

# Peter Simmonds

## List of Publications by Year in descending order

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546  
papers

51,863  
citations

944

115  
h-index

2500

196  
g-index

589  
all docs

589  
docs citations

589  
times ranked

32081  
citing authors

#	ARTICLE	IF	CITATIONS
1	The importance of enterovirus surveillance in a post-polio world. <i>Lancet Infectious Diseases</i> , The, 2022, 22, e35-e40.	4.6	38
2	Uncovering viral RNA–host cell interactions on a proteome-wide scale. <i>Trends in Biochemical Sciences</i> , 2022, 47, 23-38.	3.7	20
3	ViroidDB: a database of viroids and viroid-like circular RNAs. <i>Nucleic Acids Research</i> , 2022, 50, D432-D438.	6.5	14
4	Effects of Severe Acute Respiratory Syndrome Coronavirus 2 Strain Variation on Virus Neutralization Titers: Therapeutic Use of Convalescent Plasma. <i>Journal of Infectious Diseases</i> , 2022, 225, 971-976.	1.9	5
5	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	0.9	33
6	Highly Sensitive Lineage Discrimination of SARS-CoV-2 Variants through Allele-Specific Probe PCR. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0228321.	1.8	5
7	Combination therapy of infliximab and thiopurines, but not monotherapy with infliximab or vedolizumab, is associated with attenuated IgA and neutralisation responses to SARS-CoV-2 in inflammatory bowel disease. <i>Gut</i> , 2022, 71, 1919.2-1922.	6.1	3
8	Convalescent plasma donors show enhanced cross-reactive neutralizing antibody response to antigenic variants of SARS-CoV-2 following immunization. <i>Transfusion</i> , 2022, 62, 1347-1354.	0.8	9
9	Fatal COVID-19 outcomes are associated with an antibody response targeting epitopes shared with endemic coronaviruses. <i>JCI Insight</i> , 2022, 7, .	2.3	24
10	Detection frequencies and viral load distribution of parvovirus B19 DNA in blood and plasma donations in England. <i>Transfusion Medicine</i> , 2022, 32, 402-409.	0.5	4
11	Comparison of CpG- and UpA-mediated restriction of RNA virus replication in mammalian and avian cells and investigation of potential ZAP-mediated shaping of host transcriptome compositions. <i>Rna</i> , 2022, 28, 1089-1109.	1.6	6
12	Recommendations for the introduction of metagenomic high-throughput sequencing in clinical virology, part I: Wet lab procedure. <i>Journal of Clinical Virology</i> , 2021, 134, 104691.	1.6	42
13	Convalescent plasma therapy for the treatment of patients with COVID-19: Assessment of methods available for antibody detection and their correlation with neutralising antibody levels. <i>Transfusion Medicine</i> , 2021, 31, 167-175.	0.5	71
14	The Virus Species Concept. , 2021, , 47-52.		0
15	Association of Zinc Finger Antiviral Protein Binding to Viral Genomic RNA with Attenuation of Replication of Echovirus 7. <i>MSphere</i> , 2021, 6, .	1.3	13
16	Insect-Specific Flavivirus Replication in Mammalian Cells Is Inhibited by Physiological Temperature and the Zinc-Finger Antiviral Protein. <i>Viruses</i> , 2021, 13, 573.	1.5	15
17	Understanding the outcomes of COVID-19 – does the current model of an acute respiratory infection really fit?. <i>Journal of General Virology</i> , 2021, 102, .	1.3	25
18	SARS-CoV-2 within-host diversity and transmission. <i>Science</i> , 2021, 372, .	6.0	278

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19	The dinucleotide composition of the Zika virus genome is shaped by conflicting evolutionary pressures in mammalian hosts and mosquito vectors. <i>PLoS Biology</i> , 2021, 19, e3001201.	2.6	15
20	Potential APOBEC-mediated RNA editing of the genomes of SARS-CoV-2 and other coronaviruses and its impact on their longer term evolution. <i>Virology</i> , 2021, 556, 62-72.	1.1	74
21	Virological Characterization of Critically Ill Patients With COVID-19 in the United Kingdom: Interactions of Viral Load, Antibody Status, and B.1.1.7 Infection. <i>Journal of Infectious Diseases</i> , 2021, 224, 595-605.	1.9	20
22	Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. <i>Journal of Clinical Virology</i> , 2021, 138, 104812.	1.6	39
23	Molecular Epidemiology and Evolutionary Trajectory of Emerging Echovirus 30, Europe. <i>Emerging Infectious Diseases</i> , 2021, 27, 1616-1626.	2.0	18
24	Extensive C→U transition biases in the genomes of a wide range of mammalian RNA viruses; potential associations with transcriptional mutations, damage- or host-mediated editing of viral RNA. <i>PLoS Pathogens</i> , 2021, 17, e1009596.	2.1	32
25	Mapping of serological testing and SARS-CoV-2 seroprevalence studies performed in 20 European countries, March-June 2020. <i>Journal of Global Health</i> , 2021, 11, 05014.	1.2	1
26	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). <i>Archives of Virology</i> , 2021, 166, 2633-2648.	0.9	219
27	SARS-CoV-2 neutralising antibody testing in Europe: towards harmonisation of neutralising antibody titres for better use of convalescent plasma and comparability of trial data. <i>Eurosurveillance</i> , 2021, 26, .	3.9	31
28	Clinical validation of optimised RT-LAMP for the diagnosis of SARS-CoV-2 infection. <i>Scientific Reports</i> , 2021, 11, 16193.	1.6	21
29	European Non-Polio Enterovirus Network: Introduction of Hospital-Based Surveillance Network to Understand the True Disease Burden of Non-Polio Enterovirus and Parechovirus Infections in Europe. <i>Microorganisms</i> , 2021, 9, 1827.	1.6	18
30	A proposed division of the family Picornaviridae into subfamilies based on phylogenetic relationships and functional genomic organization. <i>Archives of Virology</i> , 2021, 166, 2927-2935.	0.9	11
31	Mutagenesis Mapping of RNA Structures within the Foot-and-Mouth Disease Virus Genome Reveals Functional Elements Localized in the Polymerase (3D <sup>pol</sup> )-Encoding Region. <i>MSphere</i> , 2021, 6, e0001521.	1.3	3
32	Comparability of six different immunoassays measuring SARS-CoV-2 antibodies with neutralizing antibody levels in convalescent plasma: From utility to prediction. <i>Transfusion</i> , 2021, 61, 2837-2843.	0.8	29
33	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	0.9	62
34	Seroprevalence and Virologic Surveillance of Enterovirus 71 and Coxsackievirus A6, United Kingdom, 2006-2017. <i>Emerging Infectious Diseases</i> , 2021, 27, 2261-2268.	2.0	15
35	A mechanistic evolutionary model explains the time-dependent pattern of substitution rates in viruses. <i>Current Biology</i> , 2021, 31, 4689-4696.e5.	1.8	30
36	Perforin, COVID-19 and a possible pathogenic auto-inflammatory feedback loop. <i>Scandinavian Journal of Immunology</i> , 2021, 94, e13102.	1.3	11

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37	Efficacy of ChAdOx1 nCoV-19 (AZD1222) vaccine against SARS-CoV-2 lineages circulating in Brazil. <i>Nature Communications</i> , 2021, 12, 5861.	5.8	38
38	Viral genome wide association study identifies novel hepatitis C virus polymorphisms associated with sofosbuvir treatment failure. <i>Nature Communications</i> , 2021, 12, 6105.	5.8	11
39	Re-emergence of enterovirus D68 in Europe after easing the COVID-19 lockdown, September 2021. <i>Eurosurveillance</i> , 2021, 26, .	3.9	36
40	Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes. <i>PLoS Biology</i> , 2021, 19, e3001442.	2.6	44
41	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	2.6	31
42	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	2.7	89
43	Use of an Outbred Rat Hepacivirus Challenge Model for Design and Evaluation of Efficacy of Different Immunization Strategies for Hepatitis C Virus. <i>Hepatology</i> , 2020, 71, 794-807.	3.6	18
44	A European multicentre evaluation of detection and typing methods for human enteroviruses and parechoviruses using RNA transcripts. <i>Journal of Medical Virology</i> , 2020, 92, 1065-1074.	2.5	11
45	Circulation of non-polio enteroviruses in 24 EU and EEA countries between 2015 and 2017: a retrospective surveillance study. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 350-361.	4.6	76
46	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020, 165, 519-525.	0.9	51
47	Impact of virus subtype and host <i>IFNL4</i> genotype on large-scale RNA structure formation in the genome of hepatitis C virus. <i>Rna</i> , 2020, 26, 1541-1556.	1.6	7
48	The First Nonmammalian Pegivirus Demonstrates Efficient In Vitro Replication and High Lymphtropism. <i>Journal of Virology</i> , 2020, 94, .	1.5	9
49	Broad and strong memory CD4+ and CD8+ T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. <i>Nature Immunology</i> , 2020, 21, 1336-1345.	7.0	1,066
50	Human cytomegalovirus evades ZAP detection by suppressing CpG dinucleotides in the major immediate early 1 gene. <i>PLoS Pathogens</i> , 2020, 16, e1008844.	2.1	33
51	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	0.9	184
52	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). <i>Archives of Virology</i> , 2020, 165, 2737-2748.	0.9	202
53	Molecular epidemiology and clinical impact of rhinovirus infections in adults during three epidemic seasons in 11 European countries (2007-2010). <i>Thorax</i> , 2020, 75, 882-890.	2.7	25
54	Pervasive RNA Secondary Structure in the Genomes of SARS-CoV-2 and Other Coronaviruses. <i>MBio</i> , 2020, 11, .	1.8	36

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55	Efficacy of NS5A inhibitors against unusual and potentially difficult-to-treat HCV subtypes commonly found in sub-Saharan Africa and South East Asia. <i>Journal of Hepatology</i> , 2020, 73, 794-799.	1.8	27
56	Perforin and resistance to SARS coronavirus 2. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 146, 52-53.	1.5	11
57	Recombination Analysis of Non-Poliovirus Members of the Enterovirus C Species: Restriction of Recombination Events to Members of the Same 3DPol Cluster. <i>Viruses</i> , 2020, 12, 706.	1.5	7
58	Rampant C $\hat{a}$ t'U Hypermutation in the Genomes of SARS-CoV-2 and Other Coronaviruses: Causes and Consequences for Their Short- and Long-Term Evolutionary Trajectories. <i>MSphere</i> , 2020, 5, .	1.3	204
59	How to recognise and deal with dubious virus sequences?. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104242.	1.0	0
60	Recommendations for the nomenclature of enteroviruses and rhinoviruses. <i>Archives of Virology</i> , 2020, 165, 793-797.	0.9	93
61	Plant Virus Genome Is Shaped by Specific Dinucleotide Restrictions That Influence Viral Infection. <i>MBio</i> , 2020, 11, .	1.8	12
62	Update: proposed reference sequences for subtypes of hepatitis E virus (species Orthohepevirus A). <i>Journal of General Virology</i> , 2020, 101, 692-698.	1.3	221
63	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. <i>Wellcome Open Research</i> , 2020, 5, 181.	0.9	81
64	SARS-CoV-2 RNA detected in blood products from patients with COVID-19 is not associated with infectious virus. <i>Wellcome Open Research</i> , 2020, 5, 181.	0.9	122
65	Convalescent plasma treatment for SARS-CoV-2 infection: analysis of the first 436 donors in England, 22 April to 12 May 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	53
66	Detection of neutralising antibodies to SARS-CoV-2 to determine population exposure in Scottish blood donors between March and May 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	64
67	Use of a small DNA virus model to investigate mechanisms of CpG dinucleotide-induced attenuation of virus replication. <i>Journal of General Virology</i> , 2020, 101, 1202-1218.	1.3	4
68	Title is missing!. , 2020, 16, e1008844.		0
69	Title is missing!. , 2020, 16, e1008844.		0
70	Title is missing!. , 2020, 16, e1008844.		0
71	Title is missing!. , 2020, 16, e1008844.		0
72	Suboptimal SVR rates in African patients with atypical genotype 1 subtypes: Implications for global elimination of hepatitis C. <i>Journal of Hepatology</i> , 2019, 71, 1099-1105.	1.8	52

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73	The First Co-Opted Endogenous Foamy Viruses and the Evolutionary History of Reptilian Foamy Viruses. <i>Viruses</i> , 2019, 11, 641.	1.5	13
74	The role of ZAP and OAS3/RNaseL pathways in the attenuation of an RNA virus with elevated frequencies of CpG and UpA dinucleotides. <i>Nucleic Acids Research</i> , 2019, 47, 8061-8083.	6.5	75
75	Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 1233-1244.	0.9	70
76	Taxonomy of the order Bunyavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 927-941.	0.9	115
77	The circadian clock components BMAL1 and REV-ERB $\beta$ regulate flavivirus replication. <i>Nature Communications</i> , 2019, 10, 377.	5.8	71
78	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019, 164, 943-946.	0.9	102
79	Increase in Enterovirus D68 Infections in Young Children, United Kingdom, 2006–2016. <i>Emerging Infectious Diseases</i> , 2019, 25, 1200-1203.	2.0	35
80	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). <i>Archives of Virology</i> , 2019, 164, 2417-2429.	0.9	257
81	Taxonomy of the order Bunyavirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1949-1965.	0.9	285
82	A Cost-Effectiveness Analysis of Shortened Direct-Acting Antiviral Treatment in Genotype 1 Noncirrhotic Treatment-Naive Patients With Chronic Hepatitis C Virus. <i>Value in Health</i> , 2019, 22, 693-703.	0.1	13
83	Taxonomy of the order Mononegavirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1967-1980.	0.9	224
84	Identification of 19 Novel Hepatitis C Virus Subtypes—Further Expanding HCV Classification. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz076.	0.4	72
85	Reply to “Evolutionary stasis of viruses”. <i>Nature Reviews Microbiology</i> , 2019, 17, 329-330.	13.6	3
86	A functional investigation of the suppression of CpG and UpA dinucleotide frequencies in plant RNA virus genomes. <i>Scientific Reports</i> , 2019, 9, 18359.	1.6	18
87	Highly Diverse Hepatitis C Strains Detected in Sub-Saharan Africa Have Unknown Susceptibility to Direct-Acting Antiviral Treatments. <i>Hepatology</i> , 2019, 69, 1426-1441.	3.6	36
88	Strategies to improve detection and management of human parechovirus infection in young infants. <i>Lancet Infectious Diseases</i> , The, 2019, 19, e51-e58.	4.6	35
89	Prisoners of war—host adaptation and its constraints on virus evolution. <i>Nature Reviews Microbiology</i> , 2019, 17, 321-328.	13.6	117
90	Resistance analysis of genotype 3 hepatitis C virus indicates subtypes inherently resistant to nonstructural protein 5A inhibitors. <i>Hepatology</i> , 2019, 69, 1861-1872.	3.6	68

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91	Potential for diagnosis of infectious disease from the 100,000 Genomes Project Metagenomic Dataset: Recommendations for reporting results. Wellcome Open Research, 2019, 4, 155.	0.9	9
92	Interferon lambda 4 impacts the genetic diversity of hepatitis C virus. ELife, 2019, 8, .	2.8	28
93	Genetic diversity and cross-species transmission of kobuviruses in Vietnam. Virus Evolution, 2018, 4, vey002.	2.2	18
94	Spectrum of Enterovirus Serotypes Causing Uncomplicated Hand, Foot, and Mouth Disease and Enteroviral Diagnostic Yield of Different Clinical Samples. Clinical Infectious Diseases, 2018, 67, 1729-1735.	2.9	31
95	Recommendations for enterovirus diagnostics and characterisation within and beyond Europe. Journal of Clinical Virology, 2018, 101, 11-17.	1.6	161
96	Genomic analysis of a novel picornavirus from a migratory waterfowl, greater white-fronted goose (Anser albifrons). Archives of Virology, 2018, 163, 1087-1090.	0.9	7
97	The genomic underpinnings of eukaryotic virus taxonomy: creating a sequence-based framework for family-level virus classification. Microbiome, 2018, 6, 38.	4.9	70
98	Classification and Genomic Diversity of Enterically Transmitted Hepatitis Viruses. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a031880.	2.9	67
99	Detection of potentially novel paramyxovirus and coronavirus viral <scp>RNA</scp> in bats and rats in the Mekong Delta region of southern Viet Nam. Zoonoses and Public Health, 2018, 65, 30-42.	0.9	33
100	Viral persistence, liver disease, and host response in a hepatitis C-like virus rat model. Hepatology, 2018, 68, 435-448.	3.6	59
101	Molecular and epidemiological evidence of patient-to-patient hepatitis C virus transmission in a Scottish emergency department. Journal of Hospital Infection, 2018, 98, 412-418.	1.4	9
102	Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. Journal of General Virology, 2018, 99, 1331-1343.	1.3	72
103	Time to Harmonize Dengue Nomenclature and Classification. Viruses, 2018, 10, 569.	1.5	14
104	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). Archives of Virology, 2018, 163, 2601-2631.	0.9	567
105	Detection and Characterization of Homologues of Human Hepatitis Viruses and Pegiviruses in Rodents and Bats in Vietnam. Viruses, 2018, 10, 102.	1.5	37
106	Virus classification – where do you draw the line?. Archives of Virology, 2018, 163, 2037-2046.	0.9	76
107	A clash of ideas – the varying uses of the “species” term in virology and their utility for classifying viruses in metagenomic datasets. Journal of General Virology, 2018, 99, 277-287.	1.3	11
108	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. Nature Genetics, 2017, 49, 666-673.	9.4	129

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109	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017, 162, 1441-1446.	0.9	72
110	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). <i>Archives of Virology</i> , 2017, 162, 2505-2538.	0.9	506
111	Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.	13.6	590
112	A New Clade of Insect-Specific Flaviviruses from Australian <i>Anopheles</i> Mosquitoes Displays Species-Specific Host Restriction. <i>MSphere</i> , 2017, 2, .	1.3	64
113	Characterization of Posa and Posa-like virus genomes in fecal samples from humans, pigs, rats, and bats collected from a single location in Vietnam. <i>Virus Evolution</i> , 2017, 3, vex022.	2.2	25
114	ICTV Virus Taxonomy Profile: Picornaviridae. <i>Journal of General Virology</i> , 2017, 98, 2421-2422.	1.3	374
115	ICTV Virus Taxonomy Profile: Flaviviridae. <i>Journal of General Virology</i> , 2017, 98, 2-3.	1.3	537
116	Proposed revision to the taxonomy of the genus Pestivirus, family Flaviviridae. <i>Journal of General Virology</i> , 2017, 98, 2106-2112.	1.3	264
117	Human parvovirus 4 (PARV4) remains elusive despite a decade of study. <i>F1000Research</i> , 2017, 6, 82.	0.8	17
118	PARV4 prevalence, phylogeny, immunology and coinfection with HIV, HBV and HCV in a multicentre African cohort. <i>Wellcome Open Research</i> , 2017, 2, 26.	0.9	11
119	CpG and UpA dinucleotides in both coding and non-coding regions of echovirus 7 inhibit replication initiation post-entry. <i>ELife</i> , 2017, 6, .	2.8	60
120	Proposed update to the taxonomy of the genera Hepacivirus and Pegivirus within the Flaviviridae family. <i>Journal of General Virology</i> , 2016, 97, 2894-2907.	1.3	139
121	Evaluation of Viremia Frequencies of a Novel Human Pegivirus by Using Bioinformatic Screening and PCR. <i>Emerging Infectious Diseases</i> , 2016, 22, 671-678.	2.0	46
122	Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.	1.8	112
123	Viral meningitis: epidemiology and diagnosis. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 1211-1212.	4.6	11
124	The use of human sewage screening for community surveillance of hepatitis E virus in the UK. <i>Journal of Medical Virology</i> , 2016, 88, 915-918.	2.5	37
125	First next-generation sequencing full-genome characterization of a hepatitis C virus genotype 7 divergent subtype. <i>Clinical Microbiology and Infection</i> , 2016, 22, 947.e1-947.e8.	2.8	21
126	Characterization of the Specificity, Functionality, and Durability of Host T-cell Responses Against the Full-Length Hepatitis E Virus. <i>Hepatology</i> , 2016, 64, 1934-1950.	3.6	42



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127	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	0.9	263
128	Exploration of acetanilide derivatives of 1-(1-phenoxymethyl)uracils as novel inhibitors of Hepatitis C Virus replication. Scientific Reports, 2016, 6, 29487.	1.6	15
129	Evolution and phylogeographic dissemination of endemic porcine picornaviruses in Vietnam. Virus Evolution, 2016, 2, vew001.	2.2	7
130	Hepatitis E virus is the leading cause of acute viral hepatitis in Lothian, Scotland. New Microbes and New Infections, 2016, 10, 6-12.	0.8	18
131	Detection of influenza C virus but not influenza D virus in Scottish respiratory samples. Journal of Clinical Virology, 2016, 74, 50-53.	1.6	51
132	Enhancement of the Replication of Hepatitis C Virus Replicons of Genotypes 1 to 4 by Manipulation of CpG and UpA Dinucleotide Frequencies and Use of Cell Lines Expressing SECL14L2 for Antiviral Resistance Testing. Antimicrobial Agents and Chemotherapy, 2016, 60, 2981-2992.	1.4	29
133	Large-scale screening and characterization of enteroviruses and kobuviruses infecting pigs in Vietnam. Journal of General Virology, 2016, 97, 378-388.	1.3	33
134	Proposed reference sequences for hepatitis E virus subtypes. Journal of General Virology, 2016, 97, 537-542.	1.3	339
135	Molecular epidemiology and the evolution of human coxsackievirus A6. Journal of General Virology, 2016, 97, 3225-3231.	1.3	37
136	Elevation of CpG frequencies in influenza A genome attenuates pathogenicity but enhances host response to infection. ELife, 2016, 5, e12735.	2.8	86
137	Development of a real time PCR for poliovirus in sewage. Journal of Clinical Virology, 2015, 70, S71.	1.6	0
138	Bones hold the key to virus history and epidemiology. Journal of Clinical Virology, 2015, 70, S81.	1.6	1
139	Bones hold the key to DNA virus history and epidemiology. Scientific Reports, 2015, 5, 17226.	1.6	27
140	Pathogenicity of hepatitis E virus genotype 3 variants. Journal of Clinical Virology, 2015, 70, S123.	1.6	0
141	Pathogenicity of individual rhinovirus species during exacerbations of cystic fibrosis. European Respiratory Journal, 2015, 45, 1748-1751.	3.1	14
142	Human Parvovirus 4 Infection among Mothers and Children in South Africa. Emerging Infectious Diseases, 2015, 21, 713-715.	2.0	10
143	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2015). Archives of Virology, 2015, 160, 1837-1850.	0.9	126
144	Methods for virus classification and the challenge of incorporating metagenomic sequence data. Journal of General Virology, 2015, 96, 1193-1206.	1.3	49

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145	Surveying the global virome: Identification and characterization of HCV-related animal hepaciviruses. <i>Antiviral Research</i> , 2015, 115, 83-93.	1.9	86
146	Genetic characterization of human coxsackievirus A6 variants associated with atypical hand, foot and mouth disease: a potential role of recombination in emergence and pathogenicity. <i>Journal of General Virology</i> , 2015, 96, 1067-1079.	1.3	55
147	Methods for virus classification and the challenge of incorporating metagenomic sequence data. <i>Journal of General Virology</i> , 2015, 96, 1193-1206.	1.3	72
148	Genome analysis of a novel, highly divergent picornavirus from common kestrel ( <i>Falco tinnunculus</i> ): The first non-enteroviral picornavirus with type-I-like IRES. <i>Infection, Genetics and Evolution</i> , 2015, 32, 425-431.	1.0	18
149	Attenuation of dengue (and other RNA viruses) with codon pair recoding can be explained by increased CpG/UpA dinucleotide frequencies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3633-4.	3.3	26
150	Virome Analysis of Transfusion Recipients Reveals a Novel Human Virus That Shares Genomic Features with Hepaciviruses and Pegiviruses. <i>MBio</i> , 2015, 6, e01466-15.	1.8	80
151	Hepatitis E virus and fulminant hepatitis – a virus or host-specific pathology?. <i>Liver International</i> , 2015, 35, 1334-1340.	1.9	31
152	The Vietnam Initiative on Zoonotic Infections (VIZIONS): A Strategic Approach to Studying Emerging Zoonotic Infectious Diseases. <i>EcoHealth</i> , 2015, 12, 726-735.	0.9	47
153	Variability and pathogenicity of hepatitis E virus genotype 3 variants. <i>Journal of General Virology</i> , 2015, 96, 3255-3264.	1.3	54
154	The influence of viral RNA secondary structure on interactions with innate host cell defences. <i>Nucleic Acids Research</i> , 2014, 42, 3314-3329.	6.5	42
155	Identification of novel anelloviruses with broad diversity in UK rodents. <i>Journal of General Virology</i> , 2014, 95, 1544-1553.	1.3	40
156	PARV4: An Emerging Tetraparvovirus. <i>PLoS Pathogens</i> , 2014, 10, e1004036.	2.1	26
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