

# Unprecedented genomic diversity of RNA viruses in art negative-sense RNA viruses

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Comparative paleovirological analysis of crustaceans identifies multiple widespread viral groups. <i>Mobile DNA</i> , 2015, 6, 16.	1.3	22
2	Genetic and Phylogenetic Characterization of Tataguine and Witwatersrand Viruses and Other Orthobunyaviruses of the Anopheles A, Capim, Guamãj, Koongol, Mapputta, Tete, and Turlock Serogroups. <i>Viruses</i> , 2015, 7, 5987-6008.	1.5	36
3	Insect-Specific Virus Discovery: Significance for the Arbovirus Community. <i>Viruses</i> , 2015, 7, 4911-4928.	1.5	211
4	Are arthropods at the heart of virus evolution?. <i>ELife</i> , 2015, 4, .	2.8	26
5	The evolution, diversity, and host associations of rhabdoviruses. <i>Virus Evolution</i> , 2015, 1, vev014.	2.2	68
6	Sequence-independent characterization of viruses based on the pattern of viral small RNAs produced by the host. <i>Nucleic Acids Research</i> , 2015, 43, 6191-6206.	6.5	104
7	Bugs full of viruses. <i>Nature Reviews Microbiology</i> , 2015, 13, 253-253.	13.6	2
8	Cell Walls and the Convergent Evolution of the Viral Envelope. <i>Microbiology and Molecular Biology Reviews</i> , 2015, 79, 403-418.	2.9	29
9	Non-random patterns in viral diversity. <i>Nature Communications</i> , 2015, 6, 8147.	5.8	65
10	Evolutionary origins of hepatitis A virus in small mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15190-15195.	3.3	99
11	A protein domain-based view of the virosphereâ€™host relationship. <i>Biochimie</i> , 2015, 119, 231-243.	1.3	7
12	Insect-specific viruses and their potential impact on arbovirus transmission. <i>Current Opinion in Virology</i> , 2015, 15, 69-74.	2.6	122
13	Is the evolution of Hantavirus driven by its host?. <i>Infection, Genetics and Evolution</i> , 2015, 35, 142-143.	1.0	3
14	Commensal Viruses of Mosquitoes: Host Restriction, Transmission, and Interaction with Arboviral Pathogens. <i>Evolutionary Bioinformatics</i> , 2016, 12s2, EBO.S40740.	0.6	66
15	Bunyaviruses of Crustaceans. , 2016, , 489-503.		2
16	Characterization of Viral Communities of Biting Midges and Identification of Novel Thogotovirus Species and Rhabdovirus Genus. <i>Viruses</i> , 2016, 8, 77.	1.5	37
17	Article Commentary: Virus Discovery Using Tick Cell Lines. <i>Evolutionary Bioinformatics</i> , 2016, 12s2, EBO.S39675.	0.6	16
18	Genomic Characterization of the Genus Nairovirus (Family Bunyaviridae). <i>Viruses</i> , 2016, 8, 164.	1.5	57

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19	Viral RNA Silencing Suppression: The Enigma of Bunyavirus NSs Proteins. <i>Viruses</i> , 2016, 8, 208.	1.5	38
20	Viral Metagenomics on Blood-Feeding Arthropods as a Tool for Human Disease Surveillance. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1743.	1.8	46
21	Virus-derived small RNAs: molecular footprints of host-pathogen interactions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2016, 7, 824-837.	3.2	31
22	Genome Sequences of Five Arboviruses in Field-Captured Mosquitoes in a Unique Rural Environment of South Korea. <i>Genome Announcements</i> , 2016, 4, .	0.8	35
23	The diversity of insect antiviral immunity: insights from viruses. <i>Current Opinion in Microbiology</i> , 2016, 32, 71-76.	2.3	70
24	Rhabdovirus-like endogenous viral elements in the genome of <i>Spodoptera frugiperda</i> insect cells are actively transcribed: Implications for adventitious virus detection. <i>Biologicals</i> , 2016, 44, 219-225.	0.5	34
25	Taxonomy of the order Mononegavirales: update 2016. <i>Archives of Virology</i> , 2016, 161, 2351-2360.	0.9	407
26	Phylogenetic analysis of a newfound bat-borne hantavirus supports a laurasiatherian host association for ancestral mammalian hantaviruses. <i>Infection, Genetics and Evolution</i> , 2016, 41, 113-119.	1.0	36
27	Changes in the composition of the RNA virome mark evolutionary transitions in green plants. <i>BMC Biology</i> , 2016, 14, 68.	1.7	37
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30	The Expanding Virosphere. <i>Cell Host and Microbe</i> , 2016, 20, 279-280.	5.1	13
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32	Conservation as vaccination. <i>EMBO Reports</i> , 2016, 17, 286-291.	2.0	5
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35	Resistance to Tosspoviruses in Vegetable Crops: Epidemiological and Molecular Aspects. <i>Annual Review of Phytopathology</i> , 2016, 54, 347-371.	3.5	98
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38	A Global Genomic Characterization of Nairoviruses Identifies Nine Discrete Genogroups with Distinctive Structural Characteristics and Host-Vector Associations. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 94, 1107-1122.	0.6	45
39	Reorganization and expansion of the nidoviral family Arteriviridae. <i>Archives of Virology</i> , 2016, 161, 755-768.	0.9	254
40	Diverse Array of New Viral Sequences Identified in Worldwide Populations of the Asian Citrus Psyllid ( <i>Diaphorina citri</i> ) Using Viral Metagenomics. <i>Journal of Virology</i> , 2016, 90, 2434-2445.	1.5	55
41	Divergent Viruses Discovered in Arthropods and Vertebrates Revise the Evolutionary History of the Flaviviridae and Related Viruses. <i>Journal of Virology</i> , 2016, 90, 659-669.	1.5	242
42	New bunya-like viruses: Highlighting their relations. <i>Infection, Genetics and Evolution</i> , 2017, 49, 164-173.	1.0	13
43	Molecular characterization of a novel orthomyxovirus from rainbow and steelhead trout ( <i>Oncorhynchus mykiss</i> ). <i>Virus Research</i> , 2017, 230, 38-49.	1.1	14
44	Genome Sequences of Three Novel Bunyaviruses, Two Novel Rhabdoviruses, and One Novel Nyamivirus from Washington State Moths. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
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47	Genetic characterization, molecular epidemiology, and phylogenetic relationships of insect-specific viruses in the taxon Negevirus. <i>Virology</i> , 2017, 504, 152-167.	1.1	68
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49	Insect-Specific Viruses. <i>Advances in Virus Research</i> , 2017, 98, 119-146.	0.9	58
50	The Envelope Proteins of the Bunyvirales. <i>Advances in Virus Research</i> , 2017, 98, 83-118.	0.9	83
51	Mosquito-specific and mosquito-borne viruses: evolution, infection, and host defense. <i>Current Opinion in Insect Science</i> , 2017, 22, 16-27.	2.2	71
52	A possible occurrence of genome reassortment among bipartite rhabdoviruses. <i>Virology</i> , 2017, 508, 18-25.	1.1	39
53	Vertically transmitted rhabdoviruses are found across three insect families and have dynamic interactions with their hosts. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162381.	1.2	32
54	Nonretroviral integrated RNA viruses in arthropod vectors: an occasional event or something more?. <i>Current Opinion in Insect Science</i> , 2017, 22, 45-53.	2.2	45

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55	A Diverse Range of Novel RNA Viruses in Geographically Distinct Honey Bee Populations. <i>Journal of Virology</i> , 2017, 91, .	1.5	138
56	Discovery of a Highly Divergent Coronavirus in the Asian House Shrew from China Illuminates the Origin of the Alphacoronaviruses. <i>Journal of Virology</i> , 2017, 91, .	1.5	37
57	Detection of a novel putative phlebovirus and first isolation of Dugbe virus from ticks in Accra, Ghana. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 640-645.	1.1	29
58	Diversity, Distribution, and Evolution of Tomato Viruses in China Uncovered by Small RNA Sequencing. <i>Journal of Virology</i> , 2017, 91, .	1.5	63
59	A novel rhabdovirus, related to Merida virus, in field-collected mosquitoes from Anatolia and Thrace. <i>Archives of Virology</i> , 2017, 162, 1903-1911.	0.9	18
60	Estimation of main diversification time-points of hantaviruses using phylogenetic analyses of complete genomes. <i>Virus Research</i> , 2017, 233, 60-69.	1.1	8
61	Sinu virus, a novel and divergent orthomyxovirus related to members of the genus Thogotovirus isolated from mosquitoes in Colombia. <i>Virology</i> , 2017, 501, 166-175.	1.1	22
62	Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017, 15, 161-168.	13.6	590
63	A chikungunya fever vaccine utilizing an insect-specific virus platform. <i>Nature Medicine</i> , 2017, 23, 192-199.	15.2	105
64	Metagenomic-based Surveillance of Pacific Coast tick <i>Dermacentor occidentalis</i> Identifies Two Novel Bunyaviruses and an Emerging Human Rickettsial Pathogen. <i>Scientific Reports</i> , 2017, 7, 12234.	1.6	42
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66	Genomes of viral isolates derived from different mosquito species. <i>Virus Research</i> , 2017, 242, 49-57.	1.1	40
67	Characterizing the virome of <i>Ixodes ricinus</i> ticks from northern Europe. <i>Scientific Reports</i> , 2017, 7, 10870.	1.6	92
68	Ecology of Filoviruses. <i>Current Topics in Microbiology and Immunology</i> , 2017, 411, 23-61.	0.7	22
69	Kanyawara Virus: A Novel Rhabdovirus Infecting Newly Discovered Nycteribiid Bat Flies Infesting Previously Unknown Pteropodid Bats in Uganda. <i>Scientific Reports</i> , 2017, 7, 5287.	1.6	32
70	Symbiosis: Viruses as Intimate Partners. <i>Annual Review of Virology</i> , 2017, 4, 123-139.	3.0	74
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74	Putative RNA viral sequences detected in an Ixodes scapularis-derived cell line. <i>Ticks and Tick-borne Diseases</i> , 2017, 8, 103-111.	1.1	23
75	The family Rhabdoviridae: mono- and bipartite negative-sense RNA viruses with diverse genome organization and common evolutionary origins. <i>Virus Research</i> , 2017, 227, 158-170.	1.1	200
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79	Viral Delivery of dsRNA for Control of Insect Agricultural Pests and Vectors of Human Disease: Prospects and Challenges. <i>Frontiers in Physiology</i> , 2017, 8, 399.	1.3	75
80	Vertebrate Reservoirs of Arboviruses: Myth, Synonym of Amplifier, or Reality?. <i>Viruses</i> , 2017, 9, 185.	1.5	56
81	The Potential for Reassortment between Oropouche and Schmallenberg Orthobunyaviruses. <i>Viruses</i> , 2017, 9, 220.	1.5	20
82	Tick-Virus Interactions: Toll Sensing. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 293.	1.8	10
83	Tick-Borne Viruses and Biological Processes at the Tick-Host-Virus Interface. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 339.	1.8	111
84	Two Negative-Strand RNA Viruses Identified in Watermelon Represent a Novel Clade in the Order Bunyavirales. <i>Frontiers in Microbiology</i> , 2017, 8, 1514.	1.5	51
85	An RNA Virome Associated to the Golden Orb-Weaver Spider Nephila clavipes. <i>Frontiers in Microbiology</i> , 2017, 8, 2097.	1.5	32
86	Presence of Apis Rhabdovirus-1 in Populations of Pollinators and Their Parasites from Two Continents. <i>Frontiers in Microbiology</i> , 2017, 8, 2482.	1.5	27
87	Comparative genomics shows that viral integrations are abundant and express piRNAs in the arboviral vectors Aedes aegypti and Aedes albopictus. <i>BMC Genomics</i> , 2017, 18, 512.	1.2	138
88	Generic amplification and next generation sequencing reveal Crimean-Congo hemorrhagic fever virus AP92-like strain and distinct tick phleboviruses in Anatolia, Turkey. <i>Parasites and Vectors</i> , 2017, 10, 335.	1.0	37
89	Unexpected differences in the population genetics of phasmavirids (Bunyavirales) from subarctic ponds. <i>Virus Evolution</i> , 2017, 3, vex015.	2.2	27
90	The complete genome sequence of CrRV-Ch01, a new member of the family Rhabdoviridae in the parasitic copepod Caligus rogercresseyi present on farmed Atlantic salmon (Salmo salar) in Chile. <i>Archives of Virology</i> , 2018, 163, 1657-1661.	0.9	7

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91	The Global Virome Project. <i>Science</i> , 2018, 359, 872-874.	6.0	324
92	Using Metagenomics to Characterize an Expanding Virosphere. <i>Cell</i> , 2018, 172, 1168-1172.	13.5	219
93	Estimating evolutionary rates in giant viruses using ancient genomes. <i>Virus Evolution</i> , 2018, 4, vey006.	2.2	7
94	High-Resolution Screening of Viral Communities and Identification of New Pathogens in Fish Using Next-Generation Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1746, 151-159.	0.4	0
95	Insect Virus Discovery by Metagenomic and Cell Culture-Based Approaches. <i>Methods in Molecular Biology</i> , 2018, 1746, 197-213.	0.4	6
96	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310.	0.9	157
97	<i>Marmota himalayana</i> in the Qinghai-Tibetan plateau as a special host for bi-segmented and unsegmented picobirnaviruses. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-8.	3.0	28
98	A new subtype of eastern tick-borne encephalitis virus discovered in Qinghai-Tibet Plateau, China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-9.	3.0	140
99	Viral Diversity of House Mice in New York City. <i>MBio</i> , 2018, 9, .	1.8	95
100	The evolutionary history of vertebrate RNA viruses. <i>Nature</i> , 2018, 556, 197-202.	13.7	596
101	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	153
102	Landscape of emerging and re-emerging infectious diseases in China: impact of ecology, climate, and behavior. <i>Frontiers of Medicine</i> , 2018, 12, 3-22.	1.5	46
103	A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018, 9, 373.	5.8	297
104	Viral discovery and diversity in trypanosomatid protozoa with a focus on relatives of the human parasite <i>Leishmania</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E506-E515.	3.3	75
105	The Discovery of Arthropod-Specific Viruses in Hematophagous Arthropods: An Open Door to Understanding the Mechanisms of Arbovirus and Arthropod Evolution?. <i>Annual Review of Entomology</i> , 2018, 63, 87-103.	5.7	45
106	A metagenomic survey identifies Tamdy orthonairovirus as well as divergent phlebo-, rhabdo-, chu- and flavi-like viruses in Anatolia, Turkey. <i>Ticks and Tick-borne Diseases</i> , 2018, 9, 1173-1183.	1.1	48
107	The Expanding Diversity of RNA Viruses in Vertebrates. <i>Trends in Microbiology</i> , 2018, 26, 465-466.	3.5	3
108	A novel virus (order Bunyvirales ) from stressed redclaw crayfish ( <i>Cherax quadricarinatus</i> ) from farms in northern Australia. <i>Virus Research</i> , 2018, 250, 7-12.	1.1	14

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109	Tick-Borne Viruses. <i>Virologica Sinica</i> , 2018, 33, 21-43.	1.2	79
110	Identification of Novel Viruses in <i>Amblyomma americanum</i> , <i>Dermacentor variabilis</i> , and <i>Ixodes scapularis</i> Ticks. <i>MSphere</i> , 2018, 3, .	1.3	88
111	Complete Genome Sequence of Pittsburgh Sewage-Associated Virus 1. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
112	Mosquito-Associated Viruses in China. <i>Virologica Sinica</i> , 2018, 33, 5-20.	1.2	59
113	The first phlebovirus-like virus infecting plants: a case study on the adaptation of negative-stranded RNA viruses to new hosts. <i>Molecular Plant Pathology</i> , 2018, 19, 1075-1089.	2.0	72
114	A decade of RNA virus metagenomics is (not) enough. <i>Virus Research</i> , 2018, 244, 218-229.	1.1	129
115	Meta-transcriptomics and the evolutionary biology of RNA viruses. <i>Virus Research</i> , 2018, 243, 83-90.	1.1	120
116	Molecular detection and sequence characterization of diverse rhabdoviruses in bats, China. <i>Virus Research</i> , 2018, 244, 208-212.	1.1	5
117	Characterization of a novel single-stranded RNA mycovirus related to invertebrate viruses from the plant pathogen <i>Verticillium dahliae</i> . <i>Archives of Virology</i> , 2018, 163, 771-776.	0.9	14
118	Adventitious viruses in insect cell lines used for recombinant protein expression. <i>Protein Expression and Purification</i> , 2018, 144, 25-32.	0.6	21
119	Metagenomics reshapes the concepts of RNA virus evolution by revealing extensive horizontal virus transfer. <i>Virus Research</i> , 2018, 244, 36-52.	1.1	190
120	Vector-borne viruses and their detection by viral metagenomics. <i>Infection Ecology and Epidemiology</i> , 2018, 8, 1553465.	0.5	3
122	<i>Culex quinquefasciatus</i> mosquitoes do not support replication of Zika virus. <i>Journal of General Virology</i> , 2018, 99, 258-264.	1.3	36
123	Draft Genome Sequence of a Novel Rhabdovirus Isolated from <i>Deinocerites</i> Mosquitoes. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
124	Hidden diversity and evolution of viruses in market fish. <i>Virus Evolution</i> , 2018, 4, vey031.	2.2	54
125	Discovery of Diverse Rodent and Bat Pestiviruses With Distinct Genomic and Phylogenetic Characteristics in Several Chinese Provinces. <i>Frontiers in Microbiology</i> , 2018, 9, 2562.	1.5	30
126	RNA Virus Fidelity Mutants: A Useful Tool for Evolutionary Biology or a Complex Challenge?. <i>Viruses</i> , 2018, 10, 600.	1.5	31
127	Plant rhabdoviruses—their origins and vector interactions. <i>Current Opinion in Virology</i> , 2018, 33, 198-207.	2.6	70



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129	Viral diversity of Rhipicephalus microplus parasitizing cattle in southern Brazil. Scientific Reports, 2018, 8, 16315.	1.6	72
130	The Unique Phylogenetic Position of a Novel Tick-Borne Phlebovirus Ensures an Ixodid Origin of the Genus <i>Phlebovirus</i> . MSphere, 2018, 3, .	1.3	36
131	Evolutionary Virology at 40. Genetics, 2018, 210, 1151-1162.	1.2	51
132	Origins and Evolution of the Global RNA Virome. MBio, 2018, 9, .	1.8	383
133	Molecular interactions between tospoviruses and thrips vectors. Current Opinion in Virology, 2018, 33, 191-197.	2.6	40
134	Diverse, Novel Mycoviruses From the Virome of a Hypovirulent Sclerotium rolfii Strain. Frontiers in Plant Science, 2018, 9, 1738.	1.7	31
135	Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome, 2018, 6, 178.	4.9	150
136	A Negative-Stranded RNA Virus Infecting Citrus Trees: The Second Member of a New Genus Within the Order Bunyavirales. Frontiers in Microbiology, 2018, 9, 2340.	1.5	53
137	A planarian nidovirus expands the limits of RNA genome size. PLoS Pathogens, 2018, 14, e1007314.	2.1	108
138	Biochemical and structural studies reveal differences and commonalities among cap-snatching endonucleases from segmented negative-strand RNA viruses. Journal of Biological Chemistry, 2018, 293, 19686-19698.	1.6	31
139	Ebola Virus Maintenance: If Not (Only) Bats, What Else?. Viruses, 2018, 10, 549.	1.5	44
140	RNA viruses in trypanosomatid parasites: a historical overview. Memorias Do Instituto Oswaldo Cruz, 2018, 113, e170487.	0.8	24
141	Notes on recombination and reassortment in multipartite/segmented viruses. Current Opinion in Virology, 2018, 33, 156-166.	2.6	44
142	Expansion of the metazoan virosphere: progress, pitfalls, and prospects. Current Opinion in Virology, 2018, 31, 17-23.	2.6	33
143	De novo assembly, characterization, functional annotation and expression patterns of the black tiger shrimp (Penaeus monodon) transcriptome. Scientific Reports, 2018, 8, 13553.	1.6	48
144	Persistent viruses in mosquito cultured cell line suppress multiplication of flaviviruses. Heliyon, 2018, 4, e00736.	1.4	26
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147	Adventitious viruses persistently infect three commonly used mosquito cell lines. <i>Virology</i> , 2018, 521, 175-180.	1.1	29
148	Aedes Anphevirus: an Insect-Specific Virus Distributed Worldwide in Aedes aegypti Mosquitoes That Has Complex Interplays with Wolbachia and Dengue Virus Infection in Cells. <i>Journal of Virology</i> , 2018, 92, .	1.5	54
149	Discovery and high prevalence of Phasi Charoen-like virus in field-captured Aedes aegypti in South China. <i>Virology</i> , 2018, 523, 35-40.	1.1	28
150	Insect-specific viruses: from discovery to potential translational applications. <i>Current Opinion in Virology</i> , 2018, 33, 33-41.	2.6	73
151	Co-Infection Patterns in Individual Ixodes scapularis Ticks Reveal Associations between Viral, Eukaryotic and Bacterial Microorganisms. <i>Viruses</i> , 2018, 10, 388.	1.5	44
152	Dichorhaviruses in their Host Plants and Mite Vectors. <i>Advances in Virus Research</i> , 2018, 102, 119-148.	0.9	51
153	Study of the Metatranscriptome of Eight Social and Solitary Wild Bee Species Reveals Novel Viruses and Bee Parasites. <i>Frontiers in Microbiology</i> , 2018, 9, 177.	1.5	60
154	A Systematic Review of the Natural Virome of Anopheles Mosquitoes. <i>Viruses</i> , 2018, 10, 222.	1.5	42
155	Virological Sampling of Inaccessible Wildlife with Drones. <i>Viruses</i> , 2018, 10, 300.	1.5	49
156	A new approach for detecting adventitious viruses shows Sf-rhabdovirus-negative Sf-RVN cells are suitable for safe biologicals production. <i>BMC Biotechnology</i> , 2018, 18, 8.	1.7	10
157	Recent insights into the tick microbiome gained through next-generation sequencing. <i>Parasites and Vectors</i> , 2018, 11, 12.	1.0	146
158	The mosquito holobiont: fresh insight into mosquito-microbiota interactions. <i>Microbiome</i> , 2018, 6, 49.	4.9	193
159	Genetic characterization of a novel picorna-like virus in Culex spp. mosquitoes from Mozambique. <i>Virology Journal</i> , 2018, 15, 71.	1.4	21
160	Metagenomic sequencing suggests a diversity of RNA interference-like responses to viruses across multicellular eukaryotes. <i>PLoS Genetics</i> , 2018, 14, e1007533.	1.5	95
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