

# David E Wentworth

## List of Publications by Year in descending order

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Version: 2024-02-01

124  
papers

7,355  
citations

53939

47  
h-index

75989

78  
g-index

135  
all docs

135  
docs citations

135  
times ranked

11115  
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced fitness of SARS-CoV-2 variant of concern Alpha but not Beta. <i>Nature</i> , 2022, 602, 307-313.	13.7	79
2	SARS-CoV-2 spike D614G change enhances replication and transmission. <i>Nature</i> , 2021, 592, 122-127.	13.7	440
3	Intranasal powder live attenuated influenza vaccine is thermostable, immunogenic, and protective against homologous challenge in ferrets. <i>Npj Vaccines</i> , 2021, 6, 59.	2.9	9
4	Susceptibility of widely diverse influenza A viruses to PB2 polymerase inhibitor pimodivir. <i>Antiviral Research</i> , 2021, 188, 105035.	1.9	15
5	Susceptibility to SARS-CoV-2 of Cell Lines and Substrates Commonly Used to Diagnose and Isolate Influenza and Other Viruses. <i>Emerging Infectious Diseases</i> , 2021, 27, 1380-1392.	2.0	21
6	N-glycosylation profiles of the SARS-CoV-2 spike D614G mutant and its ancestral protein characterized by advanced mass spectrometry. <i>Scientific Reports</i> , 2021, 11, 23561.	1.6	14
7	Spread of Antigenically Drifted Influenza A(H3N2) Viruses and Vaccine Effectiveness in the United States During the 2018-2019 Season. <i>Journal of Infectious Diseases</i> , 2020, 221, 8-15.	1.9	150
8	Detection of baloxavir resistant influenza A viruses using next generation sequencing and pyrosequencing methods. <i>Antiviral Research</i> , 2020, 182, 104906.	1.9	13
9	Detection and Characterization of Swine Origin Influenza A(H1N1) Pandemic 2009 Viruses in Humans following Zoonotic Transmission. <i>Journal of Virology</i> , 2020, 95, .	1.5	10
10	Human Monoclonal Antibody Derived from Transchromosomal Cattle Neutralizes Multiple H1 Clades of Influenza A Virus by Recognizing a Novel Conformational Epitope in the Hemagglutinin Head Domain. <i>Journal of Virology</i> , 2020, 94, .	1.5	6
11	Development of an RNA Strand-Specific Hybridization Assay To Differentiate Replicating versus Nonreplicating Influenza A Viruses. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	1.8	2
12	Genetically and Antigenically Divergent Influenza A(H9N2) Viruses Exhibit Differential Replication and Transmission Phenotypes in Mammalian Models. <i>Journal of Virology</i> , 2020, 94, .	1.5	12
13	Amino Acid Substitutions in Positions 385 and 393 of the Hydrophobic Region of VP4 May Be Associated with Rotavirus Attenuation and Cell Culture Adaptation. <i>Viruses</i> , 2020, 12, 408.	1.5	6
14	Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection. <i>Nature Communications</i> , 2020, 11, 2537.	5.8	72
15	Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. <i>eLife</i> , 2020, 9, .	2.8	35
16	Reply to "Reconciling disparate estimates of viral genetic diversity during human influenza infections". <i>Nature Genetics</i> , 2019, 51, 1301-1303.	9.4	3
17	Evaluation of A(H1N1)pdm09 LAIV vaccine candidates stability and replication efficiency in primary human nasal epithelial cells. <i>Vaccine: X</i> , 2019, 2, 100031.	0.9	10
18	Replicative Fitness of Seasonal Influenza A Viruses With Decreased Susceptibility to Baloxavir. <i>Journal of Infectious Diseases</i> , 2019, 221, 367-371.	1.9	27

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19	Susceptibility of Influenza A, B, C, and D Viruses to Baloxavir1. <i>Emerging Infectious Diseases</i> , 2019, 25, 1969-1972.	2.0	53
20	Detection of highly pathogenic avian influenza A(H5N6) viruses in waterfowl in Bangladesh. <i>Virology</i> , 2019, 534, 36-44.	1.1	13
21	Comparison of nucleic acid extraction methods for next-generation sequencing of avian influenza A virus from ferret respiratory samples. <i>Journal of Virological Methods</i> , 2019, 270, 95-105.	1.0	3
22	Insights into the antigenic advancement of influenza A(H3N2) viruses, 2011â€“2018. <i>Scientific Reports</i> , 2019, 9, 2676.	1.6	48
23	Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017â€“2018 influenza season. <i>Virus Evolution</i> , 2019, 5, vez046.	2.2	19
24	Assessing baloxavir susceptibility of influenza viruses circulating in the United States during the 2016/17 and 2017/18 seasons. <i>Eurosurveillance</i> , 2019, 24, .	3.9	86
25	Poor Immunogenicity, Not Vaccine Strain Egg Adaptation, May Explain the Low H3N2 Influenza Vaccine Effectiveness in 2012â€“2013. <i>Clinical Infectious Diseases</i> , 2018, 67, 327-333.	2.9	53
26	Non-mumps Viral Parotitis During the 2014â€“2015 Influenza Season in the United States. <i>Clinical Infectious Diseases</i> , 2018, 67, 493-501.	2.9	33
27	The transmission dynamics and diversity of human metapneumovirus in Peru. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 508-513.	1.5	6
28	Direct RNA Sequencing of the Coding Complete Influenza A Virus Genome. <i>Scientific Reports</i> , 2018, 8, 14408.	1.6	95
29	Where do all the subtypes go? Temporal dynamics of H8â€“H12 influenza A viruses in waterfowl. <i>Virus Evolution</i> , 2018, 4, vey025.	2.2	23
30	Avian Influenza Viruses in Wild Birds: Virus Evolution in a Multihost Ecosystem. <i>Journal of Virology</i> , 2018, 92, .	1.5	83
31	Monoclonal antibody against N2 neuraminidase of cold adapted A/Leningrad/134/17/57 (H2N2) enables efficient generation of live attenuated influenza vaccines. <i>Virology</i> , 2018, 522, 65-72.	1.1	3
32	Influenza-Associated Parotitis During the 2014â€“2015 Influenza Season in the United States. <i>Clinical Infectious Diseases</i> , 2018, 67, 485-492.	2.9	8
33	The effects of repeated automated plasmapheresis in goats ( <i>Capra hircus</i> ) in response to vaccination with purified influenza hemagglutinin proteins. <i>PLoS ONE</i> , 2018, 13, e0195903.	1.1	0
34	Update: Influenza Activity â€” United States, October 1, 2017â€“February 3, 2018. <i>Morbidity and Mortality Weekly Report</i> , 2018, 67, 169-179.	9.0	60
35	Update: Influenza Activity in the United States During the 2017â€“18 Season and Composition of the 2018â€“19 Influenza Vaccine. <i>Morbidity and Mortality Weekly Report</i> , 2018, 67, 634-642.	9.0	202
36	Multiplex Reverse Transcription-PCR for Simultaneous Surveillance of Influenza A and B Viruses. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3492-3501.	1.8	29

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37	Pathogenicity testing of influenza candidate vaccine viruses in the ferret model. <i>Virology</i> , 2017, 511, 135-141.	1.1	18
38	Potential for Low-Pathogenic Avian H7 Influenza A Viruses To Replicate and Cause Disease in a Mammalian Model. <i>Journal of Virology</i> , 2017, 91, .	1.5	14
39	A Pyrosequencing-Based Approach to High-Throughput Identification of Influenza A(H3N2) Virus Clades Harboring Antigenic Drift Variants. <i>Journal of Clinical Microbiology</i> , 2017, 55, 145-154.	1.8	6
40	Assessment of Molecular, Antigenic, and Pathological Features of Canine Influenza A(H3N2) Viruses That Emerged in the United States. <i>Journal of Infectious Diseases</i> , 2017, 216, S499-S507.	1.9	28
41	Antiviral Drug-Resistant Influenza B Viruses Carrying H134N Substitution in Neuraminidase, Laos, February 2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 686-690.	2.0	11
42	Pathogenicity of modified bat influenza virus with different M genes and its reassortment potential with swine influenza A virus. <i>Journal of General Virology</i> , 2017, 98, 577-584.	1.3	15
43	Evolution and spread of Venezuelan equine encephalitis complex alphavirus in the Americas. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005693.	1.3	56
44	The effective rate of influenza reassortment is limited during human infection. <i>PLoS Pathogens</i> , 2017, 13, e1006203.	2.1	42
45	Update: Influenza Activity – United States and Worldwide, May 21–September 23, 2017. <i>Morbidity and Mortality Weekly Report</i> , 2017, 66, 1043-1051.	9.0	34
46	Update: Influenza Activity – United States, October 1–November 25, 2017. <i>Morbidity and Mortality Weekly Report</i> , 2017, 66, 1318-1326.	9.0	16
47	Ecosystem Interactions Underlie the Spread of Avian Influenza A Viruses with Pandemic Potential. <i>PLoS Pathogens</i> , 2016, 12, e1005620.	2.1	48
48	Molecular Characterizations of Surface Proteins Hemagglutinin and Neuraminidase from Recent H5Nx Avian Influenza Viruses. <i>Journal of Virology</i> , 2016, 90, 5770-5784.	1.5	52
49	Introduction, Evolution, and Dissemination of Influenza A Viruses in Exhibition Swine in the United States during 2009 to 2013. <i>Journal of Virology</i> , 2016, 90, 10963-10971.	1.5	22
50	Deep Sequencing of Influenza A Virus from a Human Challenge Study Reveals a Selective Bottleneck and Only Limited Intra-host Genetic Diversification. <i>Journal of Virology</i> , 2016, 90, 11247-11258.	1.5	97
51	Molecular epidemiology of human enterovirus 71 at the origin of an epidemic of fatal hand, foot and mouth disease cases in Cambodia. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-9.	3.0	54
52	Reversion of Cold-Adapted Live Attenuated Influenza Vaccine into a Pathogenic Virus. <i>Journal of Virology</i> , 2016, 90, 8454-8463.	1.5	42
53	A Universal Next-Generation Sequencing Protocol To Generate Noninfectious Barcoded cDNA Libraries from High-Containment RNA Viruses. <i>MSystems</i> , 2016, 1, .	1.7	28
54	Implementation of new approaches for generating conventional reassortants for live attenuated influenza vaccine based on Russian master donor viruses. <i>Journal of Virological Methods</i> , 2016, 227, 33-39.	1.0	11

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55	Evolutionary Dynamics of Influenza A Viruses in US Exhibition Swine. <i>Journal of Infectious Diseases</i> , 2016, 213, 173-182.	1.9	28
56	Quantifying influenza virus diversity and transmission in humans. <i>Nature Genetics</i> , 2016, 48, 195-200.	9.4	182
57	Comparative <i>In Vitro</i> and <i>In Vivo</i> Studies of Porcine Rotavirus G9P[13] and Human Rotavirus Wa G1P[8]. <i>Journal of Virology</i> , 2016, 90, 142-151.	1.5	19
58	Genetically Diverse Low Pathogenicity Avian Influenza A Virus Subtypes Co-Circulate among Poultry in Bangladesh. <i>PLoS ONE</i> , 2016, 11, e0152131.	1.1	41
59	Phylogeography of Influenza A(H3N2) Virus in Peru, 2010–2012. <i>Emerging Infectious Diseases</i> , 2015, 21, 1330-1338.	2.0	29
60	Adaptation of Pandemic H2N2 Influenza A Viruses in Humans. <i>Journal of Virology</i> , 2015, 89, 2442-2447.	1.5	29
61	H7N9 influenza A virus in turkeys in Minnesota. <i>Journal of General Virology</i> , 2015, 96, 269-276.	1.3	12
62	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?. <i>Emerging Microbes and Infections</i> , 2015, 4, 1-9.	3.0	25
63	Evolution of Influenza B Virus in Kuala Lumpur, Malaysia, between 1995 and 2008. <i>Journal of Virology</i> , 2015, 89, 9689-9692.	1.5	10
64	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. <i>Journal of Virology</i> , 2015, 89, 5651-5667.	1.5	7
65	Spread and Persistence of Influenza A Viruses in Waterfowl Hosts in the North American Mississippi Migratory Flyway. <i>Journal of Virology</i> , 2015, 89, 5371-5381.	1.5	29
66	Equine and Canine Influenza H3N8 Viruses Show Minimal Biological Differences Despite Phylogenetic Divergence. <i>Journal of Virology</i> , 2015, 89, 6860-6873.	1.5	36
67	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> , 2015, 96, 2050-2060.	1.3	23
68	Whole genome detection of rotavirus mixed infections in human, porcine and bovine samples co-infected with various rotavirus strains collected from sub-Saharan Africa. <i>Infection, Genetics and Evolution</i> , 2015, 31, 321-334.	1.0	42
69	Global migration of influenza A viruses in swine. <i>Nature Communications</i> , 2015, 6, 6696.	5.8	128
70	The soft palate is an important site of adaptation for transmissible influenza viruses. <i>Nature</i> , 2015, 526, 122-125.	13.7	133
71	Differential Susceptibilities of Human Lung Primary Cells to H1N1 Influenza Viruses. <i>Journal of Virology</i> , 2015, 89, 11935-11944.	1.5	31
72	Phylogenetics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. <i>Journal of Virology</i> , 2015, 89, 8871-8879.	1.5	51

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73	Isolation of Type A Influenza Viruses from Red-necked Grebes ( <i>Podiceps grisegena</i> ). <i>Journal of Wildlife Diseases</i> , 2015, 51, 290-293.	0.3	2
74	Whole genome analyses of G1P[8] rotavirus strains from vaccinated and non-vaccinated South African children presenting with diarrhea. <i>Journal of Medical Virology</i> , 2015, 87, 79-101.	2.5	36
75	The contrasting phylodynamics of human influenza B viruses. <i>ELife</i> , 2015, 4, e05055.	2.8	166
76	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	1.1	34
77	Equine Influenza A(H3N8) Virus Isolated from Bactrian Camel, Mongolia. <i>Emerging Infectious Diseases</i> , 2014, 20, 2144-2147.	2.0	42
78	Whole-genome analyses of DS-1-like human G2P[4] and G8P[4] rotavirus strains from Eastern, Western and Southern Africa. <i>Virus Genes</i> , 2014, 49, 196-207.	0.7	29
79	Characterization of Uncultivable Bat Influenza Virus Using a Replicative Synthetic Virus. <i>PLoS Pathogens</i> , 2014, 10, e1004420.	2.1	58
80	Universal Influenza B Virus Genomic Amplification Facilitates Sequencing, Diagnostics, and Reverse Genetics. <i>Journal of Clinical Microbiology</i> , 2014, 52, 1330-1337.	1.8	86
81	Genomic analyses detect Eurasian lineage H10 and additional H14 influenza A viruses recovered from waterfowl in the Central United States. <i>Influenza and Other Respiratory Viruses</i> , 2014, 8, 493-498.	1.5	19
82	Genomewide Analysis of Reassortment and Evolution of Human Influenza A(H3N2) Viruses Circulating between 1968 and 2011. <i>Journal of Virology</i> , 2014, 88, 2844-2857.	1.5	137
83	The evolutionary dynamics of influenza A and B viruses in the tropical city of Managua, Nicaragua. <i>Virology</i> , 2014, 462-463, 81-90.	1.1	6
84	Analysis of Recombinant H7N9 Wild-Type and Mutant Viruses in Pigs Shows that the Q226L Mutation in HA Is Important for Transmission. <i>Journal of Virology</i> , 2014, 88, 8153-8165.	1.5	52
85	Introductions and Evolution of Human-Origin Seasonal Influenza A Viruses in Multinational Swine Populations. <i>Journal of Virology</i> , 2014, 88, 10110-10119.	1.5	88
86	Standards for Sequencing Viral Genomes in the Era of High-Throughput Sequencing. <i>MBio</i> , 2014, 5, e01360-14.	1.8	89
87	North Atlantic Migratory Bird Flyways Provide Routes for Intercontinental Movement of Avian Influenza Viruses. <i>PLoS ONE</i> , 2014, 9, e92075.	1.1	65
88	Sequencing viral genomes from a single isolated plaque. <i>Virology Journal</i> , 2013, 10, 181.	1.4	16
89	Evolution of a reassortant North American gull influenza virus lineage: drift, shift and stability. <i>Virology Journal</i> , 2013, 10, 179.	1.4	34
90	Synthetic Generation of Influenza Vaccine Viruses for Rapid Response to Pandemics. <i>Science Translational Medicine</i> , 2013, 5, 185ra68.	5.8	164

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91	Complete Genome Sequence of a Reassortant H14N2 Avian Influenza Virus from California. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
92	Migration and Persistence of Human Influenza A Viruses, Vietnam, 2001–2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 1756-1765.	2.0	16
93	Avian Influenza: Mixed Infections and Missing Viruses. <i>Viruses</i> , 2013, 5, 1964-1977.	1.5	18
94	Influenza A Virus Migration and Persistence in North American Wild Birds. <i>PLoS Pathogens</i> , 2013, 9, e1003570.	2.1	83
95	Sequence Analysis of <i>In Vivo</i> Defective Interfering-Like RNA of Influenza A H1N1 Pandemic Virus. <i>Journal of Virology</i> , 2013, 87, 8064-8074.	1.5	144
96	Asparagine Substitution at PB2 Residue 701 Enhances the Replication, Pathogenicity, and Transmission of the 2009 Pandemic H1N1 Influenza A Virus. <i>PLoS ONE</i> , 2013, 8, e67616.	1.1	54
97	Antiviral Responses by Swine Primary Bronchoepithelial Cells Are Limited Compared to Human Bronchoepithelial Cells Following Influenza Virus Infection. <i>PLoS ONE</i> , 2013, 8, e70251.	1.1	16
98	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. <i>Journal of General Virology</i> , 2012, 93, 2387-2398.	1.3	25
99	Engineering temperature sensitive live attenuated influenza vaccines from emerging viruses. <i>Vaccine</i> , 2012, 30, 3691-3702.	1.7	34
100	Genomic reassortment of influenza A virus in North American swine, 1998–2011. <i>Journal of General Virology</i> , 2012, 93, 2584-2589.	1.3	40
101	Decreased Serologic Response in Vaccinated Military Recruits during 2011 Correspond to Genetic Drift in Concurrent Circulating Pandemic A/H1N1 Viruses. <i>PLoS ONE</i> , 2012, 7, e34581.	1.1	13
102	Influenza A Virus Molecular Virology Techniques. <i>Methods in Molecular Biology</i> , 2012, 865, 175-192.	0.4	82
103	Migratory flyway and geographical distance are barriers to the gene flow of influenza virus among North American birds. <i>Ecology Letters</i> , 2012, 15, 24-33.	3.0	86
104	Innate Immune Response of Human Alveolar Macrophages during Influenza A Infection. <i>PLoS ONE</i> , 2012, 7, e29879.	1.1	113
105	Reverse genetics plasmid for cloning unstable Influenza A virus gene segments. <i>Journal of Virological Methods</i> , 2011, 173, 378-383.	1.0	19
106	Deep Sequencing Reveals Mixed Infection with 2009 Pandemic Influenza A (H1N1) Virus Strains and the Emergence of Oseltamivir Resistance. <i>Journal of Infectious Diseases</i> , 2011, 203, 168-174.	1.9	113
107	Phylogeography of the Spring and Fall Waves of the H1N1/09 Pandemic Influenza Virus in the United States. <i>Journal of Virology</i> , 2011, 85, 828-834.	1.5	54
108	Extensive Geographical Mixing of 2009 Human H1N1 Influenza A Virus in a Single University Community. <i>Journal of Virology</i> , 2011, 85, 6923-6929.	1.5	43



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109	Temporally structured metapopulation dynamics and persistence of influenza A H3N2 virus in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 19359-19364.	3.3	146
110	PB2 Residue 158 Is a Pathogenic Determinant of Pandemic H1N1 and H5 Influenza A Viruses in Mice. <i>Journal of Virology</i> , 2011, 85, 357-365.	1.5	118
111	Unseasonal Transmission of H3N2 Influenza A Virus During the Swine-Origin H1N1 Pandemic. <i>Journal of Virology</i> , 2010, 84, 5715-5718.	1.5	15
112	NS-based live attenuated H1N1 pandemic vaccines protect mice and ferrets. <i>Vaccine</i> , 2010, 28, 8015-8025.	1.7	48
113	Single-Reaction Genomic Amplification Accelerates Sequencing and Vaccine Production for Classical and Swine Origin Human Influenza A Viruses. <i>Journal of Virology</i> , 2009, 83, 10309-10313.	1.5	493
114	The early diversification of influenza A/H1N1pdm. <i>PLOS Currents</i> , 2009, 1, RRN1126.	1.4	121
115	Triaryl Pyrazoline Compound Inhibits Flavivirus RNA Replication. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 1320-1329.	1.4	107
116	Mustela Vison ACE2 Functions as a Receptor for Sars-Coronavirus. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 507-510.	0.8	12
117	Increased Viral Titers and Subtle Changes in Plaque Morphology Upon Passage of SARS-CoV in Cells from Different Species. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 259-263.	0.8	3
118	Analysis of SARS-CoV Receptor Activity of ACE2 Orthologs. <i>Advances in Experimental Medicine and Biology</i> , 2006, 581, 277-280.	0.8	5
119	Cells of human aminopeptidase N (CD13) transgenic mice are infected by human coronavirus-229E in vitro, but not in vivo. <i>Virology</i> , 2005, 335, 185-197.	1.1	35
120	Mice Susceptible to SARS Coronavirus. <i>Emerging Infectious Diseases</i> , 2004, 10, 1293-1296.	2.0	59
121	Discovery of Novel Human and Animal Cells Infected by the Severe Acute Respiratory Syndrome Coronavirus by Replication-Specific Multiplex Reverse Transcription-PCR. <i>Journal of Clinical Microbiology</i> , 2004, 42, 3196-3206.	1.8	85
122	CD209L (L-SIGN) is a receptor for severe acute respiratory syndrome coronavirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15748-15753.	3.3	536
123	Identification of a Receptor-Binding Domain of the Spike Glycoprotein of Human Coronavirus HCoV-229E. <i>Journal of Virology</i> , 2003, 77, 2530-2538.	1.5	170
124	Molecular Determinants of Species Specificity in the Coronavirus Receptor Aminopeptidase N (CD13): Influence of N-Linked Glycosylation. <i>Journal of Virology</i> , 2001, 75, 9741-9752.	1.5	102