

Changes to taxonomy and the International Code of Vir Nomenclature ratified by the International Committee

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genomic Characterization of Crimeanâ€“Congo Hemorrhagic Fever Virus in Hyalomma Tick from Spain, 2014. Vector-Borne and Zoonotic Diseases, 2017, 17, 714-719.	1.5	24
2	<scp>RNA</scp>â€“virus proteases counteracting host innate immunity. FEBS Letters, 2017, 591, 3190-3210.	2.8	64
3	Distinct Mechanism for the Formation of the Ribonucleoprotein Complex of Tomato Spotted Wilt Virus. Journal of Virology, 2017, 91, .	3.4	21
4	Detection and characterization of three zoonotic viruses in wild rodents and shrews from Shenzhen city, China. Virologica Sinica, 2017, 32, 290-297.	3.0	25
5	Complete Genome Sequence of a New Isolate of Solenopsis invicta virus 3 from Solenopsis invicta Ã— richteri Hybrid Ants. Genome Announcements, 2017, 5, .	0.8	1
6	Transcriptomic profile of tobacco in response to Tomato zongata spot orthotospovirus infection. Virology Journal, 2017, 14, 153.	3.4	9
7	An Insight into Cotton Leaf Curl Multan Betasatellite, the Most Important Component of Cotton Leaf Curl Disease Complex. Viruses, 2017, 9, 280.	3.3	37
8	Genomic Characterisation of Vinegar Hill Virus, An Australian Nairovirus Isolated in 1983 from Argas Robertsi Ticks Collected from Cattle Egrets. Viruses, 2017, 9, 373.	3.3	9
9	Targeting Host Cell Surface Nucleolin for RSV Therapy: Challenges and Opportunities. Vaccines, 2017, 5, 27.	4.4	12
10	Unexpected differences in the population genetics of phasmavirids (Bunyavirales) from subarctic ponds. Virus Evolution, 2017, 3, vex015.	4.9	27
11	ViCTree: an automated framework for taxonomic classification from protein sequences. Bioinformatics, 2018, 34, 2195-2200.	4.1	6
12	Genomic Characterization of a Novel Hepatovirus from Great Roundleaf Bats in China. Virologica Sinica, 2018, 33, 108-110.	3.0	4
13	Transmission routes of respiratory viruses among humans. Current Opinion in Virology, 2018, 28, 142-151.	5.4	440
14	Protein disulfide isomerases as potential therapeutic targets for influenza A and B viruses. Virus Research, 2018, 247, 26-33.	2.2	25
15	A Novel Hantavirus of the European Mole, Bruges Virus, Is Involved in Frequent Nova Virus Coinfections. Genome Biology and Evolution, 2018, 10, 45-55.	2.5	23
16	Interferon-Stimulated Gene (ISG)-Expression Screening Reveals the Specific Antibunyaviral Activity of ISG20. Journal of Virology, 2018, 92, .	3.4	48
17	SFTS phlebovirus promotes LC3-II accumulation and nonstructural protein of SFTS phlebovirus co-localizes with autophagy proteins. Scientific Reports, 2018, 8, 5287.	3.3	14
18	A decade of RNA virus metagenomics is (not) enough. Virus Research, 2018, 244, 218-229.	2.2	129

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19	Molecular detection and sequence characterization of diverse rhabdoviruses in bats, China. <i>Virus Research</i> , 2018, 244, 208-212.	2.2	5
20	Novel <i>Sulfolobus</i> Virus with an Exceptional Capsid Architecture. <i>Journal of Virology</i> , 2018, 92, .	3.4	15
22	A novel chrysovirus from a clinical isolate of <i>Aspergillus thermomutatus</i> affects sporulation. <i>PLoS ONE</i> , 2018, 13, e0209443.	2.5	10
23	Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. <i>Journal of General Virology</i> , 2018, 99, 1331-1343.	2.9	72
24	Non-Structural Protein NSm of Tomato Spotted Wilt Virus Is an Avirulence Factor Recognized by Resistance Genes of Tobacco and Tomato via Different Elicitor Active Sites. <i>Viruses</i> , 2018, 10, 660.	3.3	18
25	Phenotypic and genotypic analyses of an attenuated porcine reproductive and respiratory syndrome virus strain after serial passages in cultured porcine alveolar macrophages. <i>Journal of Veterinary Science</i> , 2018, 19, 358.	1.3	1
26	Neurologic Alterations Due to Respiratory Virus Infections. <i>Frontiers in Cellular Neuroscience</i> , 2018, 12, 386.	3.7	498
27	Identification of a novel nidovirus as a potential cause of large scale mortalities in the endangered Bellinger River snapping turtle (<i>Myuchelys georgesi</i>). <i>PLoS ONE</i> , 2018, 13, e0205209.	2.5	50
28	First Genome Sequence of Newcastle Disease Virus of Genotype VIIi from Jordan. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	7
29	The Unique Phylogenetic Position of a Novel Tick-Borne Phlebovirus Ensures an Ixodid Origin of the Genus <i>Phlebovirus</i> . <i>MSphere</i> , 2018, 3, .	2.9	36
30	Practical Guidance for Clinical Microbiology Laboratories: Viruses Causing Acute Respiratory Tract Infections. <i>Clinical Microbiology Reviews</i> , 2018, 32, .	13.6	85
31	Genetic characterization and molecular epidemiological analysis of novel enterovirus EV-B80 in China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-12.	6.5	23
32	Origins and Evolution of the Global RNA Virome. <i>MBio</i> , 2018, 9, .	4.1	383
33	The Ecological Significance and Implications of Transovarial Transmission among the Vector-Borne Bunyaviruses: A Review. <i>Insects</i> , 2018, 9, 173.	2.2	22
34	Construction and evaluation of HA-epitope-tag introduction onto the VP1 structural protein of a novel HY12 enterovirus. <i>Virology</i> , 2018, 525, 106-116.	2.4	5
35	Genetic Characterization and Pathogenicity of a Novel Recombined Porcine Reproductive and Respiratory Syndrome Virus 2 among Nadc30-Like, Jxa1-Like, and Mlv-Like Strains. <i>Viruses</i> , 2018, 10, 551.	3.3	42
36	Molecular characterization of an unusual new plant RNA virus reveals an evolutionary link between two different virus families. <i>PLoS ONE</i> , 2018, 13, e0206382.	2.5	8
37	An atypical RNA silencing suppression strategy provides a snapshot of the evolution of sweet potato-infecting potyviruses. <i>Scientific Reports</i> , 2018, 8, 15937.	3.3	32

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38	Protease inhibitors broadly effective against feline, ferret and mink coronaviruses. <i>Antiviral Research</i> , 2018, 160, 79-86.	4.1	31
39	Presence and Distribution of <i>Scirtothrips dorsalis</i> Hood (Thysanoptera: Thripidae) in Colombia. <i>Journal of Insect Science</i> , 2018, 18, .	1.5	7
40	Viruses of Eukaryotic Algae: Diversity, Methods for Detection, and Future Directions. <i>Viruses</i> , 2018, 10, 487.	3.3	56
41	Expansion of the metazoan virosphere: progress, pitfalls, and prospects. <i>Current Opinion in Virology</i> , 2018, 31, 17-23.	5.4	33
42	Influenza C Virus in Cattle with Respiratory Disease, United States, 2016â€“2018. <i>Emerging Infectious Diseases</i> , 2018, 24, 1926-1929.	4.3	27
43	Heartland Virus Epidemiology, Vector Association, and Disease Potential. <i>Viruses</i> , 2018, 10, 498.	3.3	83
44	Characterization, phylogeny and recombination analysis of <i>Pedilanthus</i> leaf curl virus-Petunia isolate and its associated betasatellite. <i>Virology Journal</i> , 2018, 15, 134.	3.4	12
45	The Sw-5 Gene Cluster: Tomato Breeding and Research Toward Orthotospovirus Disease Control. <i>Frontiers in Plant Science</i> , 2018, 9, 1055.	3.6	35
46	A Novel Squirrel Respirovirus with Putative Zoonotic Potential. <i>Viruses</i> , 2018, 10, 373.	3.3	11
47	Investigation of O-polysaccharides from bacterial strains of <i>Pseudomonas</i> genus as potential receptors of bacteriophage BIM BV-45. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 1065-1072.	7.5	2
48	The complete genomic sequence of a novel botybirnavirus isolated from a phytopathogenic <i>Bipolaris maydis</i> . <i>Virus Genes</i> , 2018, 54, 733-736.	1.6	16
49	The analysis of genome composition and codon bias reveals distinctive patterns between avian and mammalian circoviruses which suggest a potential recombinant origin for Porcine circovirus 3. <i>PLoS ONE</i> , 2018, 13, e0199950.	2.5	21
50	A Review of Bunyamwera, Batai, and Ngari Viruses: Understudied Orthobunyaviruses With Potential One Health Implications. <i>Frontiers in Veterinary Science</i> , 2018, 5, 69.	2.2	45
51	Viral species, viral genomes and HIV vaccine design: is the rational design of biological complexity a utopia?. <i>Archives of Virology</i> , 2018, 163, 2047-2054.	2.1	4
52	Virus classification â€“ where do you draw the line?. <i>Archives of Virology</i> , 2018, 163, 2037-2046.	2.1	76
53	Seroepidemiologic Survey of Crimean-Congo Hemorrhagic Fever Virus in Selected Risk Groups, South Africa. <i>Emerging Infectious Diseases</i> , 2018, 24, 1360-1363.	4.3	15
54	High Serum Procalcitonin Concentrations in Patients With Hemorrhagic Fever With Renal Syndrome Caused by Hantaan Virus. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 129.	3.9	13
55	Two New Lytic Bacteriophages of the Myoviridae Family Against Carbapenem-Resistant <i>Acinetobacter baumannii</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 850.	3.5	47

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56	Application of Real-Time Quantitative PCR to Detect Mink Circovirus in Naturally and Experimentally Infected Minks. <i>Frontiers in Microbiology</i> , 2018, 9, 937.	3.5	9
57	Complete Genome Sequences of a Diverse Group of 13 <i>Propionibacterium acnes</i> Bacteriophages Isolated from Urban Raw Sewage. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
58	Comparative Analysis of 37 <i>Acinetobacter</i> Bacteriophages. <i>Viruses</i> , 2018, 10, 5.	3.3	37
59	Identification of a Novel Recombinant Type 2 Porcine Reproductive and Respiratory Syndrome Virus in China. <i>Viruses</i> , 2018, 10, 151.	3.3	22
60	Oropouche Fever: A Review. <i>Viruses</i> , 2018, 10, 175.	3.3	90
61	Whole Genome Analysis of Two Novel Type 2 Porcine Reproductive and Respiratory Syndrome Viruses with Complex Genome Recombination between Lineage 8, 3, and 1 Strains Identified in Southwestern China. <i>Viruses</i> , 2018, 10, 328.	3.3	31
62	Isolation of three novel reassortant phleboviruses, Ponticelli I, II, III, and of Toscana virus from field-collected sandflies in Italy. <i>Parasites and Vectors</i> , 2018, 11, 84.	2.5	21
63	Role of the vacuolar ATPase in the Alphavirus replication cycle. <i>Heliyon</i> , 2018, 4, e00701.	3.2	6
64	Fatal Tickborne Phlebovirus Infection in Captive Cheetahs, Japan. <i>Emerging Infectious Diseases</i> , 2018, 24, 1726-1729.	4.3	46
65	First report and genetic characterization of feline kobuvirus in diarrhoeic cats in China. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 1357-1363.	3.0	21
66	Prion-like Domains in Eukaryotic Viruses. <i>Scientific Reports</i> , 2018, 8, 8931.	3.3	43
67	Investigating the viral ecology of global bee communities with high-throughput metagenomics. <i>Scientific Reports</i> , 2018, 8, 8879.	3.3	58
68	Natural infection of Neotropical bats with hantavirus in Brazil. <i>Scientific Reports</i> , 2018, 8, 9018.	3.3	21
69	Comparing patterns and scales of plant virus phylogeography: Rice yellow mottle virus in Madagascar and in continental Africa. <i>Virus Evolution</i> , 2019, 5, vez023.	4.9	22
70	Molecular diversity of Papaya ringspot virus in India: genetic recombination and mutations between the isolates from different hosts and geo-climatic locations are role players in virus evolution. <i>Indian Phytopathology</i> , 2019, 72, 497-511.	1.2	8
71	Shedding and Transmission Modes of Severe Fever With Thrombocytopenia Syndrome Phlebovirus in a Ferret Model. <i>Open Forum Infectious Diseases</i> , 2019, 6, .	0.9	14
72	Viral Metagenomics Revealed a Novel Cardiovirus in Feces of Wild Rats. <i>Intervirology</i> , 2019, 62, 45-50.	2.8	2
73	High seroconversion rate to Rift Valley fever virus in cattle and goats in far northern KwaZulu-Natal, South Africa, in the absence of reported outbreaks. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007296.	3.0	30

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74	A Novel, Highly Related Jumbo Family of Bacteriophages That Were Isolated Against <i>Erwinia</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1533.	3.5	43
75	Evolution and Interspecies Transmission of Canine Distemper Virus—An Outlook of the Diverse Evolutionary Landscapes of a Multi-Host Virus. <i>Viruses</i> , 2019, 11, 582.	3.3	63
76	The Needs for Developing Experiments on Reservoirs in Hantavirus Research: Accomplishments, Challenges and Promises for the Future. <i>Viruses</i> , 2019, 11, 664.	3.3	14
77	Hantavirus Pulmonary Syndrome Risk in Entre R��os, Argentina. <i>EcoHealth</i> , 2019, 16, 558-569.	2.0	9
78	Complete Genome Sequences of Rice Yellow Mottle Virus Isolates from the Federal Democratic Republic of Ethiopia. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
79	Identification of three linear B cell epitopes using monoclonal antibodies against bovine enterovirus VP2 protein. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 7467-7480.	3.6	5
80	Novel insights into endogenous RNA viral elements in <i>Ixodes scapularis</i> and other arbovirus vector genomes. <i>Virus Evolution</i> , 2019, 5, vez010.	4.9	34
81	Feline Virome—A Review of Novel Enteric Viruses Detected in Cats. <i>Viruses</i> , 2019, 11, 908.	3.3	18
82	Genetically Modified Rabies Virus Vector-Based Rift Valley Fever Virus Vaccine is Safe and Induces Efficacious Immune Responses in Mice. <i>Viruses</i> , 2019, 11, 919.	3.3	19
83	Genetic characterization of a novel picornavirus in Algerian bats: co-evolution analysis of bat-related picornaviruses. <i>Scientific Reports</i> , 2019, 9, 15706.	3.3	3
84	Occurrence and variability of begomoviruses associated with bhendi yellow vein mosaic and okra enation leaf curl diseases in south-western India. <i>VirusDisease</i> , 2019, 30, 511-525.	2.0	4
85	Evolution of infectious bronchitis virus in the field after homologous vaccination introduction. <i>Veterinary Research</i> , 2019, 50, 92.	3.0	40
86	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. <i>Genome Biology</i> , 2019, 20, 217.	8.8	269
87	Reliable and Standardized Animal Models to Study the Pathogenesis of Bluetongue and Schmallenberg Viruses in Ruminant Natural Host Species with Special Emphasis on Placental Crossing. <i>Viruses</i> , 2019, 11, 753.	3.3	5
88	Nonstructural Protein 11 of Porcine Reproductive and Respiratory Syndrome Virus Induces STAT2 Degradation To Inhibit Interferon Signaling. <i>Journal of Virology</i> , 2019, 93, .	3.4	28
89	Immuno-modulating properties of Tulathromycin in porcine monocyte-derived macrophages infected with porcine reproductive and respiratory syndrome virus. <i>PLoS ONE</i> , 2019, 14, e0221560.	2.5	7
90	Surveillance of <i>Culicoides</i> biting midges in northern Honshu, Japan, during the period of Akabane virus spread. <i>Journal of Veterinary Medical Science</i> , 2019, 81, 1496-1503.	0.9	2
91	Hantaviridae: Current Classification and Future Perspectives. <i>Viruses</i> , 2019, 11, 788.	3.3	94

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92	Detection of Two Highly Diverse Peribunyaviruses in Mosquitoes from Palenque, Mexico. <i>Viruses</i> , 2019, 11, 832.	3.3	8
93	Development of Multispecies Recombinant Nucleoprotein-Based Indirect ELISA for High-Throughput Screening of Crimean-Congo Hemorrhagic Fever Virus-Specific Antibodies. <i>Frontiers in Microbiology</i> , 2019, 10, 1822.	3.5	13
94	Contribution of Resident Memory CD8+ T Cells to Protective Immunity Against Respiratory Syncytial Virus and Their Impact on Vaccine Design. <i>Pathogens</i> , 2019, 8, 147.	2.8	24
95	Tropism of Newcastle disease virus strains for chicken neurons, astrocytes, oligodendrocytes, and microglia. <i>BMC Veterinary Research</i> , 2019, 15, 317.	1.9	12
96	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	11.0	94
97	Gray (<i>Oreochromis niloticus</i> x <i>O. aureus</i>) and Red (<i>Oreochromis</i> spp.) Tilapia Show Equal Susceptibility and Proinflammatory Cytokine Responses to Experimental Tilapia Lake Virus Infection. <i>Viruses</i> , 2019, 11, 893.	3.3	24
98	Immune Modulation and Immune-Mediated Pathogenesis of Emerging Tickborne Banyangviruses. <i>Vaccines</i> , 2019, 7, 125.	4.4	25
99	Evaluation of PRRSV specific, maternally derived and induced immune response in Ingelvac PRRSFLEX EU vaccinated piglets in the presence of maternally transferred immunity. <i>PLoS ONE</i> , 2019, 14, e0223060.	2.5	8
100	Host Range of Bacteriophages Against a World-Wide Collection of <i>Erwinia amylovora</i> Determined Using a Quantitative PCR Assay. <i>Viruses</i> , 2019, 11, 910.	3.3	21
101	Comprehensive codon usage analysis of porcine deltacoronavirus. <i>Molecular Phylogenetics and Evolution</i> , 2019, 141, 106618.	2.7	13
102	Identification of Two Porcine Reproductive and Respiratory Syndrome Virus Variants Sharing High Genomic Homology but with Distinct Virulence. <i>Viruses</i> , 2019, 11, 875.	3.3	22
103	Taxonomy of the order Mononegavirales: second update 2018. <i>Archives of Virology</i> , 2019, 164, 1233-1244.	2.1	70
104	Seroprevalence, cross antigenicity and circulation sphere of bat-borne hantaviruses revealed by serological and antigenic analyses. <i>PLoS Pathogens</i> , 2019, 15, e1007545.	4.7	10
105	A major-capsid-protein-based multiplex PCR assay for rapid identification of selected virulent bacteriophage types. <i>Archives of Virology</i> , 2019, 164, 819-830.	2.1	17
106	Identification and localization of Tospovirus genus-wide conserved residues in 3D models of the nucleocapsid and the silencing suppressor proteins. <i>Virology Journal</i> , 2019, 16, 7.	3.4	14
107	Genomic Sequence of a Megrivirus Strain Identified in Laying Hens in Brazil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
108	Expanding Repertoire of Plant Positive-Strand RNA Virus Proteases. <i>Viruses</i> , 2019, 11, 66.	3.3	24
109	Structure and tailspike glycosidase machinery of ORF212 from <i>E. coli</i> O157:H7 phage CBA120 (TSP3). <i>Scientific Reports</i> , 2019, 9, 7349.	3.3	23

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110	Flavors of Flaviviral RNA Structure: towards an Integrated View of RNA Function from Translation through Encapsidation. <i>BioEssays</i> , 2019, 41, 1900003.	2.5	5
111	Development and analytical validation of a group-specific RT-qPCR assay for the detection of the Simbu serogroup orthobunyaviruses. <i>Journal of Virological Methods</i> , 2019, 271, 113685.	2.1	4
112	Development of a multiplex real-time RT-PCR assay for simultaneous detection and differentiation of influenza A, B, C, and D viruses. <i>Diagnostic Microbiology and Infectious Disease</i> , 2019, 95, 59-66.	1.8	7
113	Transcriptome profiling in Rift Valley fever virus infected cells reveals modified transcriptional and alternative splicing programs. <i>PLoS ONE</i> , 2019, 14, e0217497.	2.5	18
114	Plant Viruses in Plant Molecular Pharming: Toward the Use of Enveloped Viruses. <i>Frontiers in Plant Science</i> , 2019, 10, 803.	3.6	38
115	Identification of a Novel Hypovirulence-Inducing Hypovirus From <i>Alternaria alternata</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1076.	3.5	60
116	Criean-Congo hemorrhagic fever (CCHF) seroprevalence: A systematic review and meta-analysis. <i>Acta Tropica</i> , 2019, 196, 102-120.	2.0	53
117	Taxonomy of the order Mononegavirales: update 2019. <i>Archives of Virology</i> , 2019, 164, 1967-1980.	2.1	224
118	Biochemical characterization of recombinant Avihepatovirus 3C protease and its localization. <i>Virology Journal</i> , 2019, 16, 54.	3.4	10
119	Non-cultivated Cotton Species (<i>Gossypium</i> spp.) Act as a Reservoir for Cotton Leaf Curl Begomoviruses and Associated Satellites. <i>Plants</i> , 2019, 8, 127.	3.5	5
120	Hepatitis B virus infection among oncohematologic disease patients in Central Brazil: prevalence, risk factors and immunization. <i>Hematology, Transfusion and Cell Therapy</i> , 2019, 41, 199-204.	0.2	4
121	12 novel atypical porcine pestivirus genomes from neonatal piglets with congenital tremors: A newly emerging branch and high prevalence in China. <i>Virology</i> , 2019, 533, 50-58.	2.4	24
122	Genomic characterization of orthobunyavirus of veterinary importance in America. <i>Infection, Genetics and Evolution</i> , 2019, 73, 205-209.	2.3	4
123	A novel picornavirus in feces of a rainbow lorikeet (<i>Trichoglossus moluccanus</i>) shows a close relationship to members of the genus Avihepatovirus. <i>Archives of Virology</i> , 2019, 164, 1911-1914.	2.1	6
124	Characterization of a New Member of Alphacoronavirus with Unique Genomic Features in <i>Rhinolophus</i> Bats. <i>Viruses</i> , 2019, 11, 379.	3.3	28
125	The first complete genomic sequence of cardamom mosaic virus, a member of the genus Macluravirus (family Potyviridae). <i>Archives of Virology</i> , 2019, 164, 1723-1726.	2.1	4
126	Identification and genetic characterization of a novel Orthobunyavirus species by a straightforward high-throughput sequencing-based approach. <i>Scientific Reports</i> , 2019, 9, 3398.	3.3	5
127	Terminase Large Subunit Provides a New Drug Target for Herpesvirus Treatment. <i>Viruses</i> , 2019, 11, 219.	3.3	15

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128	Whole genome characterisation of quail deltacoronavirus detected in Poland. <i>Virus Genes</i> , 2019, 55, 243-247.	1.6	6
129	Discovery and genetic characterization of diverse smacoviruses in Zambian non-human primates. <i>Scientific Reports</i> , 2019, 9, 5045.	3.3	8
130	Modulation of the somatotrophic axis, adiponectin and cytokine secretion during highly pathogenic porcine reproductive and respiratory syndrome virus type 1 (HP-PRRSV-1) infection. <i>Research in Veterinary Science</i> , 2019, 124, 263-269.	1.9	3
131	Asymmetric evolution in viral overlapping genes is a source of selective protein adaptation. <i>Virology</i> , 2019, 532, 39-47.	2.4	17
132	The CARD9-Associated C-Type Lectin, Mincle, Recognizes La Crosse Virus (LACV) but Plays a Limited Role in Early Antiviral Responses against LACV. <i>Viruses</i> , 2019, 11, 303.	3.3	29
133	Infectious Virions of Bombyx Mori Latent Virus Are Incorporated into Bombyx Mori Nucleopolyhedrovirus Occlusion Bodies. <i>Viruses</i> , 2019, 11, 316.	3.3	3
134	In defence of taxonomic governance. <i>Organisms Diversity and Evolution</i> , 2019, 19, 87-97.	1.6	7
135	Crimean Congo hemorrhagic fever serosurvey in humans for identifying high-risk populations and high-risk areas in the endemic state of Gujarat, India. <i>BMC Infectious Diseases</i> , 2019, 19, 104.	2.9	24
136	Diterpenoid compounds from <i>Wedelia trilobata</i> induce resistance to Tomato spotted wilt virus via the JA signal pathway in tobacco plants. <i>Scientific Reports</i> , 2019, 9, 2763.	3.3	15
137	Structural and functional similarities in bunyaviruses: Perspectives for pan-bunya antivirals. <i>Reviews in Medical Virology</i> , 2019, 29, e2039.	8.3	21
138	Application of a sequence-based taxonomic classification method to uncultured and unclassified marine single-stranded RNA viruses in the order Picornavirales. <i>Virus Evolution</i> , 2019, 5, vez056.	4.9	19
139	Taxonomy of Viruses. , 2019, , .		7
140	Vertical transmission in <i>Caenorhabditis</i> nematodes of RNA molecules encoding a viral RNA-dependent RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24738-24747.	7.1	26
141	Detection and diversity of maize yellow mosaic virus infecting maize in Nigeria. <i>VirusDisease</i> , 2019, 30, 538-544.	2.0	6
142	Viromics Reveal a Number of Novel RNA Viruses in Swedish Mosquitoes. <i>Viruses</i> , 2019, 11, 1027.	3.3	28
143	Seroprevalences of Newly Discovered Porcine Pestiviruses in German Pig Farms. <i>Veterinary Sciences</i> , 2019, 6, 86.	1.7	13
144	CRISPR-Cas13d mediates robust RNA virus interference in plants. <i>Genome Biology</i> , 2019, 20, 263.	8.8	124
145	Rescue of infectious Arumowot virus from cloned cDNA: Posttranslational degradation of Arumowot virus NSs protein in human cells. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007904.	3.0	4

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146	Discovery of High Abundances of Aster-Like Nanoparticles in Pelagic Environments: Characterization and Dynamics. <i>Frontiers in Microbiology</i> , 2019, 10, 2376.	3.5	8
147	Seroprevalence and Associated Risk Factors of Rift Valley Fever in Domestic Small Ruminants in the North Region of Cameroon. <i>Veterinary Medicine International</i> , 2019, 2019, 1-8.	1.5	9
148	Development of RT-qPCR and semi-nested RT-PCR assays for molecular diagnosis of hantavirus pulmonary syndrome. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007884.	3.0	22
149	Suggestive Serological Evidence of Infection with Shrew-Borne Imjin Virus (Hantaviridae) in Humans. <i>Viruses</i> , 2019, 11, 1128.	3.3	3
150	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25900-25908.	7.1	165
151	An Epidemiological and Economic Simulation Model to Evaluate Strategies for the Control of Bovine Virus Diarrhea in Germany. <i>Frontiers in Veterinary Science</i> , 2019, 6, 406.	2.2	19
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