Clinical Microbiology*, **2020**, 58,	9.7	1
119	Genetically and Antigenically Divergent Influenza A(H9N2) Viruses Exhibit Differential Replication and Transmission Phenotypes in Mammalian Models. *Journal of Virology*, **2020**, 94,	6.6	6
118	Amino Acid Substitutions in Positions 385 and 393 of the Hydrophobic Region of VP4 May Be Associated with Rotavirus Attenuation and Cell Culture Adaptation. *Viruses*, **2020**, 12,	6.2	1
117	Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. *ELife*, **2020**, 9,	8.9	8
116	Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection. *Nature Communications*, **2020**, 11, 2537	17.4	23
115	Spread of Antigenically Drifted Influenza A(H3N2) Viruses and Vaccine Effectiveness in the United States During the 2018-2019 Season. *Journal of Infectious Diseases*, **2020**, 221, 8-15	7	86
114	Detection of baloxavir resistant influenza A viruses using next generation sequencing and pyrosequencing methods. *Antiviral Research*, **2020**, 182, 104906	10.8	5
113	Detection and Characterization of Swine Origin Influenza A(H1N1) Pandemic 2009 Viruses in Humans following Zoonotic Transmission. *Journal of Virology*, **2020**, 95,	6.6	4
112	Human Monoclonal Antibody Derived from Transchromosomic Cattle Neutralizes Multiple H1 Clades of Influenza A Virus by Recognizing a Novel Conformational Epitope in the Hemagglutinin Head Domain. *Journal of Virology*, **2020**, 94,	6.6	4
111	Susceptibility of Influenza A, B, C, and D Viruses to Baloxavir. *Emerging Infectious Diseases*, **2019**, 25, 1969-1972	10.2	32

110	Detection of highly pathogenic avian influenza A(H5N6) viruses in waterfowl in Bangladesh. *Virology*, **2019**, 534, 36-44	3.6	10
109	Comparison of nucleic acid extraction methods for next-generation sequencing of avian influenza A virus from ferret respiratory samples. *Journal of Virological Methods*, **2019**, 270, 95-105	2.6	3
108	Insights into the antigenic advancement of influenza A(H3N2) viruses, 2011-2018. *Scientific Reports*, **2019**, 9, 2676	4.9	30
107	Reply to TReconciling disparate estimates of viral genetic diversity during human influenza infectionsT. *Nature Genetics*, **2019**, 51, 1301-1303	36.3	1
106	Evaluation of A(H1N1)pdm09 LAIV vaccine candidates stability and replication efficiency in primary human nasal epithelial cells. *Vaccine: X*, **2019**, 2, 100031	3.8	6
105	Assessing baloxavir susceptibility of influenza viruses circulating in the United States during the 2016/17 and 2017/18 seasons. *Eurosurveillance*, **2019**, 24,	19.8	56
104	Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017-2018 influenza season. *Virus Evolution*, **2019**, 5, vez046	3.7	7
103	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012-2013. *Clinical Infectious Diseases*, **2018**, 67, 327-333	11.6	36
102	Non-mumps Viral Parotitis During the 2014-2015 Influenza Season in the United States. *Clinical Infectious Diseases*, **2018**, 67, 493-501	11.6	22
101	The transmission dynamics and diversity of human metapneumovirus in Peru. *Influenza and Other Respiratory Viruses*, **2018**, 12, 508-513	5.6	4
100	Monoclonal antibody against N2 neuraminidase of cold adapted A/Leningrad/134/17/57 (H2N2) enables efficient generation of live attenuated influenza vaccines. *Virology*, **2018**, 522, 65-72	3.6	2
99	Influenza-Associated Parotitis During the 2014-2015 Influenza Season in the United States. *Clinical Infectious Diseases*, **2018**, 67, 485-492	11.6	5
98	The effects of repeated automated plasmapheresis in goats (Capra hircus) in response to vaccination with purified influenza hemagglutinin proteins. *PLoS ONE*, **2018**, 13, e0195903	3.7	
97	Update: Influenza Activity - United States, October 1, 2017-February 3, 2018. *Morbidity and Mortality Weekly Report*, **2018**, 67, 169-179	31.7	38
96	Update: Influenza Activity in the United States During the 2017-18 Season and Composition of the 2018-19 Influenza Vaccine. *Morbidity and Mortality Weekly Report*, **2018**, 67, 634-642	31.7	143
95	Direct RNA Sequencing of the Coding Complete Influenza A Virus Genome. *Scientific Reports*, **2018**, 8, 14408	4.9	72
94	Where do all the subtypes go? Temporal dynamics of H8-H12 influenza A viruses in waterfowl. *Virus Evolution*, **2018**, 4, vey025	3.7	14
93	Avian Influenza Viruses in Wild Birds: Virus Evolution in a Multihost Ecosystem. *Journal of Virology*, **2018**, 92,	6.6	50

92	Multiplex Reverse Transcription-PCR for Simultaneous Surveillance of Influenza A and B Viruses. *Journal of Clinical Microbiology*, **2017**, 55, 3492-3501	9.7	20
91	Antiviral Drug-Resistant Influenza B Viruses Carrying H134N Substitution in Neuraminidase, Laos, February 2016. *Emerging Infectious Diseases*, **2017**, 23, 686-690	10.2	10
90	Pathogenicity testing of influenza candidate vaccine viruses in the ferret model. *Virology*, **2017**, 511, 135-141	3.6	11
89	Potential for Low-Pathogenic Avian H7 Influenza A Viruses To Replicate and Cause Disease in a Mammalian Model. *Journal of Virology*, **2017**, 91,	6.6	10
88	A Pyrosequencing-Based Approach to High-Throughput Identification of Influenza A(H3N2) Virus Clades Harboring Antigenic Drift Variants. *Journal of Clinical Microbiology*, **2017**, 55, 145-154	9.7	6
87	Assessment of Molecular, Antigenic, and Pathological Features of Canine Influenza A(H3N2) Viruses That Emerged in the United States. *Journal of Infectious Diseases*, **2017**, 216, S499-S507	7	22
86	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. *PLoS Neglected Tropical Diseases*, **2017**, 11, e0005693	4.8	38
85	The effective rate of influenza reassortment is limited during human infection. *PLoS Pathogens*, **2017**, 13, e1006203	7.6	27
84	Update: Influenza Activity - United States and Worldwide, May 21-September 23, 2017. *Morbidity and Mortality Weekly Report*, **2017**, 66, 1043-1051	31.7	18
83	Update: Influenza Activity - United States, October 1-November 25, 2017. *Morbidity and Mortality Weekly Report*, **2017**, 66, 1318-1326	31.7	15
82	Pathogenicity of modified bat influenza virus with different M genes and its reassortment potential with swine influenza A virus. *Journal of General Virology*, **2017**, 98, 577-584	4.9	10
81	Reversion of Cold-Adapted Live Attenuated Influenza Vaccine into a Pathogenic Virus. *Journal of Virology*, **2016**, 90, 8454-63	6.6	28
80	A Universal Next-Generation Sequencing Protocol To Generate Noninfectious Barcoded cDNA Libraries from High-Containment RNA Viruses. *MSystems*, **2016**, 1,	7.6	23
79	Implementation of new approaches for generating conventional reassortants for live attenuated influenza vaccine based on Russian master donor viruses. *Journal of Virological Methods*, **2016**, 227, 33-9	2.6	8
78	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. *Journal of Infectious Diseases*, **2016**, 213, 173-82	7	17
77	Quantifying influenza virus diversity and transmission in humans. *Nature Genetics*, **2016**, 48, 195-200	36.3	132
76	Comparative In Vitro and In Vivo Studies of Porcine Rotavirus G9P[13] and Human Rotavirus Wa G1P[8]. *Journal of Virology*, **2016**, 90, 142-51	6.6	14
75	Genetically Diverse Low Pathogenicity Avian Influenza A Virus Subtypes Co-Circulate among Poultry in Bangladesh. *PLoS ONE*, **2016**, 11, e0152131	3.7	25

74	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. *PLoS Pathogens*, **2016**, 12, e1005620	7.6	35
73	Molecular Characterizations of Surface Proteins Hemagglutinin and Neuraminidase from Recent H5Nx Avian Influenza Viruses. *Journal of Virology*, **2016**, 90, 5770-5784	6.6	41
72	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. *Journal of Virology*, **2016**, 90, 10963-10971	6.6	15
71	Deep Sequencing of Influenza A Virus from a Human Challenge Study Reveals a Selective Bottleneck and Only Limited Intrahost Genetic Diversification. *Journal of Virology*, **2016**, 90, 11247-11258	6.6	68
70	Molecular epidemiology of human enterovirus 71 at the origin of an epidemic of fatal hand, foot and mouth disease cases in Cambodia. *Emerging Microbes and Infections*, **2016**, 5, e104	18.9	33
69	Long-term surveillance of H7 influenza viruses in American wild aquatic birds: are the H7N3 influenza viruses in wild birds the precursors of highly pathogenic strains in domestic poultry?. *Emerging Microbes and Infections*, **2015**, 4, e35	18.9	24
68	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. *Journal of Virology*, **2015**, 89, 9689-92	6.6	8
67	Swine Influenza Virus PA and Neuraminidase Gene Reassortment into Human H1N1 Influenza Virus Is Associated with an Altered Pathogenic Phenotype Linked to Increased MIP-2 Expression. *Journal of Virology*, **2015**, 89, 5651-67	6.6	7
66	Spread and persistence of influenza A viruses in waterfowl hosts in the North American Mississippi migratory flyway. *Journal of Virology*, **2015**, 89, 5371-81	6.6	18
65	Equine and Canine Influenza H3N8 Viruses Show Minimal Biological Differences Despite Phylogenetic Divergence. *Journal of Virology*, **2015**, 89, 6860-73	6.6	31
64	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	4.9	22
63	Whole genome detection of rotavirus mixed infections in human, porcine and bovine samples co-infected with various rotavirus strains collected from sub-Saharan Africa. *Infection, Genetics and Evolution*, **2015**, 31, 321-34	4.5	30
62	Global migration of influenza A viruses in swine. *Nature Communications*, **2015**, 6, 6696	17.4	91
61	The soft palate is an important site of adaptation for transmissible influenza viruses. *Nature*, **2015**, 526, 122-5	50.4	102
60	Differential Susceptibilities of Human Lung Primary Cells to H1N1 Influenza Viruses. *Journal of Virology*, **2015**, 89, 11935-44	6.6	24
59	Phylodynamics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. *Journal of Virology*, **2015**, 89, 8871-9	6.6	45
58	Isolation of type A influenza viruses from Red-necked Grebes (Podiceps grisegena). *Journal of Wildlife Diseases*, **2015**, 51, 290-3	1.3	1
57	Whole genome analyses of G1P[8] rotavirus strains from vaccinated and non-vaccinated South African children presenting with diarrhea. *Journal of Medical Virology*, **2015**, 87, 79-101	19.7	29

56	Phylogeography of Influenza A(H3N2) Virus in Peru, 2010-2012. *Emerging Infectious Diseases*, **2015**, 21, 1330-8	10.2	16
55	Adaptation of pandemic H2N2 influenza A viruses in humans. *Journal of Virology*, **2015**, 89, 2442-7	6.6	26
54	H7N9 influenza A virus in turkeys in Minnesota. *Journal of General Virology*, **2015**, 96, 269-276	4.9	7
53	The contrasting phylodynamics of human influenza B viruses. *ELife*, **2015**, 4, e05055	8.9	129
52	Genomewide analysis of reassortment and evolution of human influenza A(H3N2) viruses circulating between 1968 and 2011. *Journal of Virology*, **2014**, 88, 2844-57	6.6	100
51	The evolutionary dynamics of influenza A and B viruses in the tropical city of Managua, Nicaragua. *Virology*, **2014**, 462-463, 81-90	3.6	6
50	Analysis of recombinant H7N9 wild-type and mutant viruses in pigs shows that the Q226L mutation in HA is important for transmission. *Journal of Virology*, **2014**, 88, 8153-65	6.6	46
49	Introductions and evolution of human-origin seasonal influenza a viruses in multinational swine populations. *Journal of Virology*, **2014**, 88, 10110-9	6.6	69
48	Standardized metadata for human pathogen/vector genomic sequences. *PLoS ONE*, **2014**, 9, e99979	3.7	25
47	Equine influenza A(H3N8) virus isolated from Bactrian camel, Mongolia. *Emerging Infectious Diseases*, **2014**, 20, 2144-7	10.2	30
46	Whole-genome analyses of DS-1-like human G2P[4] and G8P[4] rotavirus strains from Eastern, Western and Southern Africa. *Virus Genes*, **2014**, 49, 196-207	2.3	24
45	Characterization of uncultivable bat influenza virus using a replicative synthetic virus. *PLoS Pathogens*, **2014**, 10, e1004420	7.6	45
44	Universal influenza B virus genomic amplification facilitates sequencing, diagnostics, and reverse genetics. *Journal of Clinical Microbiology*, **2014**, 52, 1330-7	9.7	64
43	Genomic analyses detect Eurasian-lineage H10 and additional H14 influenza A viruses recovered from waterfowl in the Central United States. *Influenza and Other Respiratory Viruses*, **2014**, 8, 493-8	5.6	16
42	North Atlantic migratory bird flyways provide routes for intercontinental movement of avian influenza viruses. *PLoS ONE*, **2014**, 9, e92075	3.7	46
41	Sequencing viral genomes from a single isolated plaque. *Virology Journal*, **2013**, 10, 181	6.1	15
40	Evolution of a reassortant North American gull influenza virus lineage: drift, shift and stability. *Virology Journal*, **2013**, 10, 179	6.1	25
39	Synthetic generation of influenza vaccine viruses for rapid response to pandemics. *Science Translational Medicine*, **2013**, 5, 185ra68	17.5	134

38	Complete Genome Sequence of a Reassortant H14N2 Avian Influenza Virus from California. *Genome Announcements*, **2013**, 1,		10
37	Migration and persistence of human influenza A viruses, Vietnam, 2001-2008. *Emerging Infectious Diseases*, **2013**, 19, 1756-65	10.2	14
36	Avian influenza: mixed infections and missing viruses. *Viruses*, **2013**, 5, 1964-77	6.2	15
35	Influenza a virus migration and persistence in North American wild birds. *PLoS Pathogens*, **2013**, 9, e1003570	7.6	69
34	Sequence analysis of in vivo defective interfering-like RNA of influenza A H1N1 pandemic virus. *Journal of Virology*, **2013**, 87, 8064-74	6.6	111
33	Asparagine substitution at PB2 residue 701 enhances the replication, pathogenicity, and transmission of the 2009 pandemic H1N1 influenza A virus. *PLoS ONE*, **2013**, 8, e67616	3.7	49
32	Antiviral responses by Swine primary bronchoepithelial cells are limited compared to human bronchoepithelial cells following influenza virus infection. *PLoS ONE*, **2013**, 8, e70251	3.7	12
31	Engineering temperature sensitive live attenuated influenza vaccines from emerging viruses. *Vaccine*, **2012**, 30, 3691-702	4.1	30
30	Genomic reassortment of influenza A virus in North American swine, 1998-2011. *Journal of General Virology*, **2012**, 93, 2584-2589	4.9	35
29	Decreased serologic response in vaccinated military recruits during 2011 correspond to genetic drift in concurrent circulating pandemic A/H1N1 viruses. *PLoS ONE*, **2012**, 7, e34581	3.7	12
28	Influenza A virus molecular virology techniques. *Methods in Molecular Biology*, **2012**, 865, 175-92	1.4	56
27	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. *Ecology Letters*, **2012**, 15, 24-33	10	76
26	Genomic analysis of 16 Colorado human NL63 coronaviruses identifies a new genotype, high sequence diversity in the N-terminal domain of the spike gene and evidence of recombination. *Journal of General Virology*, **2012**, 93, 2387-2398	4.9	23
25	Innate immune response of human alveolar macrophages during influenza A infection. *PLoS ONE*, **2012**, 7, e29879	3.7	83
24	Reverse genetics plasmid for cloning unstable influenza A virus gene segments. *Journal of Virological Methods*, **2011**, 173, 378-83	2.6	18
23	Deep sequencing reveals mixed infection with 2009 pandemic influenza A (H1N1) virus strains and the emergence of oseltamivir resistance. *Journal of Infectious Diseases*, **2011**, 203, 168-74	7	91
22	Phylogeography of the spring and fall waves of the H1N1/09 pandemic influenza virus in the United States. *Journal of Virology*, **2011**, 85, 828-34	6.6	46
21	Extensive geographical mixing of 2009 human H1N1 influenza A virus in a single university community. *Journal of Virology*, **2011**, 85, 6923-9	6.6	35

20	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 19359-64	11.5	130
19	PB2 residue 158 is a pathogenic determinant of pandemic H1N1 and H5 influenza a viruses in mice. *Journal of Virology*, **2011**, 85, 357-65	6.6	97
18	Unseasonal transmission of H3N2 influenza A virus during the swine-origin H1N1 pandemic. *Journal of Virology*, **2010**, 84, 5715-8	6.6	13
17	NS-based live attenuated H1N1 pandemic vaccines protect mice and ferrets. *Vaccine*, **2010**, 28, 8015-25	4.1	43
16	Single-reaction genomic amplification accelerates sequencing and vaccine production for classical and Swine origin human influenza a viruses. *Journal of Virology*, **2009**, 83, 10309-13	6.6	366
15	The early diversification of influenza A/H1N1pdm. *PLOS Currents*, **2009**, 1, RRN1126		108
14	Triaryl pyrazoline compound inhibits flavivirus RNA replication. *Antimicrobial Agents and Chemotherapy*, **2006**, 50, 1320-9	5.9	102
13	Mustela vison ACE2 functions as a receptor for SARS-coronavirus. *Advances in Experimental Medicine and Biology*, **2006**, 581, 507-10	3.6	9
12	Increased viral titers and subtle changes in plaque morphology upon passage of SARS-CoV in cells from different species. *Advances in Experimental Medicine and Biology*, **2006**, 581, 259-63	3.6	2
11	Analysis of SARS-CoV receptor activity of ACE2 orthologs. *Advances in Experimental Medicine and Biology*, **2006**, 581, 277-80	3.6	5
10	Cells of human aminopeptidase N (CD13) transgenic mice are infected by human coronavirus-229E in vitro, but not in vivo. *Virology*, **2005**, 335, 185-97	3.6	31
9	Mice susceptible to SARS coronavirus. *Emerging Infectious Diseases*, **2004**, 10, 1293-6	10.2	56
8	Discovery of novel human and animal cells infected by the severe acute respiratory syndrome coronavirus by replication-specific multiplex reverse transcription-PCR. *Journal of Clinical Microbiology*, **2004**, 42, 3196-206	9.7	67
7	CD209L (L-SIGN) is a receptor for severe acute respiratory syndrome coronavirus. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 15748-53	11.5	456
6	Identification of a receptor-binding domain of the spike glycoprotein of human coronavirus HCoV-229E. *Journal of Virology*, **2003**, 77, 2530-8	6.6	147
5	Molecular determinants of species specificity in the coronavirus receptor aminopeptidase N (CD13): influence of N-linked glycosylation. *Journal of Virology*, **2001**, 75, 9741-52	6.6	86
4	Differential neutralization and inhibition of SARS-CoV-2 variants by antibodies elicited by COVID-19 mRNA vaccines		2
3	Despite egg-adaptive mutations, the 2012-13 H3N2 influenza vaccine induced comparable antibody titers to the intended strain		2

LIST OF PUBLICATIONS

2	Avian influenza viruses in wild birds: virus evolution in a multi-host ecosystem	1
1	Direct RNA Sequencing of the Complete Influenza A Virus Genome	4