

Edward C Holmes

List of Publications by Year in descending order

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693
papers

95,289
citations

433

131
h-index

507

268
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800
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800
docs citations

800
times ranked

81803
citing authors

#	ARTICLE	IF	CITATIONS
1	Zoonotic disease and virome diversity in bats. <i>Current Opinion in Virology</i> , 2022, 52, 192-202.	2.6	60
2	Assessment of Coronavirus Disease 2019 Intervention Strategies in the Nordic Countries Using Genomic Epidemiology. <i>Open Forum Infectious Diseases</i> , 2022, 9, ofab665.	0.4	0
3	Diversity and evolution of the animal virome. <i>Nature Reviews Microbiology</i> , 2022, 20, 321-334.	13.6	82
4	Viromes of Freshwater Fish with Lacustrine and Diadromous Life Histories Differ in Composition. <i>Viruses</i> , 2022, 14, 257.	1.5	8
5	A time-series meta-transcriptomic analysis reveals the seasonal, host, and gender structure of mosquito viromes. <i>Virus Evolution</i> , 2022, 8, veac006.	2.2	20
6	Surveillance of Rodent Pests for SARS-CoV-2 and Other Coronaviruses, Hong Kong. <i>Emerging Infectious Diseases</i> , 2022, 28, 467-470.	2.0	15
7	Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic. <i>Virus Evolution</i> , 2022, 8, veac024.	2.2	37
8	Co-infecting pathogens can contribute to inflammatory responses and severe symptoms in COVID-19. <i>Journal of Thoracic Disease</i> , 2022, 14, 355-370.	0.6	5
9	Total infectome characterization of respiratory infections in pre-COVID-19 Wuhan, China. <i>PLoS Pathogens</i> , 2022, 18, e1010259.	2.1	16
10	COVID-19â€™s lessons for zoonotic disease. <i>Science</i> , 2022, 375, 1114-1115.	6.0	40
11	Virome characterization of game animals in China reveals a spectrum of emerging pathogens. <i>Cell</i> , 2022, 185, 1117-1129.e8.	13.5	106
12	Human land use impacts viral diversity and abundance in a New Zealand river. <i>Virus Evolution</i> , 2022, 8, veac032.	2.2	13
13	Unrecognized diversity of mammalian orthoreoviruses in North American bats. <i>Virology</i> , 2022, 571, 1-11.	1.1	7
14	Surveillance of Rodent Pests for SARS-CoV-2 and Other Coronaviruses, Hong Kong.. <i>Emerging Infectious Diseases</i> , 2022, 28, 467-470.	2.0	4
15	Diagnosis and analysis of unexplained cases of childhood encephalitis in Australia using metatranscriptomic sequencing. <i>Journal of General Virology</i> , 2022, 103, .	1.3	2
16	A total infectome approach to understand the etiology of infectious disease in pigs. <i>Microbiome</i> , 2022, 10, 73.	4.9	11
17	Australia as a global sink for the genetic diversity of avian influenza A virus. <i>PLoS Pathogens</i> , 2022, 18, e1010150.	2.1	9
18	Co-infection with SARS-CoV-2 Omicron and Delta variants revealed by genomic surveillance. <i>Nature Communications</i> , 2022, 13, 2745.	5.8	64

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19	Off-season RSV epidemics in Australia after easing of COVID-19 restrictions. <i>Nature Communications</i> , 2022, 13, .	5.8	135
20	Transcriptome Mining Expands Knowledge of RNA Viruses across the Plant Kingdom. <i>Journal of Virology</i> , 2022, 96, .	1.5	32
21	Resolving deep evolutionary relationships within the RNA virus phylum <i>Lentiviricota</i> . <i>Virus Evolution</i> , 2022, 8, .	2.2	11
22	Metatranscriptomic Comparison of Viromes in Endemic and Introduced Passerines in New Zealand. <i>Viruses</i> , 2022, 14, 1364.	1.5	9
23	The Ecology of Viral Emergence. <i>Annual Review of Virology</i> , 2022, 9, 173-192.	3.0	20
24	Low Intra-host and Inter-host Genetic Diversity of Carnivore Protoparvovirus 1 in Domestic Cats during a Feline Panleukopenia Outbreak. <i>Viruses</i> , 2022, 14, 1412.	1.5	1
25	The enteric virome of cats with feline panleukopenia differs in abundance and diversity from healthy cats. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	6
26	Total infectomes of 162 SARS-CoV-2 cases using meta-transcriptomic sequencing. <i>Journal of Infection</i> , 2021, 82, e44-e48.	1.7	7
27	SARS-CoV-2 replicates in respiratory ex vivo organ cultures of domestic ruminant species. <i>Veterinary Microbiology</i> , 2021, 252, 108933.	0.8	48
28	Collecting and managing taxonomic data with NCBI-taxonomist. <i>Bioinformatics</i> , 2021, 36, 5548-5550.	1.8	1
29	Addendum: A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2021, 6, 415-415.	5.9	65
30	A household case evidences shorter shedding of SARS-CoV-2 in naturally infected cats compared to their human owners. <i>Emerging Microbes and Infections</i> , 2021, 10, 376-383.	3.0	74
31	Metagenomic sequencing reveals a lack of virus exchange between native and invasive freshwater fish across the Murray-Darling Basin, Australia. <i>Virus Evolution</i> , 2021, 7, veab034.	2.2	27
32	Bioinformatics resources for SARS-CoV-2 discovery and surveillance. <i>Briefings in Bioinformatics</i> , 2021, 22, 631-641.	3.2	38
33	Virome composition in marine fish revealed by meta-transcriptomics. <i>Virus Evolution</i> , 2021, 7, veab005.	2.2	58
34	High Resolution Metatranscriptomic Characterization of the Pulmonary RNA Virome After Lung Transplantation. <i>Transplantation</i> , 2021, Publish Ahead of Print, 2546-2553.	0.5	5
35	Understanding the Impact of Resistance to Influenza Antivirals. <i>Clinical Microbiology Reviews</i> , 2021, 34, .	5.7	30
36	A Novel Rubi-Like Virus in the Pacific Electric Ray (<i>Tetronarce californica</i>) Reveals the Complex Evolutionary History of the Matonaviridae. <i>Viruses</i> , 2021, 13, 585.	1.5	12

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37	Genomic Evidence of In-Flight Transmission of SARS-CoV-2 Despite Predeparture Testing. <i>Emerging Infectious Diseases</i> , 2021, 27, 687-693.	2.0	58
38	Partial immunity and SARS-CoV-2 mutationsâ€™Response. <i>Science</i> , 2021, 372, 354-355.	6.0	2
39	Emergence and Spread of SARS-CoV-2 Lineages B.1.1.7 and P.1 in Italy. <i>Viruses</i> , 2021, 13, 794.	1.5	32
40	Field and classroom initiatives for portable sequence-based monitoring of dengue virus in Brazil. <i>Nature Communications</i> , 2021, 12, 2296.	5.8	29
41	Pathogenicity and transmissibility of a novel respirovirus isolated from a Malayan pangolin. <i>Journal of General Virology</i> , 2021, 102, .	1.3	7
42	How accurately can we assess zoonotic risk?. <i>PLoS Biology</i> , 2021, 19, e3001135.	2.6	56
43	Epidemiological and evolutionary considerations of SARS-CoV-2 vaccine dosing regimes. <i>Science</i> , 2021, 372, 363-370.	6.0	185
44	Infectious disease phylodynamics with occurrence data. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1498-1507.	2.2	14
45	Use of Genomics to Track Coronavirus Disease Outbreaks, New Zealand. <i>Emerging Infectious Diseases</i> , 2021, 27, 1317-1322.	2.0	28
46	Unbiased Characterization of the Microbiome and Virome of Questing Ticks. <i>Frontiers in Microbiology</i> , 2021, 12, 627327.	1.5	11
47	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. <i>Wellcome Open Research</i> , 2021, 6, 121.	0.9	115
48	Slippery when wet: cross-species transmission of divergent coronaviruses in bony and jawless fish and the evolutionary history of the <i>Coronaviridae</i>. <i>Virus Evolution</i> , 2021, 7, veab050.	2.2	23
49	Retrospective meta-transcriptomic identification of severe dengue in a traveller returning from Africa to Sweden, 1990. <i>One Health</i> , 2021, 12, 100217.	1.5	1
50	Retrospective screening of routine respiratory samples revealed undetected community transmission and missed intervention opportunities for SARS-CoV-2 in the United Kingdom. <i>Journal of General Virology</i> , 2021, 102, .	1.3	10
51	SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. <i>Nature Microbiology</i> , 2021, 6, 821-823.	5.9	221
52	Sequence dynamics of three influenza A virus strains grown in different MDCK cell lines, including those expressing different sialic acid receptors. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1878-1900.	0.8	5
53	After the pandemic: perspectives on the future trajectory of COVID-19. <i>Nature</i> , 2021, 596, 495-504.	13.7	260
54	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	2.2	774

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55	Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. <i>Cell</i> , 2021, 184, 4380-4391.e14.	13.5	261
56	Revealing RNA virus diversity and evolution in unicellular algae transcriptomes. <i>Virus Evolution</i> , 2021, 7, .	2.2	28
57	Vaccine nationalism and the dynamics and control of SARS-CoV-2. <i>Science</i> , 2021, 373, eabj7364.	6.0	80
58	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. <i>Wellcome Open Research</i> , 2021, 6, 121.	0.9	129
59	RNA virome abundance and diversity is associated with host age in a bird species. <i>Virology</i> , 2021, 561, 98-106.	1.1	19
60	Frequent intergenotypic recombination between the non-structural and structural genes is a major driver of epidemiological fitness in caliciviruses. <i>Virus Evolution</i> , 2021, 7, veab080.	2.2	24
61	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	13.5	330
62	Current challenges to virus discovery by meta-transcriptomics. <i>Current Opinion in Virology</i> , 2021, 51, 48-55.	2.6	56
63	Feline Calicivirus Virulent Systemic Disease: Clinical Epidemiology, Analysis of Viral Isolates and In Vitro Efficacy of Novel Antivirals in Australian Outbreaks. <i>Viruses</i> , 2021, 13, 2040.	1.5	14
64	RNA virome diversity and Wolbachia infection in individual <i>Drosophila simulans</i> flies. <i>Journal of General Virology</i> , 2021, 102, .	1.3	4
65	Metagenomic Identification of Viral Sequences in Laboratory Reagents. <i>Viruses</i> , 2021, 13, 2122.	1.5	21
66	The impact of public health interventions in the Nordic countries during the first year of SARS-CoV-2 transmission and evolution. <i>Eurosurveillance</i> , 2021, 26, .	3.9	8
67	Characterization of the Gut Microbiome and Resistomes of Wild and Zoo-Captive Macaques. <i>Frontiers in Veterinary Science</i> , 2021, 8, 778556.	0.9	3
68	Meta-transcriptomic analysis of the virome and microbiome of the invasive Indian myna (<i>Acridotheres</i>) Tj ETQq0 0 Q rgBT /Overlock 10 T	1.5	11
69	An Ecosystems Perspective on Virus Evolution and Emergence. <i>Trends in Microbiology</i> , 2020, 28, 165-175.	3.5	86
70	Human pegivirus in brain tissue of a patient with encephalitis. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 96, 114898.	0.8	11
71	The Ecology and Evolution of Influenza Viruses. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2020, 10, a038489.	2.9	97
72	Novel hepaci- and pegi-like viruses in native Australian wildlife and non-human primates. <i>Virus Evolution</i> , 2020, 6, veaa064.	2.2	21

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73	Red fox viromes in urban and rural landscapes. <i>Virus Evolution</i> , 2020, 6, veaa065.	2.2	27
74	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	1.8	33
75	Metatranscriptomic Identification of Diverse and Divergent RNA Viruses in Green and Chlorarachniophyte Algae Cultures. <i>Viruses</i> , 2020, 12, 1180.	1.5	26
76	Divergent Influenza-Like Viruses of Amphibians and Fish Support an Ancient Evolutionary Association. <i>Viruses</i> , 2020, 12, 1042.	1.5	23
77	Meta-Transcriptomic Discovery of a Divergent Circovirus and a Chaphamaparvovirus in Captive Reptiles with Proliferative Respiratory Syndrome. <i>Viruses</i> , 2020, 12, 1073.	1.5	14
78	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	3.5	18
79	Wild birds as reservoirs for diverse and abundant gamma- and deltacoronaviruses. <i>FEMS Microbiology Reviews</i> , 2020, 44, 631-644.	3.9	75
80	A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. <i>Nature Microbiology</i> , 2020, 5, 1403-1407.	5.9	2,291
81	The origins and genomic diversity of American Civil War Era smallpox vaccine strains. <i>Genome Biology</i> , 2020, 21, 175.	3.8	22
82	Identification of Novel Astroviruses in the Gastrointestinal Tract of Domestic Cats. <i>Viruses</i> , 2020, 12, 1301.	1.5	8
83	The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing. <i>Emerging Microbes and Infections</i> , 2020, 9, 1824-1834.	3.0	42
84	Diversity and circulation of Jingmen tick virus in ticks and mammals. <i>Virus Evolution</i> , 2020, 6, veaa051.	2.2	38
85	Circumpolar diversification of the <i>Ixodes uriae</i> tick virome. <i>PLoS Pathogens</i> , 2020, 16, e1008759.	2.1	27
86	Identifying the Risk of SARS-CoV-2 Infection and Environmental Monitoring in Airborne Infectious Isolation Rooms (AIIRs). <i>Virologica Sinica</i> , 2020, 35, 785-792.	1.2	14
87	Meta-transcriptomic identification of <i>Trypanosoma</i> spp. in native wildlife species from Australia. <i>Parasites and Vectors</i> , 2020, 13, 447.	1.0	14
88	Diverse and abundant resistome in terrestrial and aquatic vertebrates revealed by transcriptional analysis. <i>Scientific Reports</i> , 2020, 10, 18870.	1.6	13
89	Response to Brinkmann et al. "Re-assembly of 19th century smallpox vaccine genomes reveals the contemporaneous use of horsepox and horsepox-related viruses in the United States". <i>Genome Biology</i> , 2020, 21, 287.	3.8	2
90	Genomic Epidemiology of the First Wave of SARS-CoV-2 in Italy. <i>Viruses</i> , 2020, 12, 1438.	1.5	39

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91	Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand. <i>Nature Communications</i> , 2020, 11, 6351.	5.8	100
92	Coding-Complete Genome Sequence of Yada Yada Virus, a Novel Alphavirus Detected in Australian Mosquitoes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	10
93	Meta-Transcriptomic Identification of Divergent Amnoonviridae in Fish. <i>Viruses</i> , 2020, 12, 1254.	1.5	16
94	Blood molecular markers associated with COVID-19 immunopathology and multi-organ damage. <i>EMBO Journal</i> , 2020, 39, e105896.	3.5	123
95	Unmapped RNA Virus Diversity in Termites and Their Symbionts. <i>Viruses</i> , 2020, 12, 1145.	1.5	28
96	A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein. <i>Current Biology</i> , 2020, 30, 2196-2203.e3.	1.8	480
97	Newly identified viral genomes in pangolins with fatal disease. <i>Virus Evolution</i> , 2020, 6, veaa020.	2.2	31
98	Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins. <i>Nature</i> , 2020, 583, 282-285.	13.7	1,453
99	Identification of hepatitis C virus in the common bed bug – a potential, but uncommon route for HCV infection?. <i>Emerging Microbes and Infections</i> , 2020, 9, 1429-1431.	3.0	12
100	A Divergent Articulavirus in an Australian Gecko Identified Using Meta-Transcriptomics and Protein Structure Comparisons. <i>Viruses</i> , 2020, 12, 613.	1.5	19
101	The proximal origin of SARS-CoV-2. <i>Nature Medicine</i> , 2020, 26, 450-452.	15.2	3,871
102	A Genomic Perspective on the Origin and Emergence of SARS-CoV-2. <i>Cell</i> , 2020, 181, 223-227.	13.5	662
103	A new coronavirus associated with human respiratory disease in China. <i>Nature</i> , 2020, 579, 265-269.	13.7	9,370
104	High resolution metagenomic characterization of complex infectomes in paediatric acute respiratory infection. <i>Scientific Reports</i> , 2020, 10, 3963.	1.6	26
105	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. <i>Nature Medicine</i> , 2020, 26, 1398-1404.	15.2	283
106	Metatranscriptomic Analysis of Virus Diversity in Urban Wild Birds with Parectic Disease. <i>Journal of Virology</i> , 2020, 94, .	1.5	21
107	The use of taxon-specific reference databases compromises metagenomic classification. <i>BMC Genomics</i> , 2020, 21, 184.	1.2	30
108	We shouldn't worry when a virus mutates during disease outbreaks. <i>Nature Microbiology</i> , 2020, 5, 529-530.	5.9	136

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109	Properties and abundance of overlapping genes in viruses. <i>Virus Evolution</i> , 2020, 6, veaa009.	2.2	36
110	Discovery and Prevalence of Divergent RNA Viruses in European Field Voles and Rabbits. <i>Viruses</i> , 2020, 12, 47.	1.5	9
111	Identification of a Novel Papillomavirus Associated with Squamous Cell Carcinoma in a Domestic Cat. <i>Viruses</i> , 2020, 12, 124.	1.5	22
112	Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. <i>Lancet, The</i> , 2020, 395, 565-574.	6.3	9,430
113	CCMetagen: comprehensive and accurate identification of eukaryotes and prokaryotes in metagenomic data. <i>Genome Biology</i> , 2020, 21, 103.	3.8	91
114	Infectious KoRV-related retroviruses circulating in Australian bats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9529-9536.	3.3	31
115	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. <i>Virus Evolution</i> , 2020, 6, veaa027.	2.2	119
116	Comparative Analysis of RNA Virome Composition in Rabbits and Associated Ectoparasites. <i>Journal of Virology</i> , 2020, 94, .	1.5	30
117	Sustained RNA virome diversity in Antarctic penguins and their ticks. <i>ISME Journal</i> , 2020, 14, 1768-1782.	4.4	56
118	Extensive genetic diversity and host range of rodent-borne coronaviruses. <i>Virus Evolution</i> , 2020, 6, veaa078.	2.2	31
119	Facemask against viral respiratory infections among Hajj pilgrims: A challenging cluster-randomized trial. <i>PLoS ONE</i> , 2020, 15, e0240287.	1.1	22
120	Bat IFITM3 restriction depends on S-palmitoylation and a polymorphic site within the CD225 domain. <i>Life Science Alliance</i> , 2020, 3, e201900542.	1.3	32
121	Genomic Epidemiology of 2015â€“2016 Zika Virus Outbreak in Cape Verde. <i>Emerging Infectious Diseases</i> , 2020, 26, 1084-1090.	2.0	24
122	Metatranscriptomics as a tool to identify fungal species and subspecies in mixed communities â€“ a proof of concept under laboratory conditions. <i>IMA Fungus</i> , 2019, 10, 12.	1.7	20
123	Reply to â€“Reconciling disparate estimates of viral genetic diversity during human influenza infectionsâ€™. <i>Nature Genetics</i> , 2019, 51, 1301-1303.	9.4	3
124	Co-circulation and persistence of multiple A/H3N2 influenza variants in China. <i>Emerging Microbes and Infections</i> , 2019, 8, 1157-1167.	3.0	20
125	Meta-transcriptomic identification of hepatitis B virus in cerebrospinal fluid in patients with central nervous system disease. <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 95, 114878.	0.8	9
126	Identification of diverse arthropod associated viruses in native Australian fleas. <i>Virology</i> , 2019, 535, 189-199.	1.1	24

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127	Evolutionary history of Simbu serogroup orthobunyaviruses in the Australian epizootic system. <i>Virology</i> , 2019, 535, 32-44.	1.1	11
128	Limited Intra-host Diversity and Background Evolution Accompany 40 Years of Canine Parvovirus Host Adaptation and Spread. <i>Journal of Virology</i> , 2019, 94, .	1.5	53
129	Evolution of Termite Symbiosis Informed by Transcriptome-Based Phylogenies. <i>Current Biology</i> , 2019, 29, 3728-3734.e4.	1.8	110
130	Identification of a Novel Equine Papillomavirus in Semen from a Thoroughbred Stallion with a Penile Lesion. <i>Viruses</i> , 2019, 11, 713.	1.5	16
131	Reagent contamination in viromics: all that glitters is not gold. <i>Clinical Microbiology and Infection</i> , 2019, 25, 1167-1168.	2.8	21
132	Epidemiology and Diversity of Rickettsiales Bacteria in Humans and Animals in Jiangsu and Jiangxi provinces, China. <i>Scientific Reports</i> , 2019, 9, 13176.	1.6	36
133	Influenza Viruses in Mice: Deep Sequencing Analysis of Serial Passage and Effects of Sialic Acid Structural Variation. <i>Journal of Virology</i> , 2019, 93, .	1.5	15
134	Human Tick-Borne Diseases in Australia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 3.	1.8	37
135	Comparison of intra- and inter-host genetic diversity in rabies virus during experimental cross-species transmission. <i>PLoS Pathogens</i> , 2019, 15, e1007799.	2.1	22
136	Virome heterogeneity and connectivity in waterfowl and shorebird communities. <i>ISME Journal</i> , 2019, 13, 2603-2616.	4.4	53
137	Limited Sustained Local Transmission of HIV-1 CRF01_AE in New South Wales, Australia. <i>Viruses</i> , 2019, 11, 482.	1.5	4
138	Sustained Wolbachia-mediated blocking of dengue virus isolates following serial passage in <i>Aedes aegypti</i> cell culture. <i>Virus Evolution</i> , 2019, 5, vez012.	2.2	19
139	Expanding the RNA Virosphere by Unbiased Metagenomics. <i>Annual Review of Virology</i> , 2019, 6, 119-139.	3.0	129
140	Entrezpy: a Python library to dynamically interact with the NCBI Entrez databases. <i>Bioinformatics</i> , 2019, 35, 4511-4514.	1.8	11
141	Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?. <i>MBio</i> , 2019, 10, .	1.8	37
142	The discovery of three new hare lagoviruses reveals unexplored viral diversity in this genus. <i>Virus Evolution</i> , 2019, 5, vez005.	2.2	16
143	A reptilian endogenous foamy virus sheds light on the early evolution of retroviruses. <i>Virus Evolution</i> , 2019, 5, vez001.	2.2	19
144	Discovery of a highly divergent hepadnavirus in shrews from China. <i>Virology</i> , 2019, 531, 162-170.	1.1	6

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145	Identification of A Novel Picorna-Like Virus, Burpengary Virus, that is Negatively Associated with Chlamydial Disease in the Koala. <i>Viruses</i> , 2019, 11, 211.	1.5	6
146	Fecal Viral Diversity of Captive and Wild Tasmanian Devils Characterized Using Virion-Enriched Metagenomics and Metatranscriptomics. <i>Journal of Virology</i> , 2019, 93, .	1.5	56
147	Meta-transcriptomics reveals a diverse antibiotic resistance gene pool in avian microbiomes. <i>BMC Biology</i> , 2019, 17, 31.	1.7	76
148	Punctuated Evolution of Myxoma Virus: Rapid and Disjunct Evolution of a Recent Viral Lineage in Australia. <i>Journal of Virology</i> , 2019, 93, .	1.5	17
149	Evolutionary stasis of viruses?. <i>Nature Reviews Microbiology</i> , 2019, 17, 329-329.	13.6	8
150	Shared Common Ancestry of Rodent Alphacoronaviruses Sampled Globally. <i>Viruses</i> , 2019, 11, 125.	1.5	35
151	Meta-Transcriptomic Comparison of the RNA Viromes of the Mosquito Vectors <i>Culex pipiens</i> and <i>Culex torrentium</i> in Northern Europe. <i>Viruses</i> , 2019, 11, 1033.	1.5	64
152	Origin of the São Paulo Yellow Fever epidemic of 2017–2018 revealed through molecular epidemiological analysis of fatal cases. <i>Scientific Reports</i> , 2019, 9, 20418.	1.6	46
153	Distinct Lineages of Feline Parvovirus Associated with Epizootic Outbreaks in Australia, New Zealand and the United Arab Emirates. <i>Viruses</i> , 2019, 11, 1155.	1.5	27
154	Identification and evolution of avian endogenous foamy viruses. <i>Virus Evolution</i> , 2019, 5, vez049.	2.2	10
155	Diversity and Evolution of Novel Invertebrate DNA Viruses Revealed by Meta-Transcriptomics. <i>Viruses</i> , 2019, 11, 1092.	1.5	16
156	Intra-host growth kinetics of dengue virus in the mosquito <i>Aedes aegypti</i> . <i>PLoS Pathogens</i> , 2019, 15, e1008218.	2.1	23
157	Novel RNA viruses associated with <i>Plasmodium vivax</i> in human malaria and <i>Leucocytozoon</i> parasites in avian disease. <i>PLoS Pathogens</i> , 2019, 15, e1008216.	2.1	50
158	Metagenomic discovery and co-infection of diverse wobbly possum disease viruses and a novel hepacivirus in Australian brushtail possums. <i>One Health Outlook</i> , 2019, 1, 5.	1.4	18
159	Extensive Diversity of RNA Viruses in Australian Ticks. <i>Journal of Virology</i> , 2019, 93, .	1.5	116
160	Fogarty International Center collaborative networks in infectious disease modeling: Lessons learnt in research and capacity building. <i>Epidemics</i> , 2019, 26, 116-127.	1.5	16
161	Tracking virus outbreaks in the twenty-first century. <i>Nature Microbiology</i> , 2019, 4, 10-19.	5.9	305
162	Novel hepatitis D-like agents in vertebrates and invertebrates. <i>Virus Evolution</i> , 2019, 5, vez021.	2.2	63

#	ARTICLE	IF	CITATIONS
163	Discovery of novel highly divergent RNA viruses in European rodents and rabbits. <i>Access Microbiology</i> , 2019, 1, .	0.2	0
164	Title is missing!. , 2019, 15, e1008216.		0
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167	Using Metagenomics to Characterize an Expanding Virosphere. <i>Cell</i> , 2018, 172, 1168-1172.	13.5	219
168	Estimating evolutionary rates in giant viruses using ancient genomes. <i>Virus Evolution</i> , 2018, 4, vey006.	2.2	7
169	The evolutionary history of vertebrate RNA viruses. <i>Nature</i> , 2018, 556, 197-202.	13.7	596
170	Sudden emergence of human infections with H7N9 avian influenza A virus in Hubei province, central China. <i>Scientific Reports</i> , 2018, 8, 2486.	1.6	4
171	A Single Amino Acid Change in the Response Regulator PhoP, Acquired during <i>Yersinia pestis</i> Evolution, Affects PhoP Target Gene Transcription and Polymyxin B Susceptibility. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	16
172	Interplay between co-divergence and cross-species transmission in the evolutionary history of bat coronaviruses. <i>Infection, Genetics and Evolution</i> , 2018, 58, 279-289.	1.0	56
173	Emergence and Adaptation of a Novel Highly Pathogenic H7N9 Influenza Virus in Birds and Humans from a 2013 Human-Infecting Low-Pathogenic Ancestor. <i>Journal of Virology</i> , 2018, 92, .	1.5	99
174	Meta-transcriptomics and the evolutionary biology of RNA viruses. <i>Virus Research</i> , 2018, 243, 83-90.	1.1	120
175	Rabbit Hemorrhagic Disease Virus 2 (RHDV2; GI.2) Is Replacing Endemic Strains of RHDV in the Australian Landscape within 18 Months of Its Arrival. <i>Journal of Virology</i> , 2018, 92, .	1.5	85
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177	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018, 4, vey031.	2.2	54
178	A Divergent Hepatitis D-Like Agent in Birds. <i>Viruses</i> , 2018, 10, 720.	1.5	69
179	Evolutionary Virology at 40. <i>Genetics</i> , 2018, 210, 1151-1162.	1.2	51
180	A Simple Method to Detect Candidate Overlapping Genes in Viruses Using Single Genome Sequences. <i>Molecular Biology and Evolution</i> , 2018, 35, 2572-2581.	3.5	27

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181	The phylogenomics of evolving virus virulence. <i>Nature Reviews Genetics</i> , 2018, 19, 756-769.	7.7	152
182	Virus-virus interactions and host ecology are associated with RNA virome structure in wild birds. <i>Molecular Ecology</i> , 2018, 27, 5263-5278.	2.0	77
183	Transcriptome Analysis and In Situ Hybridization for FcaGHV1 in Feline Lymphoma. <i>Viruses</i> , 2018, 10, 464.	1.5	6
184	An Atypical Parvovirus Drives Chronic Tubulointerstitial Nephropathy and Kidney Fibrosis. <i>Cell</i> , 2018, 175, 530-543.e24.	13.5	89
185	Evolution of Human Respiratory Syncytial Virus (RSV) over Multiple Seasons in New South Wales, Australia. <i>Viruses</i> , 2018, 10, 476.	1.5	28
186	Unbiased whole genome deep sequencing of Rotavirus Group A positive samples from rural Kenya, 2012-14 reveals high frequency of coinfection and genetic reassortment. <i>International Journal of Infectious Diseases</i> , 2018, 73, 203.	1.5	2
187	Draft genome assembly of the invasive cane toad, <i>Rhinella marina</i> . <i>GigaScience</i> , 2018, 7, .	3.3	60
188	No detectable effect of <i>Wolbachia wMel</i> on the prevalence and abundance of the RNA virome of <i>Drosophila melanogaster</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181165.	1.2	53
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193	Pandemics: spend on surveillance, not prediction. <i>Nature</i> , 2018, 558, 180-182.	13.7	120
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198	Continental synchronicity of human influenza virus epidemics despite climactic variation. <i>PLoS Pathogens</i> , 2018, 14, e1006780.	2.1	38

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200	Complete genome of <i>Aedes aegypti</i> anphevirus in the Aag2 mosquito cell line. <i>Journal of General Virology</i> , 2018, 99, 832-836.	1.3	13
201	The impact of host genetic diversity on virus evolution and emergence. <i>Ecology Letters</i> , 2018, 21, 253-263.	3.0	33
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204	Diversity, evolution and population dynamics of avian influenza viruses circulating in the live poultry markets in China. <i>Virology</i> , 2017, 505, 33-41.	1.1	24
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212	Establishment and cryptic transmission of Zika virus in Brazil and the Americas. <i>Nature</i> , 2017, 546, 406-410.	13.7	515
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215	Multiple Sources of Genetic Diversity of Influenza A Viruses during the Hajj. <i>Journal of Virology</i> , 2017, 91, .	1.5	11
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218	Characterizing the virome of <i>Ixodes ricinus</i> ticks from northern Europe. <i>Scientific Reports</i> , 2017, 7, 10870.	1.6	92
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227	<i>Francisella tularensis</i> ssp. <i>holarctica</i> in Ringtail Possums, Australia. <i>Emerging Infectious Diseases</i> , 2017, 23, 1198-1201.	2.0	49
228	Spread of Canine Influenza A(H3N2) Virus, United States, 1950-1957. <i>Emerging Infectious Diseases</i> , 2017, 23, 1950-1957.	2.0	70
229	Persistent infections in immunocompromised hosts are rarely sources of new pathogen variants. <i>Virus Evolution</i> , 2017, 3, vex018.	2.2	21
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232	Highly Divergent Dengue Virus Type 2 in Traveler Returning from Borneo to Australia. <i>Emerging Infectious Diseases</i> , 2016, 22, 2146-2148.	2.0	29
233	Molecular Evolution and Phylogeography of Co-circulating IHNV and VHSV in Italy. <i>Frontiers in Microbiology</i> , 2016, 7, 1306.	1.5	33
234	Genome-scale rates of evolutionary change in bacteria. <i>Microbial Genomics</i> , 2016, 2, e000094.	1.0	224

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