List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genomic analysis of uncultured marine viral communities. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14250-14255.	7.1	874
2	The Marine Viromes of Four Oceanic Regions. PLoS Biology, 2006, 4, e368.	5.6	867
3	Functional metagenomic profiling of nine biomes. Nature, 2008, 452, 629-632.	27.8	842
4	Metagenomic Analyses of an Uncultured Viral Community from Human Feces. Journal of Bacteriology, 2003, 185, 6220-6223.	2.2	699
5	Here a virus, there a virus, everywhere the same virus?. Trends in Microbiology, 2005, 13, 278-284.	7.7	687
6	Virus taxonomy in the age of metagenomics. Nature Reviews Microbiology, 2017, 15, 161-168.	28.6	590
7	RNA Viral Community in Human Feces: Prevalence of Plant Pathogenic Viruses. PLoS Biology, 2005, 4, e3.	5.6	589
8	Laboratory procedures to generate viral metagenomes. Nature Protocols, 2009, 4, 470-483.	12.0	530
9	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. Applied and Environmental Microbiology, 2007, 73, 7059-7066.	3.1	480
10	Marine Viruses: Truth or Dare. Annual Review of Marine Science, 2012, 4, 425-448.	11.6	457
11	Phage puppet masters of the marine microbial realm. Nature Microbiology, 2018, 3, 754-766.	13.3	438
12	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	17.5	414
13	Using pyrosequencing to shed light on deep mine microbial ecology. BMC Genomics, 2006, 7, 57.	2.8	405
14	Viral and microbial community dynamics in four aquatic environments. ISME Journal, 2010, 4, 739-751.	9.8	387
15	Diversity of bacteria associated with the Caribbean coral Montastraea franksi. Coral Reefs, 2001, 20, 85-91.	2.2	361
16	Viral diversity and dynamics in an infant gut. Research in Microbiology, 2008, 159, 367-373.	2.1	288
17	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
18	Densovirus associated with sea-star wasting disease and mass mortality. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17278-17283	7.1	276

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19	Diversity and population structure of a near–shore marine–sediment viral community. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 565-574.	2.6	272
20	Transposases are the most abundant, most ubiquitous genes in nature. Nucleic Acids Research, 2010, 38, 4207-4217.	14.5	270
21	Metagenomic analysis of viruses in reclaimed water. Environmental Microbiology, 2009, 11, 2806-2820.	3.8	259
22	<i>Pepper Mild Mottle Virus</i> as an Indicator of Fecal Pollution. Applied and Environmental Microbiology, 2009, 75, 7261-7267.	3.1	259
23	A field guide to eukaryotic circular single-stranded DNA viruses: insights gained from metagenomics. Archives of Virology, 2012, 157, 1851-1871.	2.1	254
24	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. Nature, 2008, 452, 340-343.	27.8	251
25	Exploring the viral world through metagenomics. Current Opinion in Virology, 2011, 1, 289-297.	5.4	235
26	Role of elevated organic carbon levels and microbial activity in coral mortality. Marine Ecology - Progress Series, 2006, 314, 119-125.	1.9	233
27	Exploring the Vast Diversity of Marine Viruses. Oceanography, 2007, 20, 135-139.	1.0	224
28	Metagenomic and stable isotopic analyses of modern freshwater microbialites in Cuatro Ciénegas, Mexico. Environmental Microbiology, 2009, 11, 16-34.	3.8	204
29	Global distribution of nearly identical phage-encoded DNA sequences. FEMS Microbiology Letters, 2004, 236, 249-256.	1.8	193
30	FastGroupII: a web-based bioinformatics platform for analyses of large 16S rDNA libraries. BMC Bioinformatics, 2006, 7, 57.	2.6	186
31	Broad Surveys of DNA Viral Diversity Obtained through Viral Metagenomics of Mosquitoes. PLoS ONE, 2011, 6, e20579.	2.5	185
32	Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. PeerJ, 2016, 4, e2777.	2.0	185
33	PHACCS, an online tool for estimating the structure and diversity of uncultured viral communities using metagenomic information. BMC Bioinformatics, 2005, 6, 41.	2.6	182
34	Diverse circular ssDNA viruses discovered in dragonflies (Odonata: Epiprocta). Journal of General Virology, 2012, 93, 2668-2681.	2.9	163
35	Phage Community Dynamics in Hot Springs. Applied and Environmental Microbiology, 2004, 70, 1633-1640.	3.1	162
36	Evaluation of Filtration and DNA Extraction Methods for Environmental DNA Biodiversity Assessments across Multiple Trophic Levels. Frontiers in Marine Science, 2017, 4, .	2.5	160

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37	The complete genomic sequence of the marine phage Roseophage SIO1 shares homology with nonmarine phages. Limnology and Oceanography, 2000, 45, 408-418.	3.1	154
38	Environmental DNA reveals seasonal shifts and potential interactions in a marine community. Nature Communications, 2020, 11, 254.	12.8	154
39	Eukaryotic Circular Rep-Encoding Single-Stranded DNA (CRESS DNA) Viruses: Ubiquitous Viruses With Small Genomes and a Diverse Host Range. Advances in Virus Research, 2019, 103, 71-133.	2.1	151
40	Method for discovering novel DNA viruses in blood using viral particle selection and shotgun sequencing. BioTechniques, 2005, 39, 729-736.	1.8	150
41	ICTV Virus Taxonomy Profile: Circoviridae. Journal of General Virology, 2017, 98, 1997-1998.	2.9	147
42	Diverse circovirus-like genome architectures revealed by environmental metagenomics. Journal of General Virology, 2009, 90, 2418-2424.	2.9	145
43	Coral-associated Archaea. Marine Ecology - Progress Series, 2004, 273, 89-96.	1.9	140
44	A bacterial metapopulation adapts locally to phage predation despite global dispersal. Genome Research, 2008, 18, 293-297.	5.5	135
45	Frequent Detection of Highly Diverse Variants of <i>Cardiovirus</i> , <i>Cosavirus</i> , <i>Bocavirus</i> , and <i>Circovirus</i> in Sewage Samples Collected in the United States. Journal of Clinical Microbiology, 2009, 47, 3507-3513.	3.9	135
46	Comparative metagenomics of microbial traits within oceanic viral communities. ISME Journal, 2011, 5, 1178-1190.	9.8	135
47	Ocean time-series reveals recurring seasonal patterns of virioplankton dynamics in the northwestern Sargasso Sea. ISME Journal, 2012, 6, 273-284.	9.8	133
48	Pepper mild mottle virus: A plant pathogen with a greater purpose in (waste)water treatment development and public health management. Water Research, 2018, 144, 1-12.	11.3	130
49	Eukaryotic Viruses in Wastewater Samples from the United States. Applied and Environmental Microbiology, 2009, 75, 1402-1409.	3.1	126
50	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2015). Archives of Virology, 2015, 160, 1837-1850.	2.1	126
51	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. BMC Evolutionary Biology, 2013, 13, 33.	3.2	123
52	Discovery of a Novel Single-Stranded DNA Virus from a Sea Turtle Fibropapilloma by Using Viral Metagenomics. Journal of Virology, 2009, 83, 2500-2509.	3.4	119
53	<i>Cressdnaviricota</i> : a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. Journal of Virology, 2020, 94, .	3.4	118
54	A case study of enteric virus removal and insights into the associated risk of water reuse for two wastewater treatment pond systems in Bolivia. Water Research, 2014, 65, 257-270.	11.3	112

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55	Dragonfly cyclovirus, a novel single-stranded DNA virus discovered in dragonflies (Odonata:) Tj ETQq1 1 0.784314	ŀrg₿T /O	verlock 10 Th
56	Evaluation of marine zooplankton community structure through environmental DNA metabarcoding. Limnology and Oceanography: Methods, 2018, 16, 209-221.	2.0	108
57	Global distribution of nearly identical phage-encoded DNA sequences. FEMS Microbiology Letters, 2004, 236, 249-256.	1.8	105
58	Exploring the Diversity of Plant DNA Viruses and Their Satellites Using Vector-Enabled Metagenomics on Whiteflies. PLoS ONE, 2011, 6, e19050.	2.5	102
59	Diversity and distribution of single-stranded DNA phages in the North Atlantic Ocean. ISME Journal, 2011, 5, 822-830.	9.8	99
60	Membrane vesicles in sea water: heterogeneous DNA content and implications for viral abundance estimates. ISME Journal, 2017, 11, 394-404.	9.8	96
61	Development of <i>phoH</i> as a Novel Signature Gene for Assessing Marine Phage Diversity. Applied and Environmental Microbiology, 2011, 77, 7730-7739.	3.1	90
62	Single-stranded DNA phages: from early molecular biology tools to recent revolutions in environmental microbiology. FEMS Microbiology Letters, 2016, 363, fnw027.	1.8	88
63	Novel anellovirus discovered from a mortality event of captive California sea lions. Journal of General Virology, 2009, 90, 1256-1261.	2.9	85
64	Managing Microbial Risks from Indirect Wastewater Reuse for Irrigation in Urbanizing Watersheds. Environmental Science & Technology, 2016, 50, 6803-6813.	10.0	83
65	Diversity of virus–host systems in hypersaline Lake Retba, Senegal. Environmental Microbiology, 2011, 13, 1956-1972.	3.8	82
66	Use of Fluorescently Labeled Phage in the Detection and Identification of Bacterial Species. Applied Spectroscopy, 2003, 57, 1138-1144.	2.2	80
67	Widespread association of a Rickettsiales-like bacterium with reef-building corals. Environmental Microbiology, 2004, 6, 1137-1148.	3.8	79
68	Diversity of environmental single-stranded DNA phages revealed by PCR amplification of the partial major capsid protein. ISME Journal, 2014, 8, 2093-2103.	9.8	71
69	Novel circular single-stranded DNA viruses identified in marine invertebrates reveal high sequence diversity and consistent predicted intrinsic disorder patterns within putative structural proteins. Frontiers in Microbiology, 2015, 6, 696.	3.5	69
70	Assessing eukaryotic biodiversity in the Florida Keys National Marine Sanctuary through environmental DNA metabarcoding. Ecology and Evolution, 2019, 9, 1029-1040.	1.9	69
71	Molecular and microscopic evidence of viruses in marine copepods. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1375-1380.	7.1	67
72	Genomic analysis of multiple Roseophage SIO1 strains. Environmental Microbiology, 2009, 11, 2863-2873.	3.8	64

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73	Metagenomic identification of a novel anellovirus in Pacific harbor seal (Phoca vitulina richardsii) lung samples and its detection in samples from multiple years. Journal of General Virology, 2011, 92, 1318-1323.	2.9	61
74	Phage Encoded H-NS: A Potential Achilles Heel in the Bacterial Defence System. PLoS ONE, 2011, 6, e20095.	2.5	59
75	Metagenomic Analysis of Lysogeny in Tampa Bay: Implications for Prophage Gene Expression. PLoS ONE, 2008, 3, e3263.	2.5	58
76	Variability and host density independence in inductions-based estimates of environmental lysogeny. Nature Microbiology, 2017, 2, 17064.	13.3	57
77	High global diversity of cycloviruses amongst dragonflies. Journal of General Virology, 2013, 94, 1827-1840.	2.9	56
78	Diverse and highly recombinant anelloviruses associated with Weddell seals in Antarctica. Virus Evolution, 2017, 3, vex017.	4.9	55
79	Metagenomic sequencing for virus identification in a public-health setting. Journal of General Virology, 2010, 91, 2846-2856.	2.9	53
80	The Ferrojan Horse Hypothesis: Iron-Virus Interactions in the Ocean. Frontiers in Marine Science, 2016, 3, .	2.5	53
81	Faecal pollution along the southeastern coast of Florida and insight into the use of pepper mild mottle virus as an indicator. Journal of Applied Microbiology, 2016, 121, 1469-1481.	3.1	53
82	Unprecedented Diversity of ssDNA Phages from the Family Microviridae Detected within the Gut of a Protochordate Model Organism (Ciona robusta). Viruses, 2018, 10, 404.	3.3	53
83	Widespread occurrence of phage-encoded exotoxin genes in terrestrial and aquatic environments in Southern California. FEMS Microbiology Letters, 2006, 261, 141-149.	1.8	52
84	Power law rank–abundance models for marine phage communities. FEMS Microbiology Letters, 2007, 273, 224-228.	1.8	51
85	Virus discovery in all three major lineages of terrestrial arthropods highlights the diversity of single-stranded DNA viruses associated with invertebrates. PeerJ, 2018, 6, e5761.	2.0	51
86	Comparative metagenomics: natural populations of induced prophages demonstrate highly unique, lower diversity viral sequences. Environmental Microbiology, 2014, 16, 570-585.	3.8	50
87	Microbial source tracking in shellfish harvesting waters in the Gulf of Nicoya, Costa Rica. Water Research, 2017, 111, 177-184.	11.3	48
88	RNA Viral Metagenome of Whiteflies Leads to the Discovery and Characterization of a Whitefly-Transmitted Carlavirus in North America. PLoS ONE, 2014, 9, e86748.	2.5	46
89	Discovery of a novel mastrevirus and alphasatellite-like circular DNA in dragonflies (Epiprocta) from Puerto Rico. Virus Research, 2013, 171, 231-237.	2.2	45
90	Spatial heterogeneity of bacterial communities in the mucus of Montastraea annularis. Marine Ecology - Progress Series, 2011, 426, 29-40.	1.9	45

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91	Deep sequencing of the viral <i>phoH</i> gene reveals temporal variation, depth-specific composition, and persistent dominance of the same viral <i>phoH</i> genes in the Sargasso Sea. PeerJ, 2015, 3, e997.	2.0	44
92	A Framework for a Marine Biodiversity Observing Network Within Changing Continental Shelf Seascapes. Oceanography, 2014, 27, 18-23.	1.0	43
93	Microbial communities associated with skeletal tumors onPorites compressa. FEMS Microbiology Letters, 2005, 243, 431-436.	1.8	42
94	Pepper mild mottle virus: Agricultural menace turned effective tool for microbial water quality monitoring and assessing (waste)water treatment technologies. PLoS Pathogens, 2019, 15, e1007639.	4.7	41
95	Begomovirus-Associated Satellite DNA Diversity Captured Through Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae). Viruses, 2016, 8, 36.	3.3	40
96	Relationships among microbial indicators of fecal pollution, microbial source tracking markers, and pathogens in Costa Rican coastal waters. Water Research, 2021, 188, 116507.	11.3	40
97	Vector-Enabled Metagenomic (VEM) Surveys Using Whiteflies (Aleyrodidae) Reveal Novel Begomovirus Species in the New and OldWorlds. Viruses, 2015, 7, 5553-5570.	3.3	39
98	Bacterial communities associated with the ctenophores Mnemiopsis leidyi and Beroe ovata. FEMS Microbiology Ecology, 2012, 82, 90-101.	2.7	37
99	Novel cyclovirus discovered in the Florida woods cockroach Eurycotis floridana (Walker). Archives of Virology, 2013, 158, 1389-1392.	2.1	35
100	Diversity of DNA and RNA Viruses in Indoor Air As Assessed via Metagenomic Sequencing. Environmental Science & Technology, 2018, 52, 1014-1027.	10.0	35
101	Spatially Resolved Genomic, Stable Isotopic, and Lipid Analyses of a Modern Freshwater Microbialite from Cuatro Ciénegas, Mexico. Astrobiology, 2012, 12, 685-698.	3.0	33
102	Metagenomic identification, seasonal dynamics, and potential transmission mechanisms of a <i>Daphnia</i> â€associated singleâ€stranded DNA virus in two temperate lakes. Limnology and Oceanography, 2013, 58, 1605-1620.	3.1	33
103	Affordable Enteric Virus Detection Techniques Are Needed to Support Changing Paradigms in Water Quality Management. Clean - Soil, Air, Water, 2015, 43, 8-12.	1.1	29
104	Multidimensional metrics for estimating phage abundance, distribution, gene density, and sequence coverage in metagenomes. Frontiers in Microbiology, 2015, 6, 381.	3.5	28
105	Removal of Six Estrogenic Endocrine-Disrupting Compounds (EDCs) from Municipal Wastewater Using Aluminum Electrocoagulation. Water (Switzerland), 2016, 8, 128.	2.7	28
106	Reduction of nutrients, microbes and personal care products in domestic wastewater by a benchtop electrocoagulation unit. Scientific Reports, 2015, 5, 9380.	3.3	26
107	Metagenomic identification of a nodavirus and a circular ssDNA virus in semi-purified viral nucleic acids from the hepatopancreas of healthy Farfantepenaeus duorarum shrimp. Diseases of Aquatic Organisms, 2013, 105, 237-242.	1.0	26
108	Discovery of a novel circular DNA virus in the Forbes sea star, Asterias forbesi. Archives of Virology, 2015, 160, 2349-2351.	2.1	24

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109	Disparity between planktonic fish egg and larval communities as indicated by DNA barcoding. Marine Ecology - Progress Series, 2014, 503, 195-204.	1.9	23
110	Genomic evolution, recombination, and inter-strain diversity of chelonid alphaherpesvirus 5 from Florida and Hawaii green sea turtles with fibropapillomatosis. PeerJ, 2018, 6, e4386.	2.0	23
111	Prokaryotic and Viral Community Composition of Freshwater Springs in Florida, USA. MBio, 2020, 11, .	4.1	22
112	PhiSiGns: an online tool to identify signature genes in phages and design PCR primers for examining phage diversity. BMC Bioinformatics, 2012, 13, 37.	2.6	21
113	Distinct Lineage of Vesiculovirus from Big Brown Bats, United States. Emerging Infectious Diseases, 2013, 19, 1978-1980.	4.3	21
114	Population genomics of three deep-sea cephalopod species reveals connectivity between the Gulf of Mexico and northwestern Atlantic Ocean. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 158, 103222.	1.4	21
115	Discovery, Prevalence, and Persistence of Novel Circular Single-Stranded DNA Viruses in the Ctenophores Mnemiopsis leidyi and Beroe ovata. Frontiers in Microbiology, 2015, 6, 1427.	3.5	18
116	Isolation and Characterization of a Shewanella Phage–Host System from the Gut of the Tunicate, Ciona intestinalis. Viruses, 2017, 9, 60.	3.3	18
117	DNA barcoding of fish eggs collected off northwestern Cuba and across the Florida Straits demonstrates egg transport by mesoscale eddies. Fisheries Oceanography, 2020, 29, 340-348.	1.7	18
118	The gut virome of the protochordate model organism, Ciona intestinalis subtype A. Virus Research, 2018, 244, 137-146.	2.2	17
119	Regeneration of macronutrients and trace metals during phytoplankton decay: An experimental study. Limnology and Oceanography, 2020, 65, 1936-1960.	3.1	17
120	Water column stratification structures viral community composition in the Sargasso Sea. Aquatic Microbial Ecology, 2015, 76, 85-94.	1.8	16
121	<scp>DNA</scp> barcoding reveals clear delineation between spawning sites for neritic versus oceanic fishes in the Gulf of Mexico. Fisheries Oceanography, 2019, 28, 228-239.	1.7	14
122	Zoonotic Infection With Pigeon Paramyxovirus Type 1 Linked to Fatal Pneumonia. Journal of Infectious Diseases, 2018, 218, 1037-1044.	4.0	11
123	Discovery of Four Novel Circular Single-Stranded DNA Viruses in Fungus-Farming Termites. Genome Announcements, 2018, 6, .	0.8	11
124	Genome Sequence of PM2-Like Phage Cr39582, Induced from a Pseudoalteromonas sp. Isolated from the Gut of Ciona robusta. Genome Announcements, 2018, 6, .	0.8	10
125	Spatial and Temporal Dynamics of Prokaryotic and Viral Community Assemblages in a Lotic System (Manatee Springs, Florida). Applied and Environmental Microbiology, 2021, 87, e0064621.	3.1	10

126 Phage Ecology and Bacterial Pathogenesis. , 0, , 66-91.

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127	Development of a Serological Assay for the Sea Lion (Zalophus californianus) Anellovirus, ZcAV. Scientific Reports, 2015, 5, 9637.	3.3	7
128	A Brilliant Impostor?. Oceanography, 2014, 27, 14-14.	1.0	5
129	Genome Sequence of <i>Euphorbia mosaic virus</i> from Passionfruit and <i>Euphorbia heterophylla</i> in Florida. Genome Announcements, 2017, 5, .	0.8	5
130	Discovery of a novel potexvirus in the seagrass <i>Thalassia testudinum</i> from Tampa Bay, Florida. Limnology and Oceanography Letters, 2019, 4, 1-8.	3.9	5
131	Prevalence of a vertically transmitted single-stranded DNA virus in spinybacked orbweavers (Gasteracantha cancriformis) from Florida, USA. Journal of General Virology, 2019, 100, 1253-1265.	2.9	5
132	Phage Eco-Locator: a web tool for visualization and analysis of phage genomes in metagenomic data sets. BMC Bioinformatics, 2011, 12, .	2.6	4
133	Adaptation of the polony technique to quantify <i>Gokushovirinae</i> , a diverse group of singleâ€stranded <scp>DNA</scp> phage. Environmental Microbiology, 2021, 23, 6622-6636.	3.8	3
134	Genome Sequence of Vibrio natriegens Phage vB_VnaS-AQKL99. Microbiology Resource Announcements, 2020, 9, .	0.6	2
135	MOLECULAR SURVEILLANCE OF PLANT VIRUSES: IDENTIFICATION OF NEW AND EMERGING VIRUSES OF TOMATO BEFORE THEY CAUSE EPIDEMICS. Acta Horticulturae, 2015, , 127-131.	0.2	1
136	Near-Complete Genome Sequence of a Novel Single-Stranded RNA Virus Discovered in Indoor Air. Genome Announcements, 2018, 6, .	0.8	1
137	DNA Detectives: Outreach Activity Teaching Students to Identify Fish Eggs Using DNA Barcoding â€. Journal of Microbiology and Biology Education, 2021, 22, .	1.0	1
138	First-year graduate courses foster inclusion. Nature Geoscience, 2021, 14, 539-540.	12.9	1
139	Dissolved Inorganic Carbon-Accumulating Complexes from Autotrophic Bacteria from Extreme Environments. Journal of Bacteriology, 2021, 203, e0037721.	2.2	1
140	Diversity and population structure of uncultured marine viral communities. , 2003, , .		0
141	Elementary Student Outreach Activity Demonstrating the Use of Phage Therapy Heroes to Combat Bacterial Infections. Journal of Microbiology and Biology Education, 2018, 19, .	1.0	0