

Arvind Varsani

List of Publications by Year in descending order

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Version: 2024-02-01

335
papers

19,310
citations

18482

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355
all docs

355
docs citations

355
times ranked

12506
citing authors

#	ARTICLE	IF	CITATIONS
1	SDT: A Virus Classification Tool Based on Pairwise Sequence Alignment and Identity Calculation. PLoS ONE, 2014, 9, e108277.	2.5	1,208
2	ICTV Virus Taxonomy Profile: Geminiviridae. Journal of General Virology, 2017, 98, 131-133.	2.9	676
3	Revision of Begomovirus taxonomy based on pairwise sequence comparisons. Archives of Virology, 2015, 160, 1593-1619.	2.1	664
4	Virus taxonomy in the age of metagenomics. Nature Reviews Microbiology, 2017, 15, 161-168.	28.6	590
5	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.	2.1	567
6	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). Archives of Virology, 2017, 162, 2505-2538.	2.1	506
7	VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. Microbiome, 2021, 9, 37.	11.1	441
8	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	17.5	414
9	Global Organization and Proposed Megataxonomy of the Virus World. Microbiology and Molecular Biology Reviews, 2020, 84, .	6.6	378
10	Revisiting the taxonomy of the family Circoviridae: establishment of the genus Cyclovirus and removal of the genus Gyrovirus. Archives of Virology, 2017, 162, 1447-1463.	2.1	285
11	VIRIDICâ€”A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses, 2020, 12, 1268.	3.3	274
12	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). Archives of Virology, 2016, 161, 2921-2949.	2.1	263
13	The Spread of Tomato Yellow Leaf Curl Virus from the Middle East to the World. PLoS Pathogens, 2010, 6, e1001164.	4.7	259
14	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). Archives of Virology, 2019, 164, 2417-2429.	2.1	257
15	RDP5: a computer program for analyzing recombination in, and removing signals of recombination from, nucleotide sequence datasets. Virus Evolution, 2021, 7, veaa087.	4.9	257
16	Recombination Patterns in Aphthoviruses Mirror Those Found in Other Picornaviruses. Journal of Virology, 2006, 80, 11827-11832.	3.4	247
17	Capulavirus and Grablovirus: two new genera in the family Geminiviridae. Archives of Virology, 2017, 162, 1819-1831.	2.1	240
18	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	2.1	219

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19	Establishment of three new genera in the family Geminiviridae: Becurtovirus, Eragrovirus and Turncurtovirus. Archives of Virology, 2014, 159, 2193-2203.	2.1	218
20	Widely Conserved Recombination Patterns among Single-Stranded DNA Viruses. Journal of Virology, 2009, 83, 2697-2707.	3.4	216
21	A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus Mastrevirus (family Geminiviridae). Archives of Virology, 2013, 158, 1411-1424.	2.1	216
22	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). Archives of Virology, 2020, 165, 2737-2748.	2.1	202
23	The Ancient Evolutionary History of Polyomaviruses. PLoS Pathogens, 2016, 12, e1005574.	4.7	190
24	Recombination in Eukaryotic Single Stranded DNA Viruses. Viruses, 2011, 3, 1699-1738.	3.3	188
25	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	2.1	184
26	Begomovirus "melting pot"™ in the south-west Indian Ocean islands: molecular diversity and evolution through recombination. Journal of General Virology, 2007, 88, 3458-3468.	2.9	170
27	Evolution and ecology of plant viruses. Nature Reviews Microbiology, 2019, 17, 632-644.	28.6	166
28	Diverse circular ssDNA viruses discovered in dragonflies (Odonata: Epiprocta). Journal of General Virology, 2012, 93, 2668-2681.	2.9	163
29	ICTV Virus Taxonomy Profile: Circoviridae. Journal of General Virology, 2017, 98, 1997-1998.	2.9	147
30	Alphasatellitidae: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. Archives of Virology, 2018, 163, 2587-2600.	2.1	133
31	Geometagenomics illuminates the impact of agriculture on the distribution and prevalence of plant viruses at the ecosystem scale. ISME Journal, 2018, 12, 173-184.	9.8	132
32	Discovery of several thousand highly diverse circular DNA viruses. ELife, 2020, 9, .	6.0	131
33	Genomoviridae: a new family of widespread single-stranded DNA viruses. Archives of Virology, 2016, 161, 2633-2643.	2.1	129
34	Multiple origins of prokaryotic and eukaryotic single-stranded DNA viruses from bacterial and archaeal plasmids. Nature Communications, 2019, 10, 3425.	12.8	127
35	An 81-Nucleotide Deletion in SARS-CoV-2 ORF7a Identified from Sentinel Surveillance in Arizona (January to March 2020). Journal of Virology, 2020, 94, .	3.4	121
36	Recombination, decreased host specificity and increased mobility may have driven the emergence of maize streak virus as an agricultural pathogen. Journal of General Virology, 2008, 89, 2063-2074.	2.9	121

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37	A unicellular algal virus, <i>Emiliania huxleyi</i> virus 86, exploits an animal-like infection strategy. <i>Journal of General Virology</i> , 2009, 90, 2306-2316.	2.9	119
38	<i>Cressdnaviricota</i> : a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. <i>Journal of Virology</i> , 2020, 94, .	3.4	118
39	Brazilian Begomovirus Populations Are Highly Recombinant, Rapidly Evolving, and Segregated Based on Geographical Location. <i>Journal of Virology</i> , 2013, 87, 5784-5799.	3.4	115
40	Maize streak virus: an old and complex “emerging” pathogen. <i>Molecular Plant Pathology</i> , 2010, 11, 1-12.	4.2	113
41	A protocol for the rapid isolation of full geminivirus genomes from dried plant tissue. <i>Journal of Virological Methods</i> , 2008, 149, 97-102.	2.1	110
42	Dragonfly cyclovirus, a novel single-stranded DNA virus discovered in dragonflies (Odonata: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 542 T	2.9	110
43	Six novel begomoviruses infecting tomato and associated weeds in Southeastern Brazil. <i>Archives of Virology</i> , 2008, 153, 1985-1989.	2.1	108
44	Preservation of viral genomes in 700-y-old caribou feces from a subarctic ice patch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16842-16847.	7.1	107
45	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.	2.1	102
46	ICTV Virus Taxonomy Profile: Geminiviridae 2021. <i>Journal of General Virology</i> , 2021, 102, .	2.9	97
47	Sequence-based taxonomic framework for the classification of uncultured single-stranded DNA viruses of the family Genomoviridae. <i>Virus Evolution</i> , 2017, 3, vew037.	4.9	93
48	High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants. <i>Water Research</i> , 2021, 205, 117710.	11.3	93
49	Development of <i>phoH</i> as a Novel Signature Gene for Assessing Marine Phage Diversity. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7730-7739.	3.1	90
50	Revisiting the classification of curtoviruses based on genome-wide pairwise identity. <i>Archives of Virology</i> , 2014, 159, 1873-1882.	2.1	89
51	Kombucha: a novel model system for cooperation and conflict in a complex multi-species microbial ecosystem. <i>PeerJ</i> , 2019, 7, e7565.	2.0	89
52	Appearances Can Be Deceptive: Revealing a Hidden Viral Infection with Deep Sequencing in a Plant Quarantine Context. <i>PLoS ONE</i> , 2014, 9, e102945.	2.5	89
53	Rapid host adaptation by extensive recombination. <i>Journal of General Virology</i> , 2009, 90, 734-746.	2.9	88
54	Expression of Human papillomavirus type 16 major capsid protein in transgenic <i>Nicotiana tabacum</i> cv. Xanthi. <i>Archives of Virology</i> , 2003, 148, 1771-1786.	2.1	78

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55	Complex Recombination Patterns Arising during Geminivirus Coinfections Preserve and Demarcate Biologically Important Intra-Genome Interaction Networks. <i>PLoS Pathogens</i> , 2011, 7, e1002203.	4.7	78
56	Chimeric Human Papillomavirus Type 16 (HPV-16) L1 Particles Presenting the Common Neutralizing Epitope for the L2 Minor Capsid Protein of HPV-6 and HPV-16. <i>Journal of Virology</i> , 2003, 77, 8386-8393.	3.4	76
57	Characterisation of a diverse range of circular replication-associated protein encoding DNA viruses recovered from a sewage treatment oxidation pond. <i>Infection, Genetics and Evolution</i> , 2015, 31, 73-86.	2.3	76
58	Ongoing geographical spread of Tomato yellow leaf curl virus. <i>Virology</i> , 2016, 498, 257-264.	2.4	76
59	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017, 162, 1441-1446.	2.1	72
60	Pervasive Chimerism in the Replication-Associated Proteins of Uncultured Single-Stranded DNA Viruses. <i>Viruses</i> , 2018, 10, 187.	3.3	72
61	Global genetic diversity and geographical and host-species distribution of beak and feather disease virus isolates. <i>Journal of General Virology</i> , 2011, 92, 752-767.	2.9	71
62	A highly divergent South African geminivirus species illuminates the ancient evolutionary history of this family. <i>Virology Journal</i> , 2009, 6, 36.	3.4	70
63	Novel myco-like DNA viruses discovered in the faecal matter of various animals. <i>Virus Research</i> , 2013, 177, 209-216.	2.2	70
64	Identification of diverse circular single-stranded DNA viruses in adult dragonflies and damselflies (Insecta: Odonata) of Arizona and Oklahoma, USA. <i>Infection, Genetics and Evolution</i> , 2015, 30, 278-287.	2.3	67
65	Diverse circular replication-associated protein encoding viruses circulating in invertebrates within a lake ecosystem. <i>Infection, Genetics and Evolution</i> , 2016, 39, 304-316.	2.3	66
66	Successful application of FTA® Classic Card technology and use of bacteriophage Φ 29 DNA polymerase for large-scale field sampling and cloning of complete maize streak virus genomes. <i>Journal of Virological Methods</i> , 2007, 140, 100-105.	2.1	65
67	Circular replication-associated protein encoding DNA viruses identified in the faecal matter of various animals in New Zealand. <i>Infection, Genetics and Evolution</i> , 2016, 43, 151-164.	2.3	65
68	Post-translational cleavage of recombinantly expressed nitrilase from <i>Rhodococcus rhodochrous</i> J1 yields a stable, active helical form. <i>FEBS Journal</i> , 2007, 274, 2099-2108.	4.7	63
69	Smacoviridae: a new family of animal-associated single-stranded DNA viruses. <i>Archives of Virology</i> , 2018, 163, 2005-2015.	2.1	63
70	Molecular characterisation of a novel cassava associated circular ssDNA virus. <i>Virus Research</i> , 2012, 166, 130-135.	2.2	62
71	Alfalfa Leaf Curl Virus: an Aphid-Transmitted Geminivirus. <i>Journal of Virology</i> , 2015, 89, 9683-9688.	3.4	62
72	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	2.1	62

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73	Reconstructing the History of Maize Streak Virus Strain A Dispersal To Reveal Diversification Hot Spots and Its Origin in Southern Africa. <i>Journal of Virology</i> , 2011, 85, 9623-9636.	3.4	61
74	Transient expression of Human papillomavirus type 16 L1 protein in <i>Nicotiana benthamiana</i> using an infectious tobamovirus vector. <i>Virus Research</i> , 2006, 120, 91-96.	2.2	59
75	Evidence of ancient papillomavirus recombination. <i>Journal of General Virology</i> , 2006, 87, 2527-2531.	2.9	59
76	Plant-Produced Cottontail Rabbit Papillomavirus L1 Protein Protects against Tumor Challenge: a Proof-of-Concept Study. <i>Vaccine Journal</i> , 2006, 13, 845-853.	3.1	59
77	Experimental observations of rapid Maize streak virus evolution reveal a strand-specific nucleotide substitution bias. <i>Virology Journal</i> , 2008, 5, 104.	3.4	58
78	Further characterization of tomato-infecting begomoviruses in Brazil. <i>Archives of Virology</i> , 2012, 157, 747-752.	2.1	58
79	The global distribution of Banana bunchy top virus reveals little evidence for frequent recent, human-mediated long distance dispersal events. <i>Virus Evolution</i> , 2015, 1, vev009.	4.9	58
80	Dating the origins of the maize-adapted strain of maize streak virus, MSV-A. <i>Journal of General Virology</i> , 2009, 90, 3066-3074.	2.9	57
81	Extensive recombination detected among beak and feather disease virus isolates from breeding facilities in Poland. <i>Journal of General Virology</i> , 2013, 94, 1086-1095.	2.9	56
82	High global diversity of cycloviruses amongst dragonflies. <i>Journal of General Virology</i> , 2013, 94, 1827-1840.	2.9	56
83	Genome diversity and evidence of recombination and reassortment in nanoviruses from Europe. <i>Journal of General Virology</i> , 2014, 95, 1178-1191.	2.9	56
84	Apparent competition drives community-wide parasitism rates and changes in host abundance across ecosystem boundaries. <i>Nature Communications</i> , 2016, 7, 12644.	12.8	56
85	Genetic analysis of maize streak virus isolates from Uganda reveals widespread distribution of a recombinant variant. <i>Journal of General Virology</i> , 2007, 88, 3154-3165.	2.9	55
86	Diverse and highly recombinant anelloviruses associated with Weddell seals in Antarctica. <i>Virus Evolution</i> , 2017, 3, vex017.	4.9	55
87	Viruses associated with Antarctic wildlife: From serology based detection to identification of genomes using high throughput sequencing. <i>Virus Research</i> , 2018, 243, 91-105.	2.2	55
88	Taxonomic update for mammalian anelloviruses (family Anelloviridae). <i>Archives of Virology</i> , 2021, 166, 2943-2953.	2.1	55
89	Molecular characterisation of beak and feather disease virus (BFDV) in New Zealand and its implications for managing an infectious disease. <i>Archives of Virology</i> , 2012, 157, 1651-1663.	2.1	54
90	Towards inferring the global movement of beak and feather disease virus. <i>Virology</i> , 2014, 450-451, 24-33.	2.4	53

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91	Diverse small circular single-stranded DNA viruses identified in a freshwater pond on the McMurdo Ice Shelf (Antarctica). <i>Infection, Genetics and Evolution</i> , 2014, 26, 132-138.	2.3	53
92	Diverse small circular DNA viruses circulating amongst estuarine molluscs. <i>Infection, Genetics and Evolution</i> , 2015, 31, 284-295.	2.3	53
93	Cycloviruses, gemycircularviruses and other novel replication-associated protein encoding circular viruses in Pacific flying fox (<i>Pteropus tonganus</i>) faeces. <i>Infection, Genetics and Evolution</i> , 2016, 39, 279-292.	2.3	53
94	Predicting the zoonotic capacity of mammals to transmit SARS-CoV-2. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211651.	2.6	53
95	Experimental evidence indicating that mastreviruses probably did not co-diverge with their hosts. <i>Virology Journal</i> , 2009, 6, 104.	3.4	51
96	Unique genome organization of non-mammalian papillomaviruses provides insights into the evolution of viral early proteins. <i>Virus Evolution</i> , 2017, 3, vex027.	4.9	51
97	Binomial nomenclature for virus species: a consultation. <i>Archives of Virology</i> , 2020, 165, 519-525.	2.1	51
98	Virus discovery in all three major lineages of terrestrial arthropods highlights the diversity of single-stranded DNA viruses associated with invertebrates. <i>PeerJ</i> , 2018, 6, e5761.	2.0	51
99	A novel papillomavirus in Adélie penguin (<i>Pygoscelis adeliae</i>) faeces sampled at the Cape Crozier colony, Antarctica. <i>Journal of General Virology</i> , 2014, 95, 1352-1365.	2.9	50
100	Evolutionary history of ssDNA bacilladnaviruses features horizontal acquisition of the capsid gene from ssRNA nodaviruses. <i>Virology</i> , 2017, 504, 114-121.	2.4	50
101	East African cassava mosaic-like viruses from Africa to Indian ocean islands: molecular diversity, evolutionary history and geographical dissemination of a bipartite begomovirus. <i>BMC Evolutionary Biology</i> , 2012, 12, 228.	3.2	48
102	Turnip curly top virus, a highly divergent geminivirus infecting turnip in Iran. <i>Virus Research</i> , 2010, 152, 169-175.	2.2	47
103	Discovery of a novel mastrevirus and alphasatellite-like circular DNA in dragonflies (Eiprocta) from Puerto Rico. <i>Virus Research</i> , 2013, 171, 231-237.	2.2	45
104	Identification and molecular characterization of a single-stranded circular DNA virus with similarities to <i>Sclerotinia sclerotiorum</i> hypovirulence-associated DNA virus 1. <i>Archives of Virology</i> , 2014, 159, 1527-1531.	2.1	45
105	Evidence of inter-component recombination, intra-component recombination and reassortment in banana bunchy top virus. <i>Journal of General Virology</i> , 2012, 93, 1103-1119.	2.9	44
106	Mimicking filtration and transport of rotavirus and adenovirus in sand media using DNA-labeled, protein-coated silica nanoparticles. <i>Water Research</i> , 2014, 62, 167-179.	11.3	44
107	Notes on recombination and reassortment in multipartite/segmented viruses. <i>Current Opinion in Virology</i> , 2018, 33, 156-166.	5.4	44
108	Fulfilling Koch's postulates for beet curly top Iran virus and proposal for consideration of new genus in the family Geminiviridae. <i>Archives of Virology</i> , 2013, 158, 435-443.	2.1	43

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109	Establishment of five new genera in the family Geminiviridae: Citlodavirus, Maldovirus, Mulcrilevirus, Opunvirus, and Topilevirus. Archives of Virology, 2022, 167, 695-710.	2.1	43
110	Passion Fruit Chlorotic Mottle Virus: Molecular Characterization of a New Divergent Geminivirus in Brazil. Viruses, 2018, 10, 169.	3.3	42
111	Novel circular DNA viruses identified in Procordulia grayi and Xanthocnemis zealandica larvae using metagenomic approaches. Infection, Genetics and Evolution, 2014, 22, 134-141.	2.3	41
112	Identification of an avian polyomavirus associated with AdÃ©lie penguins (Pygoscelis adeliae). Journal of General Virology, 2015, 96, 851-857.	2.9	41
113	Discovery of Sclerotinia sclerotiorum Hypovirulence-Associated Virus-1 in Urban River Sediments of Heathcote and Styx Rivers in Christchurch City, New Zealand. Genome Announcements, 2013, 1, .	0.8	40
114	Begomovirus-Associated Satellite DNA Diversity Captured Through Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae). Viruses, 2016, 8, 36.	3.3	40
115	Molecular characterization and prevalence of two capulaviruses: Alfalfa leaf curl virus from France and Euphorbia caput-medusae latent virus from South Africa. Virology, 2016, 493, 142-153.	2.4	40
116	Integrating Viral Metagenomics into an Ecological Framework. Annual Review of Virology, 2021, 8, 133-158.	6.7	40
117	Molecular characterisation of dicot-infecting mastreviruses from Australia. Virus Research, 2012, 166, 13-22.	2.2	39
118	Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae) Reveal Novel Begomovirus Species in the New and Old Worlds. Viruses, 2015, 7, 5553-5570.	3.3	39
119	Genome sequences of a capulavirus infecting Plantago lanceolata in the Åland archipelago of Finland. Archives of Virology, 2017, 162, 2041-2045.	2.1	39
120	Evidence that dicot-infecting mastreviruses are particularly prone to inter-species recombination and have likely been circulating in Australia for longer than in Africa and the Middle East. Virology, 2013, 444, 282-291.	2.4	37
121	Discovery of a novel circular single-stranded DNA virus from porcine faeces. Archives of Virology, 2013, 158, 283-289.	2.1	36
122	Pigeon circoviruses display patterns of recombination, genomic secondary structure and selection similar to those of beak and feather disease viruses. Journal of General Virology, 2014, 95, 1338-1351.	2.9	36
123	Identification of a polyomavirus in Weddell seal (Leptonychotes weddellii) from the Ross Sea (Antarctica). Archives of Virology, 2017, 162, 1403-1407.	2.1	36
124	Single Stranded DNA Viruses Associated with Capybara Faeces Sampled in Brazil. Viruses, 2019, 11, 710.	3.3	36
125	From Spatial Metagenomics to Molecular Characterization of Plant Viruses: A Geminivirus Case Study. Advances in Virus Research, 2018, 101, 55-83.	2.1	34
126	Adsorption of Rotavirus, MS2 Bacteriophage and Surface-Modified Silica Nanoparticles to Hydrophobic Matter. Food and Environmental Virology, 2015, 7, 261-268.	3.4	33

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127	Genetic Characterization of a Recombinant Myxoma Virus in the Iberian Hare (<i>Lepus granatensis</i>). <i>Viruses</i> , 2019, 11, 530.	3.3	33
128	Family Genomoviridae: 2021 taxonomy update. <i>Archives of Virology</i> , 2021, 166, 2911-2926.	2.1	33
129	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	2.1	33
130	Complete sequences of tomato leaf curl Palampur virus isolates infecting cucurbits in Iran. <i>Archives of Virology</i> , 2009, 154, 1015-1018.	2.1	32
131	Genetic diversity and distribution of tomato-infecting begomoviruses in Iran. <i>Virus Genes</i> , 2009, 38, 311-319.	1.6	32
132	A deletion and point mutation study of the human papillomavirus type 16 major capsid gene. <i>Virus Research</i> , 2006, 122, 154-163.	2.2	31
133	Evidence of Pervasive Biologically Functional Secondary Structures within the Genomes of Eukaryotic Single-Stranded DNA Viruses. <i>Journal of Virology</i> , 2014, 88, 1972-1989.	3.4	31
134	Diverse single-stranded DNA viruses associated with honey bees (<i>Apis mellifera</i>). <i>Infection, Genetics and Evolution</i> , 2019, 71, 179-188.	2.3	31
135	Single-Stranded DNA Viruses in Antarctic Cryoconite Holes. <i>Viruses</i> , 2019, 11, 1022.	3.3	31
136	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	5.4	31
137	Identification of a Nanovirus-Alphasatellite Complex in <i>Sophora alopecuroides</i> . <i>Virus Research</i> , 2017, 235, 24-32.	2.2	30
138	Identification of circular single-stranded DNA viruses in faecal samples of Canada lynx (<i>Lynx</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 T Juan Mountains. <i>Infection, Genetics and Evolution</i> , 2018, 64, 1-8.	2.3	30
139	Diversity of Beet curly top Iran virus isolated from different hosts in Iran. <i>Virus Genes</i> , 2013, 46, 571-575.	1.6	29
140	Sex-Based Differences in AdÃ©lie Penguin (<i>Pygoscelis adeliae</i>) Chick Growth Rates and Diet. <i>PLoS ONE</i> , 2016, 11, e0149090.	2.5	29
141	A new isolate of beak and feather disease virus from endemic wild red-fronted parakeets (<i>Cyanoramphus novaezelandiae</i>) in New Zealand. <i>Archives of Virology</i> , 2010, 155, 613-620.	2.1	28
142	The Mechanism of the Amidases. <i>Journal of Biological Chemistry</i> , 2013, 288, 28514-28523.	3.4	28
143	Identification of novel Bromus- and Trifolium-associated circular DNA viruses. <i>Archives of Virology</i> , 2015, 160, 1303-1311.	2.1	28
144	Comparison of Illumina de novo assembled and Sanger sequenced viral genomes: A case study for RNA viruses recovered from the plant pathogenic fungus <i>Sclerotinia sclerotiorum</i> . <i>Virus Research</i> , 2016, 219, 51-57.	2.2	28

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145	Tracking effluent discharges in undisturbed stony soil and alluvial gravel aquifer using synthetic DNA tracers. <i>Science of the Total Environment</i> , 2017, 592, 144-152.	8.0	27
146	Comparative analysis of Panicum streak virus and Maize streak virus diversity, recombination patterns and phylogeography. <i>Virology Journal</i> , 2009, 6, 194.	3.4	26
147	Identification of Phytoplasmas Associated with Cultivated and Ornamental Plants in Kerman Province, Iran. <i>Journal of Phytopathology</i> , 2010, 158, 713-720.	1.0	26
148	Replicative intermediates of maize streak virus found during leaf development. <i>Journal of General Virology</i> , 2010, 91, 1077-1081.	2.9	26
149	Evidence of multiple introductions of beak and feather disease virus into the Pacific islands of Nouvelle-Calédonie (New Caledonia). <i>Journal of General Virology</i> , 2012, 93, 2466-2472.	2.9	26
150	Divergent evolutionary and epidemiological dynamics of cassava mosaic geminiviruses in Madagascar. <i>BMC Evolutionary Biology</i> , 2016, 16, 182.	3.2	26
151	Transmission of the Bean-Associated Cytorhabdovirus by the Whitefly Bemisia tabaci MEAM1. <i>Viruses</i> , 2020, 12, 1028.	3.3	26
152	Virus Discovery in Desert Tortoise Fecal Samples: Novel Circular Single-Stranded DNA Viruses. <i>Viruses</i> , 2020, 12, 143.	3.3	26
153	Metagenomic identification of a nodavirus and a circular ssDNA virus in semi-purified viral nucleic acids from the hepatopancreas of healthy Farfantepenaeus duorarum shrimp. <i>Diseases of Aquatic Organisms</i> , 2013, 105, 237-242.	1.0	26
154	Panicum streak virus diversity is similar to that observed for maize streak virus. <i>Archives of Virology</i> , 2008, 153, 601-604.	2.1	25
155	Incidence and natural hosts of Tomato leaf curl Palampur virus in Iran. <i>Australasian Plant Pathology</i> , 2013, 42, 195-203.	1.0	25
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157	Novel sugarcane streak and sugarcane streak Reunion mastreviruses from southern Africa and La Réunion. <i>Archives of Virology</i> , 2008, 153, 605-609.	2.1	24
158	Genetic diversity and host range studies of turnip curly top virus. <i>Virus Genes</i> , 2013, 46, 345-353.	1.6	24
159	Discovery of a novel circular DNA virus in the Forbes sea star, Asterias forbesi. <i>Archives of Virology</i> , 2015, 160, 2349-2351.	2.1	24
160	Unravelling the Single-Stranded DNA Virome of the New Zealand Blackfly. <i>Viruses</i> , 2019, 11, 532.	3.3	24
161	Australian monocot-infecting mastrevirus diversity rivals that in Africa. <i>Virus Research</i> , 2012, 169, 127-136.	2.2	23
162	Molecular characterisation of an avihepadnavirus isolated from Psittacula krameri (ring-necked) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	2.1	23

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164	Molecular diversity of turncurtoviruses in Iran. <i>Archives of Virology</i> , 2016, 161, 551-561.	2.1	22
165	Unveiling Crucivirus Diversity by Mining Metagenomic Data. <i>MBio</i> , 2020, 11, .	4.1	22
166	Restoration of native folding of single-stranded DNA sequences through reverse mutations: An indication of a new epigenetic mechanism. <i>Archives of Biochemistry and Biophysics</i> , 2006, 453, 108-122.	3.0	21
167	A unique isolate of beak and feather disease virus isolated from budgerigars (<i>Melopsittacus</i>) Tj ETQq1 1 0.784314 ggBT /Overlock 10 TF	2.1	21
168	Analysis of Iranian Potato virus S isolates. <i>Virus Genes</i> , 2011, 43, 281-288.	1.6	21
169	First Report of Maize yellow mosaic virus Infecting Maize in Brazil. <i>Plant Disease</i> , 2017, 101, 2156.	1.4	21
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171	Structural and biochemical characterization of a nitrilase from the thermophilic bacterium, <i>Geobacillus pallidus</i> RAPc8. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 143-153.	3.6	20
172	Novel ssDNA virus recovered from estuarine Mollusc (<i>Amphibola crenata</i>) whose replication associated protein (Rep) shares similarities with Rep-like sequences of bacterial origin. <i>Journal of General Virology</i> , 2013, 94, 1104-1110.	2.9	20
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175	A novel geminivirus identified in tomato and cleome plants sampled in Brazil. <i>Virus Research</i> , 2017, 240, 175-179.	2.2	20
176	Occurrence of a novel mastrevirus in sugarcane germplasm collections in Florida, Guadeloupe and R��union. <i>Virology Journal</i> , 2017, 14, 146.	3.4	20
177	Risk assessment of SARS-CoV-2 in Antarctic wildlife. <i>Science of the Total Environment</i> , 2021, 755, 143352.	8.0	20
178	Viral Aggregation: The Knowns and Unknowns. <i>Viruses</i> , 2022, 14, 438.	3.3	20
179	Intergeneric recombination between a new, spinach-infecting curtovirus and a new geminivirus belonging to the genus Becurtovirus: first New World exemplar. <i>Archives of Virology</i> , 2013, 158, 2245-2254.	2.1	19
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182	New strains of chickpea chlorotic dwarf virus discovered on diseased papaya and tomato plants in Burkina Faso. <i>Archives of Virology</i> , 2017, 162, 1791-1794.	2.1	19
183	Fish polyomaviruses belong to two distinct evolutionary lineages. <i>Journal of General Virology</i> , 2018, 99, 567-573.	2.9	19
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185	First World Report of Cucurbit Aphid-Borne Yellows Virus Infecting Passionfruit. <i>Plant Disease</i> , 2018, 102, 2665-2665.	1.4	18
186	Identification of a Novel Adenovirus Penguin Circovirus at Cape Crozier (Ross Island, Antarctica). <i>Viruses</i> , 2019, 11, 1088.	3.3	18
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198	A new African streak virus species from Nigeria. <i>Archives of Virology</i> , 2008, 153, 1407-1410.	2.1	15

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210	Identification of Starling Circovirus in an Estuarine Mollusc (Amphibola crenata) in New Zealand Using Metagenomic Approaches. Genome Announcements, 2013, 1, .	0.8	14
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212	Discovery of the first maize-infecting mastrevirus in the Americas using a vector-enabled metagenomics approach. Archives of Virology, 2018, 163, 263-267.	2.1	14
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227	Symptom evolution following the emergence of maize streak virus. ELife, 2020, 9, .	6.0	13
228	Diverse single-stranded DNA viruses identified in New Zealand (Aotearoa) South Island robin (Petroica) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.4	13
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233	The Westward Journey of Alfalfa Leaf Curl Virus. Viruses, 2018, 10, 542.	3.3	12
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236	Recombination patterns in dicot-infecting mastreviruses mirror those found in monocot-infecting mastreviruses. <i>Archives of Virology</i> , 2011, 156, 1463-1469.	2.1	11
237	A novel maize-infecting mastrevirus from La Réunion Island. <i>Archives of Virology</i> , 2012, 157, 1617-1621.	2.1	11
238	Analysis of watermelon chlorotic stunt virus and tomato leaf curl Palampur virus mixed and pseudo-recombination infections. <i>Virus Genes</i> , 2015, 51, 408-416.	1.6	11
239	Molecular diversity, geographic distribution and host range of monocot-infecting mastreviruses in Africa and surrounding islands. <i>Virus Research</i> , 2017, 238, 171-178.	2.2	11
240	Genomoviruses associated with mountain and western pine beetles. <i>Virus Research</i> , 2018, 256, 17-20.	2.2	11
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249	Genome Sequences of Two Single-Stranded DNA Viruses Identified in <i>Varroa destructor</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	10
250	Identification and Distribution of Novel Cressdnaviruses and Circular Molecules in Four Penguin Species in South Georgia and the Antarctic Peninsula. <i>Viruses</i> , 2020, 12, 1029.	3.3	10
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268	Comparative analysis of common regions found in babuviruses and alphasatellite molecules. <i>Archives of Virology</i> , 2017, 162, 849-855.	2.1	8
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270	Identification of a new turncurtovirus in the leafhopper <i>Circulifer haematocephus</i> and the host plant species <i>Sesamum indicum</i> . <i>Virus Genes</i> , 2018, 54, 840-845.	1.6	8

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279	Genome Sequences of Microviruses Associated with <i>Coptotermes formosanus</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
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281	Genome characterization of parsley severe stunt-associated virus in Iran. <i>Virus Genes</i> , 2021, 57, 293-301.	1.6	7
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286	Adaptive evolution by recombination is not associated with increased mutation rates in Maize streak virus. <i>BMC Evolutionary Biology</i> , 2012, 12, 252.	3.2	6
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292	Known and New Emerging Viruses Infecting Blueberry. Plants, 2021, 10, 2172.	3.5	6
293	Diverse Single-Stranded DNA Viruses Identified in Chicken Buccal Swabs. Microorganisms, 2021, 9, 2602.	3.6	6
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301	First report of <i>Chickpea chlorotic dwarf virus</i> naturally infecting chickpea in Tunisia. New Disease Reports, 2015, 32, 16-16.	0.8	5
302	In Silico Characterisation of Putative Prophages in Lactobacillaceae Used in Probiotics for Vaginal Health. Microorganisms, 2022, 10, 214.	3.6	5
303	Coevolutionary Analysis Implicates Toll-Like Receptor 9 in Papillomavirus Restriction. MBio, 2022, 13, e0005422.	4.1	5
304	Detection of human, porcine and canine picornaviruses in municipal sewage sludge using pan-enterovirus amplicon-based long-read Illumina sequencing. Emerging Microbes and Infections, 2022, 11, 1339-1342.	6.5	5
305	Genome Sequence of a Single-Stranded DNA Virus Identified in Gila Monster Feces. Microbiology Resource Announcements, 2018, 7, .	0.6	4
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309	Poxvirus infection in house finches (<i>Haemorhous mexicanus</i>): Genome sequence analysis and patterns of infection in wild birds. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	3.0	4
310	Canine picornaviruses detected in wastewater in Arizona, USA 2019 and 2021. <i>Infection, Genetics and Evolution</i> , 2022, 103, 105315.	2.3	4
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