

# Marine DNA Viral Macro- and Microdiversity from Pole

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Anticancer Drug Discovery Potential of Marine Invertebrates from Russian Pacific. <i>Marine Drugs</i> , 2019, 17, 474.	4.6	16
2	Bacteriophages in Natural and Artificial Environments. <i>Pathogens</i> , 2019, 8, 100.	2.8	124
3	Evolution and ecology of plant viruses. <i>Nature Reviews Microbiology</i> , 2019, 17, 632-644.	28.6	166
4	Viral Communities in the Global Deep Ocean Conveyor Belt Assessed by Targeted Viromics. <i>Frontiers in Microbiology</i> , 2019, 10, 1801.	3.5	21
5	Pole-to-pole ocean viromes. <i>Nature Methods</i> , 2019, 16, 575-575.	19.0	0
6	A Review on Viral Metagenomics in Extreme Environments. <i>Frontiers in Microbiology</i> , 2019, 10, 2403.	3.5	54
7	Studying the gut virome in the metagenomic era: challenges and perspectives. <i>BMC Biology</i> , 2019, 17, 84.	3.8	113
8	Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. <i>Marine Drugs</i> , 2019, 17, 576.	4.6	26
9	Absolute quantification of infecting viral particles by chip-based digital polymerase chain reaction. <i>Environmental Microbiology Reports</i> , 2019, 11, 855-860.	2.4	4
10	Unique structure and function of viral rhodopsins. <i>Nature Communications</i> , 2019, 10, 4939.	12.8	59
11	Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019, 179, 1068-1083.e21.	28.9	268
12	Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019, 179, 1084-1097.e21.	28.9	271
13	Metagenomic Analysis of the Diversity of DNA Viruses in the Surface and Deep Sea of the South China Sea. <i>Frontiers in Microbiology</i> , 2019, 10, 1951.	3.5	34
14	Culture-Dependent Bioprospecting of Bacterial Isolates From the Canadian High Arctic Displaying Antibacterial Activity. <i>Frontiers in Microbiology</i> , 2019, 10, 1836.	3.5	22
15	Bottom-up biofilm eradication using bacteriophage-loaded magnetic nanocomposites: a computational and experimental study. <i>Environmental Science: Nano</i> , 2019, 6, 3539-3550.	4.3	19
16	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	11.0	94
17	Neo-virology: The raison d'être of viruses. <i>Virus Research</i> , 2019, 274, 197751.	2.2	4
18	The Tara Pacific expedition – A pan-ecosystemic approach of the ‘omics’ complexity of coral reef holobionts across the Pacific Ocean. <i>PLoS Biology</i> , 2019, 17, e3000483.	5.6	48

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19	Scientistsâ€™ warning to humanity: microorganisms and climate change. Nature Reviews Microbiology, 2019, 17, 569-586.	28.6	1,138
20	Combinatorial approach for screening and assessment of multiple therapeutic enzymes from marine isolate <i>Pseudomonas aeruginosa</i> AR01. RSC Advances, 2019, 9, 16989-17001.	3.6	5
21	Droplet Digital PCR for Estimating Absolute Abundances of Widespread Pelagibacter Viruses. Frontiers in Microbiology, 2019, 10, 1226.	3.5	29
22	Arctic an unexpected hotspot for viral diversity. Nature Reviews Microbiology, 2019, 17, 398-398.	28.6	0
23	Drowning in Viruses. Cell, 2019, 177, 1084-1085.	28.9	4
24	Trends of Microdiversity Reveal Depth-Dependent Evolutionary Strategies of Viruses in the Mediterranean. MSystems, 2019, 4, .	3.8	26
25	Taxonomy of Viruses. , 2019, , .		7
26	Diverse, Abundant, and Novel Viruses Infecting the Marine <i>Roseobacter</i> RCA Lineage. MSystems, 2019, 4, .	3.8	27
27	Single-Stranded DNA Viruses in Antarctic Cryoconite Holes. Viruses, 2019, 11, 1022.	3.3	31
28	Metabolic and biogeochemical consequences of viral infection in aquatic ecosystems. Nature Reviews Microbiology, 2020, 18, 21-34.	28.6	222
29	The spinal cord-gut-immune axis as a master regulator of health and neurological function after spinal cord injury. Experimental Neurology, 2020, 323, 113085.	4.1	46
30	Plankton of the Open Arctic Ocean. , 2020, , 495-506.		0
31	Phage-specific metabolic reprogramming of virocells. ISME Journal, 2020, 14, 881-895.	9.8	133
32	Long-term stability and Red Queen-like strain dynamics in marine viruses. Nature Microbiology, 2020, 5, 265-271.	13.3	62
33	Phytoplankton in the <i>Tara</i> Ocean. Annual Review of Marine Science, 2020, 12, 233-265.	11.6	96
34	The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. Cell Host and Microbe, 2020, 28, 724-740.e8.	11.0	352
35	Phytoplankton dynamics in a changing Arctic Ocean. Nature Climate Change, 2020, 10, 892-903.	18.8	162
36	Entamoeba and Giardia parasites implicated as hosts of CRESS viruses. Nature Communications, 2020, 11, 4620.	12.8	34

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37	Adsorption Sequencing as a Rapid Method to Link Environmental Bacteriophages to Hosts. IScience, 2020, 23, 101439.	4.1	23
38	Single-virus genomics and beyond. Nature Reviews Microbiology, 2020, 18, 705-716.	28.6	18
39	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. Nature Microbiology, 2020, 5, 1262-1270.	13.3	156
40	Diel cycling of the cosmopolitan abundant Pelagibacter virus 37â€¢F6: one of the most abundant viruses on earth. Environmental Microbiology Reports, 2020, 12, 214-219.	2.4	8
41	Genomeâ€¢resolved viral ecology in a marine oxygen minimum zone. Environmental Microbiology, 2021, 23, 2858-2874.	3.8	15
42	VIRIDICâ€¢A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses, 2020, 12, 1268.	3.3	274
43	Aquatic virus culture collection: an absent (but necessary) safety net for environmental microbiologists. Applied Phycology, 2022, 3, 211-225.	1.3	7
44	Viral Metagenomic Content Reflects Seawater Ecological Quality in the Coastal Zone. Viruses, 2020, 12, 806.	3.3	10
45	Assessing Viral Abundance and Community Composition in Four Contrasting Regions of the Southern Ocean. Life, 2020, 10, 107.	2.4	10
46	Viral elements and their potential influence on microbial processes along the permanently stratified Cariaco Basin redoxcline. ISME Journal, 2020, 14, 3079-3092.	9.8	36
47	Seasonal Regime Shift in the Viral Communities of a Permafrost Thaw Lake. Viruses, 2020, 12, 1204.	3.3	5
48	Quantification of Lysogeny Caused by Phage Coinfections in Microbial Communities from Biophysical Principles. MSystems, 2020, 5, .	3.8	28
49	Femtoplankton: Whatâ€¢s New?. Viruses, 2020, 12, 881.	3.3	4
50	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. Nature Ecology and Evolution, 2020, 4, 1639-1649.	7.8	78
51	Prevalence of temperate viruses in deep South China Sea and western Pacific Ocean. Deep-Sea Research Part I: Oceanographic Research Papers, 2020, 166, 103403.	1.4	4
52	Comparative viromes of <i>Culicoides</i> and mosquitoes reveal their consistency and diversity in viral profiles. Briefings in Bioinformatics, 2021, 22, .	6.5	9
53	The ocean genome and future prospects for conservation and equity. Nature Sustainability, 2020, 3, 588-596.	23.7	38
54	Tara Oceans: towards global ocean ecosystems biology. Nature Reviews Microbiology, 2020, 18, 428-445.	28.6	227

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55	MHC Class I Regulation: The Origin Perspective. <i>Cancers</i> , 2020, 12, 1155.	3.7	12
56	A single-cell view on alga-virus interactions reveals sequential transcriptional programs and infection states. <i>Science Advances</i> , 2020, 6, eaba4137.	10.3	55
57	Deep Roots and Splendid Boughs of the Global Plant Virome. <i>Annual Review of Phytopathology</i> , 2020, 58, 23-53.	7.8	73
58	VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences. <i>Microbiome</i> , 2020, 8, 90.	11.1	482
59	Diversity within species: interpreting strains in microbiomes. <i>Nature Reviews Microbiology</i> , 2020, 18, 491-506.	28.6	222
60	A tissue level atlas of the healthy human virome. <i>BMC Biology</i> , 2020, 18, 55.	3.8	50
61	Coral Reef Microorganisms in a Changing Climate. <i>IScience</i> , 2020, 23, 100972.	4.1	52
62	Investigating the Diversity of Marine Bacteriophage in Contrasting Water Masses Associated with the East Australian Current (EAC) System. <i>Viruses</i> , 2020, 12, 317.	3.3	3
63	5 challenges in understanding the role of the virome in health and disease. <i>PLoS Pathogens</i> , 2020, 16, e1008318.	4.7	30
64	Extreme Viral Partitioning in a Marine-Derived High Arctic Lake. <i>MSphere</i> , 2020, 5, .	2.9	16
65	Viral Ecogenomics of Arctic Cryopeg Brine and Sea Ice. <i>MSystems</i> , 2020, 5, .	3.8	23
66	Expansion of known ssRNA phage genomes: From tens to over a thousand. <i>Science Advances</i> , 2020, 6, eaay5981.	10.3	112
67	Phage protein receptors have multiple interaction partners and high expressions. <i>Bioinformatics</i> , 2020, 36, 2975-2979.	4.1	12
68	Villains or heroes? The raison d'Être of viruses. <i>Clinical and Translational Immunology</i> , 2020, 9, e01114.	3.8	7
69	Double-stranded DNA viroplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. <i>ISME Journal</i> , 2020, 14, 1304-1315.	9.8	65
70	The arms race between bacteria and their phage foes. <i>Nature</i> , 2020, 577, 327-336.	27.8	514
71	Coming-of-Age Characterization of Soil Viruses: A User's Guide to Virus Isolation, Detection within Metagenomes, and Viromics. <i>Soil Systems</i> , 2020, 4, 23.	2.6	61
72	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. <i>Nature Microbiology</i> , 2020, 5, 668-674.	13.3	198

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73	Impact of phages on soil bacterial communities and nitrogen availability under different assembly scenarios. Microbiome, 2020, 8, 52.	11.1	82
74	Newly-discovered interactions between bacteriophages and the process of calcium carbonate precipitation. Geochimica Et Cosmochimica Acta, 2021, 292, 482-498.	3.9	13
75	Planet Microbe: a platform for marine microbiology to discover and analyze interconnected omics and environmental data. Nucleic Acids Research, 2021, 49, D792-D802.	14.5	14
76	The Greater Virus World and Its Evolution. , 2021, , 38-46.		0
77	Culturing novel and abundant pelagiphages in the ocean. Environmental Microbiology, 2021, 23, 1145-1161.	3.8	27
78	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. Nucleic Acids Research, 2021, 49, D764-D775.	14.5	240
79	Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. ISME Journal, 2021, 15, 981-998.	9.8	71
80	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. Nature Biotechnology, 2021, 39, 578-585.	17.5	569
81	Viral discovery in the "realm" of <sc>COVID</sc>19. Environmental Microbiology Reports, 2021, 13, 62-67.	2.4	0
82	<sc>T4</sc>-like myovirus community shaped by dispersal and deterministic processes in the South China Sea. Environmental Microbiology, 2021, 23, 1038-1052.	3.8	5
83	A single-cell polony method reveals low levels of infected <i>Prochlorococcus</i> in oligotrophic waters despite high cyanophage abundances. ISME Journal, 2021, 15, 41-54.	9.8	40
84	Porcine reproductive and respiratory syndrome virus whole-genome sequencing efficacy with field clinical samples using a poly(A)-tail viral genome purification method. Journal of Veterinary Diagnostic Investigation, 2021, 33, 216-226.	1.1	8
85	Marine Bacteriophages. , 2021, , 322-341.		7
86	Rapid discovery of novel prophages using biological feature engineering and machine learning. NAR Genomics and Bioinformatics, 2021, 3, lqaa109.	3.2	39
88	Prokaryotic virus host predictor: a Gaussian model for host prediction of prokaryotic viruses in metagenomics. BMC Biology, 2021, 19, 5.	3.8	50
89	Virome composition in marine fish revealed by meta-transcriptomics. Virus Evolution, 2021, 7, veab005.	4.9	58
90	Characterization of the gut DNA and RNA Viromes in a Cohort of Chinese Residents and Visiting Pakistanis. Virus Evolution, 2021, 7, veab022.	4.9	21
91	Housekeeping in the Hydrosphere: Microbial Cooking, Cleaning, and Control under Stress. Life, 2021, 11, 152.	2.4	8

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92	Interaction dynamics and virus–host range for estuarine actinophages captured by epicPCR. <i>Nature Microbiology</i> , 2021, 6, 630-642.	13.3	29
93	Metaviromics coupled with phage-host identification to open the viral “black box”™. <i>Journal of Microbiology</i> , 2021, 59, 311-323.	2.8	10
94	VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. <i>Microbiome</i> , 2021, 9, 37.	11.1	441
96	Large-scale genome sequencing reveals the driving forces of viruses in microalgal evolution. <i>Cell Host and Microbe</i> , 2021, 29, 250-266.e8.	11.0	48
97	Metagenomic tools in microbial ecology research. <i>Current Opinion in Biotechnology</i> , 2021, 67, 184-191.	6.6	77
98	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021, 9, e10911.	2.0	44
99	Deep sea sediments associated with cold seeps are a subsurface reservoir of viral diversity. <i>ISME Journal</i> , 2021, 15, 2366-2378.	9.8	93
100	VirION2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature. <i>PeerJ</i> , 2021, 9, e11088.	2.0	25
103	Streamlining CRISPR spacer-based bacterial host predictions to decipher the viral dark matter. <i>Nucleic Acids Research</i> , 2021, 49, 3127-3138.	14.5	72
104	Genomic Characterization and Distribution Pattern of a Novel Marine OM43 Phage. <i>Frontiers in Microbiology</i> , 2021, 12, 651326.	3.5	7
105	Recognizing species as a new focus of virus research. <i>PLoS Pathogens</i> , 2021, 17, e1009318.	4.7	12
107	Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , 2021, 19, 501-513.	28.6	77
108	Hybrid assembly of an agricultural slurry virome reveals a diverse and stable community with the potential to alter the metabolism and virulence of veterinary pathogens. <i>Microbiome</i> , 2021, 9, 65.	11.1	182
109	Examining horizontal gene transfer in microbial communities. <i>Nature Reviews Microbiology</i> , 2021, 19, 442-453.	28.6	136
110	Uncultivated Viral Populations Dominate Estuarine Viromes on the Spatiotemporal Scale. <i>MSystems</i> , 2021, 6, .	3.8	13
111	Quantitative Assessment of Nucleocytoplasmic Large DNA Virus and Host Interactions Predicted by Co-occurrence Analyses. <i>MSphere</i> , 2021, 6, .	2.9	22
112	Phylogenomic Insights into Distribution and Adaptation of Bdellovibrionota in Marine Waters. <i>Microorganisms</i> , 2021, 9, 757.	3.6	14
113	Environmental dissolved <sc>DNA</sc> harbours meaningful biological information on microbial community structure. <i>Environmental Microbiology</i> , 2021, 23, 2669-2682.	3.8	3

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114	A thermal trade-off between viral production and degradation drives virus-phytoplankton population dynamics. <i>Ecology Letters</i> , 2021, 24, 1133-1144.	6.4	10
117	Comparison of ultrafiltration and iron chloride flocculation in the preparation of aquatic viromes from contrasting sample types. <i>PeerJ</i> , 2021, 9, e11111.	2.0	18
118	Prophage Genomics and Ecology in the Family Rhodobacteraceae. <i>Microorganisms</i> , 2021, 9, 1115.	3.6	22
122	Diversity and distribution of viruses inhabiting the deepest ocean on Earth. <i>ISME Journal</i> , 2021, 15, 3094-3110.	9.8	55
124	Computational Viromics: Applications of the Computational Biology in Viromics Studies. <i>Virologica Sinica</i> , 2021, 36, 1256-1260.	3.0	3
126	Viruses as “Truffle Hounds”: Molecular Tools for Untangling Brain Cellular Pathology. <i>Trends in Neurosciences</i> , 2021, 44, 352-365.	8.6	7
127	Metaviromes Reveal the Dynamics of Pseudomonas Host-Specific Phages Cultured and Uncultured by Plaque Assay. <i>Viruses</i> , 2021, 13, 959.	3.3	7
129	Viruses infecting a warm water picoeukaryote shed light on spatial co-occurrence dynamics of marine viruses and their hosts. <i>ISME Journal</i> , 2021, 15, 3129-3147.	9.8	10
131	PHROG: families of prokaryotic virus proteins clustered using remote homology. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab067.	3.2	134
132	Phage-encoded ten-eleven translocation dioxygenase (TET) is active in C5-cytosine hypermodification in DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
133	The landscape of lysogeny across microbial community density, diversity and energetics. <i>Environmental Microbiology</i> , 2021, 23, 4098-4111.	3.8	50
134	Application of machine learning in bacteriophage research. <i>BMC Microbiology</i> , 2021, 21, 193.	3.3	26
135	A catalog of tens of thousands of viruses from human metagenomes reveals hidden associations with chronic diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	138
136	Expanding standards in viromics: in silico evaluation of dsDNA viral genome identification, classification, and auxiliary metabolic gene curation. <i>PeerJ</i> , 2021, 9, e11447.	2.0	51
137	Spinal Cord Injury Changes the Structure and Functional Potential of Gut Bacterial and Viral Communities. <i>MSystems</i> , 2021, 6, .	3.8	28
138	Going to extremes “a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
139	Exploring Codon Adjustment Strategies towards Escherichia coli-Based Production of Viral Proteins Encoded by HTH1, a Novel Prophage of the Marine Bacterium <i>Hypnocyclicus thermotrophus</i> . <i>Viruses</i> , 2021, 13, 1215.	3.3	3
140	efam: an expanded, metaproteome-supported HMM profile database of viral protein families. <i>Bioinformatics</i> , 2021, 37, 4202-4208.	4.1	15



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141	Prospects for viruses infecting eukaryotic microalgae in biotechnology. <i>Biotechnology Advances</i> , 2022, 54, 107790.	11.7	5
142	Metagenomic and viromic data mining reveals viral threats in biologically treated domestic wastewater. <i>Environmental Science and Ecotechnology</i> , 2021, 7, 100105.	13.5	23
143	Glacier ice archives nearly 15,000-year-old microbes and phages. <i>Microbiome</i> , 2021, 9, 160.	11.1	59
144	Genomic diversity, life strategies and ecology of marine HTVC010P-type pelagiphages. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
145	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	3.8	5
146	Fishing for the Virome of Tropical Tuna. <i>Viruses</i> , 2021, 13, 1291.	3.3	8
147	Ecogenomics and Adaptation Strategies of Southern Ocean Viral Communities. <i>MSystems</i> , 2021, 6, e0039621.	3.8	11
148	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	10.3	54
149	Fishing for phages in metagenomes: what do we catch, what do we miss?. <i>Current Opinion in Virology</i> , 2021, 49, 142-150.	5.4	10
150	Functional strain redundancy and persistent phage infection in Swiss hard cheese starter cultures. <i>ISME Journal</i> , 2022, 16, 388-399.	9.8	24
152	Characterization and Genomic Analysis of <i>Marinobacter</i> Phage vB_MalS-PS3, Representing a New Lambda-Like Temperate Siphoviral Genus Infecting Algae-Associated Bacteria. <i>Frontiers in Microbiology</i> , 2021, 12, 726074.	3.5	7
153	Revealing RNA virus diversity and evolution in unicellular algae transcriptomes. <i>Virus Evolution</i> , 2021, 7, .	4.9	28
154	Interactions between bacterial and phage communities in natural environments. <i>Nature Reviews Microbiology</i> , 2022, 20, 49-62.	28.6	193
157	Characterization and genomic analysis of the first <i>Oceanospirillum</i> phage, vB_OliS_CJ44, representing a novel siphoviral cluster. <i>BMC Genomics</i> , 2021, 22, 675.	2.8	7
158	Pathways of thymidine hypermodification. <i>Nucleic Acids Research</i> , 2022, 50, 3001-3017.	14.5	12
159	Biominalization processes in modern calcareous tufa: Possible roles of viruses, vesicles and extracellular polymeric substances (Corvino Valley “ Southern Italy). <i>Sedimentology</i> , 2022, 69, 399-422.	3.1	11
160	Viral Characteristics of the Warm Atlantic and Cold Arctic Water Masses in the Nordic Seas. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0116021.	3.1	12
161	Integrating Viral Metagenomics into an Ecological Framework. <i>Annual Review of Virology</i> , 2021, 8, 133-158.	6.7	40

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163	High-throughput identification of viral termini and packaging mechanisms in virome datasets using PhageTermVirome. Scientific Reports, 2021, 11, 18319.	3.3	6
164	Highly diverse flavobacterial phages isolated from North Sea spring blooms. ISME Journal, 2022, 16, 555-568.	9.8	32
165	Arms race in a cell: genomic, transcriptomic, and proteomic insights into intracellular phageâ€“bacteria interplay in deep-sea snail holobionts. Microbiome, 2021, 9, 182.	11.1	7
166	Viral footprints across Gulfs of Kathiawar Peninsula and Arabian Sea: Unraveled from pelagic sediment metagenomic data. Virus Research, 2021, 302, 198485.	2.2	4
168	Monsavirus in monkey rectal swab and throat swab specimens in China: Proposal for Posaliviridae as a new family in Picornavirales. Virus Research, 2021, 303, 198501.	2.2	2
169	Parasites, pathogens, and other symbionts of copepods. Trends in Parasitology, 2021, 37, 875-889.	3.3	19
170	Viral Community and Virus-Associated Antibiotic Resistance Genes in Soils Amended with Organic Fertilizers. Environmental Science & Technology, 2021, 55, 13881-13890.	10.0	49
172	Bacteriophage Ecology. , 2021, , 253-294.		9
174	Efficient dilution-to-extinction isolation of novel virusâ€“host model systems for fastidious heterotrophic bacteria. ISME Journal, 2021, 15, 1585-1598.	9.8	26
175	Aerobic and anaerobic iron oxidizers together drive denitrification and carbon cycling at marine iron-rich hydrothermal vents. ISME Journal, 2021, 15, 1271-1286.	9.8	46
176	Phage diversity, genomics and phylogeny. Nature Reviews Microbiology, 2020, 18, 125-138.	28.6	455
177	Seasonal and diel patterns of abundance and activity of viruses in the Red Sea. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29738-29747.	7.1	27
178	Cenote-Taker 2 democratizes virus discovery and sequence annotation. Virus Evolution, 2021, 7, veaa100.	4.9	82
206	Discovery of several thousand highly diverse circular DNA viruses. ELife, 2020, 9, .	6.0	131
207	Towards optimized viral metagenomes for double-stranded and single-stranded DNA viruses from challenging soils. PeerJ, 2019, 7, e7265.	2.0	48
208	Genomics of host-pathogen interactions: challenges and opportunities across ecological and spatiotemporal scales. PeerJ, 2019, 7, e8013.	2.0	23
209	Benchmarking protocols for the metagenomic analysis of stream biofilm viromes. PeerJ, 2019, 7, e8187.	2.0	9
210	A new family of â€œmegaphagesâ€“abundant in the marine environment. ISME Communications, 2021, 1, .	4.2	12

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211	Genomic Characterization of Two Novel RCA Phages Reveals New Insights into the Diversity and Evolution of Marine Viruses. <i>Microbiology Spectrum</i> , 2021, 9, e0123921.	3.0	6
212	Genome and Ecology of a Novel <i>Alteromonas</i> Podovirus, ZP6, Representing a New Viral Genus, <i>Mareflavirus</i> . <i>Microbiology Spectrum</i> , 2021, 9, e0046321.	3.0	13
214	Hundreds of thousands of marine viruses discovered in world's oceans. <i>Nature</i> , 2019, , .	27.8	1
216	Not all viruses in nature are human enemies: a perspective on aquatic virus ecology in Brazil. <i>Acta Limnologica Brasiliensia</i> , 0, 32, .	0.4	1
218	Viral infection of prokaryotic plankton during early formation of the North Atlantic Deep Water. <i>Aquatic Microbial Ecology</i> , 2020, 84, 175-189.	1.8	3
220	COVID-19 VE HAYVANLAR. <i>Veteriner Farmakoloji Ve Toksikoloji Derneği Bülteni</i> , 2020, 11, 49-60.	0.1	2
222	Clinical practices underlie COVID-19 patient respiratory microbiome composition and its interactions with the host. <i>Nature Communications</i> , 2021, 12, 6243.	12.8	42
223	Microbial Ecology of Oxygen Minimum Zones Amidst Ocean Deoxygenation. <i>Frontiers in Microbiology</i> , 2021, 12, 748961.	3.5	25
226	Bacteriophage Ecology. , 2020, , 1-42.		4
227	Phage Communication and the Ecological Implications on Microbial Interactions, Diversity, and Function. , 2020, , 71-86.		1
230	The origin and impeded dissemination of the DNA phosphorothioation system in prokaryotes. <i>Nature Communications</i> , 2021, 12, 6382.	12.8	14
232	The gut virome in inflammatory bowel diseases. <i>Current Opinion in Virology</i> , 2021, 51, 190-198.	5.4	18
234	Unexpected myriad of co-occurring viral strains and species in one of the most abundant and microdiverse viruses on Earth. <i>ISME Journal</i> , 2022, 16, 1025-1035.	9.8	8
236	Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes. <i>PLoS Biology</i> , 2021, 19, e3001442.	5.6	44
237	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. <i>Microbiome</i> , 2021, 9, 233.	11.1	53
238	Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021, 51, 207-215.	5.4	31
239	Saline lakes on the Qinghai-Tibet Plateau harbor unique viral assemblages mediating microbial environmental adaption. <i>IScience</i> , 2021, 24, 103439.	4.1	13
240	A Catalogue of 48,425 Nonredundant Viruses From Oral Metagenomes Expands the Horizon of the Human Oral Virome. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
241	Spaceflight Virology: What Do We Know about Viral Threats in the Spaceflight Environment?. <i>Astrobiology</i> , 2022, 22, 210-224.	3.0	11
242	Release the iron: does the infection of magnetotactic bacteria by phages play a role in making iron available in aquatic environments?. <i>Journal of Oceanology and Limnology</i> , 2021, 39, 2063-2069.	1.3	3
243	Organochlorine contamination enriches virus-encoded metabolism and pesticide degradation associated auxiliary genes in soil microbiomes. <i>ISME Journal</i> , 2022, 16, 1397-1408.	9.8	45
244	Metagenomic analysis of viral community in the Yangtze River expands known eukaryotic and prokaryotic virus diversity in freshwater. <i>Virologica Sinica</i> , 2022, 37, 60-69.	3.0	13
245	High molecular weight DNA extraction strategies for long-read sequencing of complex metagenomes. <i>Molecular Ecology Resources</i> , 2022, 22, 1786-1802.	4.8	24
246	Communities of T4-like bacteriophages associated with bacteria in Lake Baikal: diversity and biogeography. <i>PeerJ</i> , 0, 10, e12748.	2.0	3
249	Novel Viral Communities Potentially Assisting in Carbon, Nitrogen, and Sulfur Metabolism in the Upper Slope Sediments of Mariana Trench. <i>MSystems</i> , 2022, 7, e0135821.	3.8	22
250	Newly identified HMO-2011-type phages reveal genomic diversity and biogeographic distributions of this marine viral group. <i>ISME Journal</i> , 2022, 16, 1363-1375.	9.8	8
252	Viral tag and grow: a scalable approach to capture and characterize infectious virus-host pairs. <i>ISME Communications</i> , 2022, 2, .	4.2	4
253	Virus genomics: what is being overlooked?. <i>Current Opinion in Virology</i> , 2022, 53, 101200.	5.4	14
255	Marine Viruses: Agents of Chaos, Promoters of Order. <i>The Microbiomes of Humans, Animals, Plants, and the Environment</i> , 2022, , 297-325.	0.6	1
256	A Five-Fold Expansion of the Global RNA Virome Reveals Multiple New Clades of RNA Bacteriophages. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4
257	A holistic genome dataset of bacteria, archaea and viruses of the Pearl River estuary. <i>Scientific Data</i> , 2022, 9, 49.	5.3	12
258	Evolving Perspective on the Origin and Diversification of Cellular Life and the Virosphere. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	13
260	A Novel and Ubiquitous Marine Methylophage Provides Insights into Viral-Host Coevolution and Possible Host-Range Expansion in Streamlined Marine Heterotrophic Bacteria. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0025522.	3.1	2
261	Diversity and origins of bacterial and archaeal viruses on sinking particles reaching the abyssal ocean. <i>ISME Journal</i> , 2022, 16, 1627-1635.	9.8	18
262	Computational Tools for the Analysis of Uncultivated Phage Genomes. <i>Microbiology and Molecular Biology Reviews</i> , 2022, 86, e0000421.	6.6	13
263	MetaPop: a pipeline for macro- and microdiversity analyses and visualization of microbial and viral metagenome-derived populations. <i>Microbiome</i> , 2022, 10, 49.	11.1	24

#	ARTICLE	IF	CITATIONS
264	Diatoms and Their Microbiomes in Complex and Changing Polar Oceans. <i>Frontiers in Microbiology</i> , 2022, 13, 786764.	3.5	7
265	Record-Breaking Rain Event Altered Estuarine Viral Assemblages. <i>Microorganisms</i> , 2022, 10, 729.	3.6	5
266	Infection strategy and biogeography distinguish cosmopolitan groups of marine jumbo bacteriophages. <i>ISME Journal</i> , 2022, 16, 1657-1667.	9.8	27
267	Characterization and Genomic Analysis of the First Podophage Infecting <i>Shewanella</i> , Representing a Novel Viral Cluster. <i>Frontiers in Microbiology</i> , 2022, 13, 853973.	3.5	3
268	Viruses affect picocyanobacterial abundance and biogeography in the North Pacific Ocean. <i>Nature Microbiology</i> , 2022, 7, 570-580.	13.3	25
269	Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome. <i>Science</i> , 2022, 376, 156-162.	12.6	124
270	There's more to RNA viruses than diseases. <i>Science</i> , 2022, 376, 138-139.	12.6	1
271	A mixed blessing of viruses in wastewater treatment plants. <i>Water Research</i> , 2022, 215, 118237.	11.3	21
272	Viral diversity and biogeochemical potential revealed in different prawn-culture sediments by virus-enriched metagenome analysis. <i>Environmental Research</i> , 2022, 210, 112901.	7.5	7
273	Spatial dynamics of active microeukaryotes along a latitudinal gradient: Diversity, assembly process, and co-occurrence relationships. <i>Environmental Research</i> , 2022, 212, 113234.	7.5	5
274	Decadal vision in oceanography 2021: Mid-latitude ocean. <i>Oceanography in Japan</i> , 2021, 30, 127-154.	0.5	1
275	Biogeography of culturable marine bacteria from both poles reveals that "everything is not everywhere" at the genomic level. <i>Environmental Microbiology</i> , 2022, 24, 98-109.	3.8	5
276	Bacteriophages and their microbial hosts in terrestrial biotopes of Antarctica. <i>Antarctic Science</i> , 2022, 34, 120-136.	0.9	3
277	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. <i>ISME Communications</i> , 2021, 1, .	4.2	13
279	Editorial for the Special Issue: The Role of the Virome in Health and Disease. <i>Microorganisms</i> , 2022, 10, 20.	3.6	2
280	Eco-evolutionary responses of the microbial loop to surface ocean warming and consequences for primary production. <i>ISME Journal</i> , 2022, 16, 1130-1139.	9.8	5
281	From Trees to Clouds: PhageClouds for Fast Comparison of ~4640,000 Phage Genomic Sequences and Host-Centric Visualization Using Genomic Network Graphs. <i>Phage</i> , 2021, 2, 194-203.	1.7	14
284	Three new clades of putative viral RNA-dependent RNA polymerases with rare or unique catalytic triads discovered in libraries of ORFans from powdery mildews and the yeast of oenological interest <i>Starmarella bacillari</i> . <i>Virus Evolution</i> , 2022, 8, .	4.9	12

#	ARTICLE	IF	CITATIONS
298	Viral Metagenomics Reveals Widely Diverse Viral Community of Freshwater Amazonian Lake. <i>Frontiers in Public Health</i> , 2022, 10, 869886.	2.7	2
299	Organizing the Global Diversity of Microviruses. <i>MBio</i> , 2022, 13, e0058822.	4.1	21
301	Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022, 2, 100123.	6.5	70
302	Optimized Metavirome Analysis of Marine DNA Virus Communities for Taxonomic Profiling. <i>Ocean Science Journal</i> , 2022, 57, 259-268.	1.3	3
303	vRhyme enables binning of viral genomes from metagenomes. <i>Nucleic Acids Research</i> , 2022, 50, e83-e83.	14.5	30
304	Patterns and ecological drivers of viral communities in acid mine drainage sediments across Southern China. <i>Nature Communications</i> , 2022, 13, 2389.	12.8	25
305	The First Cbk-Like Phage Infecting <i>Erythrobacter</i> , Representing a Novel Siphoviral Genus. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	1
306	A snapshot of the global drinking water virome: Diversity and metabolic potential vary with residual disinfectant use. <i>Water Research</i> , 2022, 218, 118484.	11.3	14
307	On the Comparison of Bacteriophage Populations. <i>Lecture Notes in Computer Science</i> , 2022, , 3-20.	1.3	1
309	A catalog of 48,425 nonredundant viruses from oral metagenomes expands the horizon of the human oral virome. <i>IScience</i> , 2022, 25, 104418.	4.1	20
310	Schrödinger and the Possible Existence of Different Types of Life. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	0
311	Nutrient levels and prokaryotes affect viral communities in plateau lakes. <i>Science of the Total Environment</i> , 2022, 839, 156033.	8.0	2
313	Thousands of small, novel genes predicted in global phage genomes. <i>Cell Reports</i> , 2022, 39, 110984.	6.4	21
314	Gut virome profiling identifies a widespread bacteriophage family associated with metabolic syndrome. <i>Nature Communications</i> , 2022, 13, .	12.8	32
315	The OceanDNA MAG catalog contains over 50,000 prokaryotic genomes originated from various marine environments. <i>Scientific Data</i> , 2022, 9, .	5.3	29
316	Long-Read Metagenomics Improves the Recovery of Viral Diversity from Complex Natural Marine Samples. <i>MSystems</i> , 2022, 7, .	3.8	11
317	The Case for Studying New Viruses of New Hosts. <i>Annual Review of Virology</i> , 2022, 9, 157-172.	6.7	3
318	Nanotechnology: New frontiers in anti-HIV therapy. , 2022, , 129-171.		0

#	ARTICLE	IF	CITATIONS
319	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	12.6	41
320	Accurate identification of bacteriophages from metagenomic data using Transformer. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	14
321	Virioplankton assemblages from challenger deep, the deepest place in the oceans. <i>IScience</i> , 2022, 25, 104680.	4.1	7
325	Auxiliary Metabolic Gene Functions in Pelagic and Benthic Viruses of the Baltic Sea. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	21
326	Phage Therapy: Genomics to Applications and Future Prospects. , 2022, , 109-145.		2
327	Trawling the ocean virome. <i>Nature Methods</i> , 2022, 19, 928-931.	19.0	1
328	Why the ocean virome matters. <i>Nature Methods</i> , 2022, 19, 924-927.	19.0	4
329	Into the Dark: Exploring the Deep Ocean with Single-Virus Genomics. <i>Viruses</i> , 2022, 14, 1589.	3.3	4
331	Recent insights into aquatic viruses: Emerging and reemerging pathogens, molecular features, biological effects, and novel investigative approaches. , 2022, 1, 100062.		11
332	Complete gammaproteobacterial endosymbiont genome assembly from a seep tubeworm <i>Lamellibrachia satsuma</i> . <i>Journal of Microbiology</i> , 2022, 60, 916-927.	2.8	1
334	Isolation and Characterization of the Lytic <i>Pseudoxanthomonas kaohsiungensi</i> Phage PW916. <i>Viruses</i> , 2022, 14, 1709.	3.3	4
335	Genomes from Uncultivated Pelagiphages Reveal Multiple Phylogenetic Clades Exhibiting Extensive Auxiliary Metabolic Genes and Cross-Family Multigene Transfers. <i>MSystems</i> , 2022, 7, .	3.8	4
336	Diverse viromes in polar regions: A retrospective study of metagenomic data from Antarctic animal feces and Arctic frozen soil in 2012â€“2014. <i>Virologica Sinica</i> , 2022, 37, 883-893.	3.0	4
338	Plankton Planet: A frugal, cooperative measure of aquatic life at the planetary scale. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	2
339	Distribution of rare <sc>N4</sc> â€“like viruses in temperate estuaries unveiled by viromics. <i>Environmental Microbiology</i> , 0, , .	3.8	0
341	Virome analysis in lakes of the South Shetland Islands, Antarctica - 2020. <i>Science of the Total Environment</i> , 2022, 852, 158537.	8.0	4
342	Host-pathogen protein-nucleic acid interactions: A comprehensive review. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 4415-4436.	4.1	9
343	Microbial Rhodopsins. <i>Methods in Molecular Biology</i> , 2022, , 1-52.	0.9	11

#	ARTICLE	IF	CITATIONS
344	Dysbiotic Oral and Gut Viromes in Untreated and Treated Rheumatoid Arthritis Patients. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	12
345	Expansion of the global RNA virome reveals diverse clades of bacteriophages. <i>Cell</i> , 2022, 185, 4023-4037.e18.	28.9	96
346	Metatranscriptomics reveals a shift in microbial community composition and function during summer months in a coastal marine environment. <i>Environmental DNA</i> , 2023, 5, 920-933.	5.8	4
348	Integrated analysis of intestinal microbiota and metabolomic reveals that decapod iridescent virus 1 (DIV1) infection induces secondary bacterial infection and metabolic reprogramming in <i>Marsupenaeus japonicus</i> . <i>Frontiers in Immunology</i> , 0, 13, .	4.8	2
349	Viruses in Subsurface Environments. <i>Annual Review of Virology</i> , 2022, 9, 99-119.	6.7	4
350	Marine DNA methylation patterns are associated with microbial community composition and inform virus-host dynamics. <i>Microbiome</i> , 2022, 10, .	11.1	8
351	Ecogenomics reveals viral communities across the Challenger Deep oceanic trench. <i>Communications Biology</i> , 2022, 5, .	4.4	9
353	Marine viruses and climate change: Virioplankton, the carbon cycle, and our future ocean. <i>Advances in Virus Research</i> , 2022, , 67-146.	2.1	1
355	Crop management shapes the diversity and activity of DNA and RNA viruses in the rhizosphere. <i>Microbiome</i> , 2022, 10, .	11.1	12
356	Viruses in astrobiology. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	5
357	Highly diverse ribonucleic acid viruses in the viromes of eukaryotic host species in Yunnan province, China. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	1
361	Over two decades of research on the marine RNA virosphere. , 2022, 1, .		3
362	Engineering indel and substitution variants of diverse and ancient enzymes using Graphical Representation of Ancestral Sequence Predictions (GRASP). <i>PLoS Computational Biology</i> , 2022, 18, e1010633.	3.2	16
363	Response of soil viral communities to land use changes. <i>Nature Communications</i> , 2022, 13, .	12.8	25
364	Quantitative Stable-Isotope Probing (qSIP) with Metagenomics Links Microbial Physiology and Activity to Soil Moisture in Mediterranean-Climate Grassland Ecosystems. <i>MSystems</i> , 2022, 7, .	3.8	9
365	Marine viral particles reveal an expansive repertoire of phage-parasitizing mobile elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	14
366	Ecological dynamics and impacts of viruses in Chinese and global estuaries. <i>Water Research</i> , 2022, 226, 119237.	11.3	3
367	Discovering marine biodiversity in the 21st century. <i>Advances in Marine Biology</i> , 2022, , 23-115.	1.4	7



#	ARTICLE	IF	CITATIONS
368	Abundant and cosmopolitan lineage of cyanopodoviruses lacking a DNA polymerase gene. ISME Journal, 2023, 17, 252-262.	9.8	4
370	Viral community-wide auxiliary metabolic genes differ by lifestyles, habitats, and hosts. Microbiome, 2022, 10, .	11.1	35
371	Ecological and functional roles of bacteriophages in contrasting environments: marine, terrestrial and human gut. Current Opinion in Microbiology, 2022, 70, 102229.	5.1	29
372	MarineMetagenomeDB: a public repository for curated and standardized metadata for marine metagenomes. Environmental Microbiomes, 2022, 17, .	5.0	8
373	Environmental Factors and Their Threshold Affecting the Survival of Five Aquatic Animal Viruses in Different Animal Cells. Viruses, 2022, 14, 2546.	3.3	2
374	What the Phage: a scalable workflow for the identification and analysis of phage sequences. GigaScience, 2022, 11, .	6.4	12
375	Higher biotic than abiotic natural variability of the plankton ecosystem revealed by a time series along a subantarctic transect. Journal of Marine Systems, 2023, 238, 103843.	2.1	3
376	Diversity and potential functional characteristics of phage communities colonizing microplastic biofilms. Environmental Research, 2023, 219, 115103.	7.5	6
378	Co-transfer of functionally interdependent genes contributes to genome mosaicism in lambdoid phages. Microbial Genomics, 2022, 8, .	2.0	0
380	Diversité et importance écologique des virus dans le milieu marin. Medecine/Sciences, 2022, 38, 1008-1015.	0.2	0
382	Guidance for creating individual and batch latinized binomial virus species names. Journal of General Virology, 2022, 103, .	2.9	12
383	Virus classification for viral genomic fragments using PhaGCN2. Briefings in Bioinformatics, 2023, 24, .	6.5	22
385	Virus diversity and interactions with hosts in deep-sea hydrothermal vents. Microbiome, 2022, 10, .	11.1	12
386	Mieux connaître les virus présents sur Terre grâce aux métatagénomiques. Medecine/Sciences, 2022, 38, 999-1007.	0.2	1
387	Genome-scale top-down strategy to generate viable genome-reduced phages. Nucleic Acids Research, 2022, 50, 13183-13197.	14.5	6
388	Characterization and genomic Analysis of a novel Pseudomonas phage vB_PsaP_M1, representing a new viral family, Psaeviridae. Frontiers in Marine Science, 0, 9, .	2.5	2
389	Reekeek- and roodoodoviruses, two different Microviridae clades constituted by the smallest DNA phages. Virus Evolution, 2023, 9, .	4.9	5
391	Novel integrative elements and genomic plasticity in ocean ecosystems. Cell, 2023, 186, 47-62.e16.	28.9	25

#	ARTICLE	IF	CITATIONS
392	Covariance of Marine Nucleocytoplasmic Large DNA Viruses with Eukaryotic Plankton Communities in the Sub-Arctic Kongsfjorden Ecosystem: A Metagenomic Analysis of Marine Microbial Ecosystems. <i>Microorganisms</i> , 2023, 11, 169.	3.6	5
393	A remarkably diverse and well-organized virus community in a filter-feeding oyster. <i>Microbiome</i> , 2023, 11, .	11.1	5
394	FastViromeExplorer-Novel: Recovering Draft Genomes of Novel Viruses and Phages in Metagenomic Data. <i>Journal of Computational Biology</i> , 0, , .	1.6	0
395	Significant Differences in Planktonic Virus Communities Between “Cellular Fraction” (0.22–3.0 $\mu\text{m}$ ) and “Viral Fraction” (<0.22 $\mu\text{m}$ ) in the Ocean. <i>Microbial Ecology</i> , 2023, 86, 825-842.	2.8	3
397	Pitfalls of genotyping microbial communities with rapidly growing genome collections. <i>Cell Systems</i> , 2023, 14, 160-176.e3.	6.2	6
398	ViralCC retrieves complete viral genomes and virus-host pairs from metagenomic Hi-C data. <i>Nature Communications</i> , 2023, 14, .	12.8	4
399	Viral infection in the ocean—A journey across scales. <i>PLoS Biology</i> , 2023, 21, e3001966.	5.6	9
401	Genomic diversity and ecological distribution of marine <i>Pseudoalteromonas</i> phages. <i>Marine Life Science and Technology</i> , 2023, 5, 271-285.	4.6	4
403	Genome-centric view of the microbiome in a new deep-sea glass sponge species <i>Bathydorus</i> sp.. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	2
404	Environmental viromes reveal global virosphere of deep-sea sediment RNA viruses. <i>Journal of Advanced Research</i> , 2024, 56, 87-102.	9.5	1
405	Prevalence of Viral Frequency-Dependent Infection in Coastal Marine Prokaryotes Revealed Using Monthly Time Series Virome Analysis. <i>MSystems</i> , 2023, 8, .	3.8	3
407	Viral and Bacterial Communities Collaborate through Complementary Assembly Processes in Soil to Survive Organochlorine Contamination. <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	5
408	Spatiotemporal Dynamics of Coastal Viral Community Structure and Potential Biogeochemical Roles Affected by an <i>Ulva</i> proliferans Green Tide. <i>MSystems</i> , 2023, 8, .	3.8	2
409	Characterization and genomic analysis of a novel <i>Synechococcus</i> phage S-H9-2 belonging to <i>Bristolvirus</i> genus isolated from the Yellow Sea. <i>Virus Research</i> , 2023, 328, 199072.	2.2	1
411	Diversity and potential function of pig gut DNA viruses. <i>Heliyon</i> , 2023, 9, e14020.	3.2	2
413	Seasonal and Spatially Distributed Viral Metagenomes from Comau Fjord (42°S), Patagonia. <i>Microbiology Resource Announcements</i> , 2023, 12, .	0.6	0
414	Potential Auxiliary Metabolic Capabilities and Activities Reveal Biochemical Impacts of Viruses in Municipal Wastewater Treatment Plants. <i>Environmental Science &amp; Technology</i> , 2023, 57, 5485-5498.	10.0	9
415	Discovery of an Abundant Viral Genus in Polar Regions through the Isolation and Genomic Characterization of a New Virus against <i>Oceanospirillaceae</i> . <i>Applied and Environmental Microbiology</i> , 2023, 89, .	3.1	4

#	ARTICLE	IF	CITATIONS
417	A First Insight into the Microbial and Viral Communities of Comau Fjordâ€™A Unique Human-Impacted Ecosystem in Patagonia (42âˆ™ S). Microorganisms, 2023, 11, 904.	3.6	1
418	Pan-Arctic plankton community structure and its global connectivity. Elementa, 2023, 11, .	3.2	2
419	Unexplored diversity and ecological functions of transposable phages. ISME Journal, 2023, 17, 1015-1028.	9.8	2
420	Genomic analysis and characterization of phages infecting the marine Roseobacter CHAB-I-5 lineage reveal a globally distributed and abundant phage genus. Frontiers in Microbiology, 0, 14, .	3.5	0
421	Environmental viromes reveal the global distribution signatures of deep-sea DNA viruses. Journal of Advanced Research, 2024, 57, 107-117.	9.5	1
422	Mirusviruses link herpesviruses to giant viruses. Nature, 2023, 616, 783-789.	27.8	28
423	A Pseudomonas Lysogenic Bacteriophage Crossing the Antarctic and Arctic, Representing a New Genus of Autographiviridae. International Journal of Molecular Sciences, 2023, 24, 7662.	4.1	3
425	Virome reveals effect of Ulva prolifera green tide on the structural and functional profiles of virus communities in coastal environments. Science of the Total Environment, 2023, 883, 163609.	8.0	2
427	Highly diverse and unknown viruses may enhance Antarctic endolithsâ€™ adaptability. Microbiome, 2023, 11, .	11.1	3
428	Distribution and survival strategies of endemic and cosmopolitan diazotrophs in the Arctic Ocean. ISME Journal, 2023, 17, 1340-1350.	9.8	2
429	Water mass age structures the auxiliary metabolic gene content of free-living and particle-attached deep ocean viral communities. Microbiome, 2023, 11, .	11.1	4
430	Metavirome Profiling and Dynamics of the DNA Viral Community in Seawater in Chuuk State, Federated States of Micronesia. Viruses, 2023, 15, 1293.	3.3	1
431	Gut phageome of the giant panda ( <i>Ailuropoda melanoleuca</i> ) reveals greater diversity than relative species. MSystems, 2023, 8, .	3.8	0
432	<i>Psychrobacter</i> Phage Encoding an Antibiotics Resistance Gene Represents a Novel Caudoviral Family. Microbiology Spectrum, 2023, 11, .	3.0	1
433	Divergent endophytic viromes and phage genome repertoires among banana (Musa) species. Frontiers in Microbiology, 0, 14, .	3.5	0
438	Metatranscriptomics unmasks Mollusca virome with a remarkable presence of rhabdovirus in cephalopods. Frontiers in Marine Science, 0, 10, .	2.5	1
439	Topâ€™heavy trophic structure within benthic viral dark matter. Environmental Microbiology, 2023, 25, 2303-2320.	3.8	2
440	Molecular Detection and Identification of Pathogens, Pathotypes, and Genes. , 2023, , 503-593.		0

#	ARTICLE	IF	CITATIONS
441	Characterization and genomic analysis of phage vB_ValR_NF, representing a new viral family prevalent in the <i>Ulva prolifera</i> blooms. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	1
442	Highly host-linked viromes in the built environment possess habitat-dependent diversity and functions for potential virus-host coevolution. <i>Nature Communications</i> , 2023, 14, .	12.8	2
443	The Ocean Genome: Conservation and the Fair, Equitable and Sustainable Use of Marine Genetic Resources. , 2023, , 91-140.		0
445	Metagenomic Analyses Reveal the Influence of Depth Layers on Marine Biodiversity on Tropical and Subtropical Regions. <i>Microorganisms</i> , 2023, 11, 1668.	3.6	2
446	Virus impacted community adaptation in oligotrophic groundwater environment revealed by Hi-C coupled metagenomic and viromic study. <i>Journal of Hazardous Materials</i> , 2023, 458, 131944.	12.4	2
447	Viromes of Coastal Waters of the North Caspian Sea: Initial Assessment of Diversity and Functional Potential. <i>Diversity</i> , 2023, 15, 813.	1.7	0
449	Diversity and Pathobiology of an Ilarvirus Unexpectedly Detected in Diverse Plants and Global Sequencing Data. <i>Phytopathology</i> , 2023, 113, 1729-1744.	2.2	4
450	Guidelines for public database submission of uncultivated virus genome sequences for taxonomic classification. <i>Nature Biotechnology</i> , 2023, 41, 898-902.	17.5	4
451	CodingDiv: analyzing SNP-level microdiversity to discriminate between coding and noncoding regions in viral genomes. <i>Bioinformatics</i> , 2023, 39, .	4.1	0
452	Novel pelagiphage isolate <i>Polarivirus skadi</i> is a polar specialist that dominates SAR11-associated bacteriophage communities at high latitudes. <i>ISME Journal</i> , 2023, 17, 1660-1670.	9.8	5
455	Small protein modules dictate prophage fates during polylysogeny. <i>Nature</i> , 2023, 620, 625-633.	27.8	4
456	Abundance and ecological footprint of <i>Pseudoalteromonas</i> phage vB_PhoS_XC in the <i>Ulva prolifera</i> green tide. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	0
457	Characterization and genomic analysis of a novel lytic phage vB_PstM_ZRG1 infecting <i>Stutzerimonas stutzeri</i> , representing a new viral genus, <i>Elithevirus</i> . <i>Virus Research</i> , 2023, 334, 199183.	2.2	0
458	Virus-pathogen interactions improve water quality along the Middle Route of the South-to-North Water Diversion Canal. <i>ISME Journal</i> , 2023, 17, 1719-1732.	9.8	1
460	Presence and role of viruses in anaerobic digestion of food waste under environmental variability. <i>Microbiome</i> , 2023, 11, .	11.1	2
461	Lower viral evolutionary pressure under stable versus fluctuating conditions in subzero Arctic brines. <i>Microbiome</i> , 2023, 11, .	11.1	3
464	Unveiling the hidden role of aquatic viruses in hydrocarbon pollution bioremediation. <i>Journal of Hazardous Materials</i> , 2023, 459, 132299.	12.4	0
466	Genome mining shows that retroviruses are pervasively invading vertebrate genomes. <i>Nature Communications</i> , 2023, 14, .	12.8	2

#	ARTICLE	IF	CITATIONS
467	Ocean-wide comparisons of mesopelagic planktonic community structures. ISME Communications, 2023, 3, .	4.2	1
468	Interrogating the viral dark matter of the rumen ecosystem with a global virome database. Nature Communications, 2023, 14, .	12.8	9
469	Identification and genomic analysis of temperate <i>Halomonas</i> bacteriophage vB_HmeY_H4907 from the surface sediment of the Mariana Trench at a depth of 8,900 m. Microbiology Spectrum, 2023, 11, .	3.0	0
470	Genomic diversity and biogeographic distributions of a novel lineage of bacteriophages that infect marine OM43 bacteria. Microbiology Spectrum, 2023, 11, .	3.0	2
471	Diversity, Relationship, and Distribution of Virophages and Large Algal Viruses in Global Ocean Viromes. Viruses, 2023, 15, 1582.	3.3	0
472	Linking extreme seasonality and gene expression in Arctic marine protists. Scientific Reports, 2023, 13, .	3.3	0
473	Phage-microbe dynamics after sterile faecal filtrate transplantation in individuals with metabolic syndrome: a double-blind, randomised, placebo-controlled clinical trial assessing efficacy and safety. Nature Communications, 2023, 14, .	12.8	2
474	Holistic view of the seascape dynamics and environment impact on macro-scale genetic connectivity of marine plankton populations. BMC Ecology and Evolution, 2023, 23, .	1.6	0
475	A systematic analysis of marine lysogens and proviruses. Nature Communications, 2023, 14, .	12.8	4
476	Novel <i>scp</i> RNA viruses from the Atlantic Ocean: Ecogenomics, biogeography, and total viroplankton mass contribution from surface to the deep ocean. Environmental Microbiology, 2023, 25, 3151-3160.	3.8	2
477	Viruses in deep-sea cold seep sediments harbor diverse survival mechanisms and remain genetically conserved within species. ISME Journal, 2023, 17, 1774-1784.	9.8	3
478	Diversity and function of mountain and polar supraglacial DNA viruses. Science Bulletin, 2023, , .	9.0	0
479	Genomic adaptation of giant viruses in polar oceans. Nature Communications, 2023, 14, .	12.8	0
480	Extracellular vesicles are the main contributor to the non-viral protected extracellular sequence space. ISME Communications, 2023, 3, .	4.2	2
481	Viruses participate in the organomineralization of travertines. Scientific Reports, 2023, 13, .	3.3	1
482	Characterization and genomic analysis of an oceanic cyanophage infecting marine <i>Synechococcus</i> reveal a novel genus. Frontiers in Microbiology, 0, 14, .	3.5	0
483	MARVD2: a machine learning enhanced tool to discriminate between archaeal and bacterial viruses in viral datasets. ISME Communications, 2023, 3, .	4.2	1
485	Development and validation of a real-time PCR assay protocol for the specific detection and quantification of pelagiphages in seawater samples. Marine Environmental Research, 2023, 191, 106168.	2.5	0

#	ARTICLE	IF	CITATIONS
486	Characterization and genomic analysis of Stutzerimonas stutzeri phage vB_PstS_ZQG1, representing a novel viral genus. Virus Research, 2023, 336, 199226.	2.2	2
489	Microviruses: A World Beyond $\phi$ X174. Annual Review of Virology, 2023, 10, 99-118.	6.7	2
491	Open questions in the social lives of viruses. Journal of Evolutionary Biology, 2023, 36, 1551-1567.	1.7	6
492	Breaking the Ice: A Review of Phages in Polar Ecosystems. Methods in Molecular Biology, 2024, , 31-71.	0.9	1
493	A novel long-tailed myovirus represents a new T4-like cyanophage cluster. Frontiers in Microbiology, 2023, 14, .	3.5	0
494	Viral Diversity in Benthic Abyssal Ecosystems: Ecological and Methodological Considerations. Viruses, 2023, 15, 2282.	3.3	0
495	PhaGenus: genus-level classification of bacteriophages using a Transformer model. Briefings in Bioinformatics, 2023, 24, .	6.5	0
496	Depth-driven patterns in lytic viral diversity, auxiliary metabolic gene content, and productivity in offshore oligotrophic waters. Frontiers in Microbiology, 2023, 14, .	3.5	0
497	Quantification of Virion-Sense and Complementary-Sense DNA Strands of Circular Single-Stranded DNA Viruses. Methods in Molecular Biology, 2024, , 93-109.	0.9	0
498	Contrasting drivers of abundant phage and prokaryotic communities revealed in diverse coastal ecosystems. ISME Communications, 2023, 3, .	4.2	0
499	Identification of over ten thousand candidate structured RNAs in viruses and phages. Computational and Structural Biotechnology Journal, 2023, 21, 5630-5639.	4.1	0
500	Phylogenetic diversity and functional potential of large and cell-associated viruses in the Bay of Bengal. MSphere, 2023, 18, .	2.9	0
501	Diversity and connectedness of brine shrimp viruses in global hypersaline ecosystems. Science China Life Sciences, 2023, 66, .	4.9	1
503	Enhanced Bacterium-Phage Symbiosis in Attached Microbial Aggregates on a Membrane Surface Facing Elevated Hydraulic Stress. Environmental Science & Technology, 2023, 57, 17324-17337.	10.0	1
505	VIGA: a one-stop tool for eukaryotic virus identification and genome assembly from next-generation-sequencing data. Briefings in Bioinformatics, 2023, 25, .	6.5	0
506	Purification and Up-Concentration of Bacteriophages and Viruses from Fecal Samples. Methods in Molecular Biology, 2024, , 105-110.	0.9	0
507	Structural and Genomic Diversity of Bacteriophages. Methods in Molecular Biology, 2024, , 3-16.	0.9	0
508	Vibrio cyclitrophicus phage encoding gene transfer agent fragment, representing a novel viral family. Virus Research, 2024, 339, 199270.	2.2	0

#	ARTICLE	IF	CITATIONS
509	Structural changes in the gut virome of patients with atherosclerotic cardiovascular disease. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	2
510	Bacteriophage Taxonomy: A Continually Evolving Discipline. <i>Methods in Molecular Biology</i> , 2024, , 27-45.	0.9	0
511	Prokaryotic virus host prediction with graph contrastive augmentaion. <i>PLoS Computational Biology</i> , 2023, 19, e1011671.	3.2	0
512	Viruses under the Antarctic Ice Shelf are active and potentially involved in global nutrient cycles. <i>Nature Communications</i> , 2023, 14, .	12.8	1
514	Revealing viral diversity in the Napahai plateau wetland based on metagenomics. <i>Antonie Van Leeuwenhoek</i> , 2024, 117, .	1.7	0
515	Prophage enhances the ability of deep-sea bacterium <i>Shewanella psychrophila</i> WP2 to utilize D-amino acid. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
516	<i>Shewanella</i> phage encoding a putative anti-CRISPR-like gene represents a novel potential viral family. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
517	PhageScope: a well-annotated bacteriophage database with automatic analyses and visualizations. <i>Nucleic Acids Research</i> , 2024, 52, D756-D761.	14.5	2
518	Viral metagenomics reveals diverse virus-host interactions throughout the soil depth profile. <i>MBio</i> , 2023, 14, .	4.1	0
519	Megataxonomy and global ecology of the virosphere. <i>ISME Journal</i> , 2024, 18, .	9.8	0
520	Diversities and interactions of phages and bacteria in deep-sea sediments as revealed by metagenomics. <i>Frontiers in Microbiology</i> , 0, 14, .	3.5	0
521	Genome analysis of vB_SupP_AX, a novel N4-like phage infecting <i>Sulfitobacter</i> . <i>International Microbiology</i> , 0, , .	2.4	0
522	The structure and assembly mechanisms of T4-like cyanophages community in the South China Sea. <i>Microbiology Spectrum</i> , 2024, 12, .	3.0	0
523	Virome profiling of fig wasps ( <i>Ceratosolen</i> spp.) reveals virus diversity spanning four realms. <i>Virology</i> , 2024, 591, 109992.	2.4	0
524	Host species and geography impact bee-associated RNA virus communities with evidence for isolation by distance in viral populations. <i>ISME Communications</i> , 2024, 4, .	4.2	0
526	The role of phages for microdiverse bacterial communities in proglacial stream biofilms. , 0, 2, .		0
527	Large language models improve annotation of prokaryotic viral proteins. <i>Nature Microbiology</i> , 2024, 9, 537-549.	13.3	2
528	Comparative evaluation of bioinformatic tools for virus-host prediction and their application to a highly diverse community in the Cuatro CiÃ©negas Basin, Mexico. <i>PLoS ONE</i> , 2024, 19, e0291402.	2.5	0

#	ARTICLE	IF	CITATIONS
529	Eco-evolutionary dynamics of gut phageome in wild gibbons (Hoolock tianxing) with seasonal diet variations. Nature Communications, 2024, 15, .	12.8	0
530	Distribution patterns and functional diversity of DNA viruses determined by ecological niches in huge river ecosystems. Virology, 2024, 593, 110015.	2.4	0
532	Identification of HDV-like theta ribozymes involved in tRNA-based recoding of gut bacteriophages. Nature Communications, 2024, 15, .	12.8	0
533	The long and short of it: benchmarking viromics using Illumina, Nanopore and PacBio sequencing technologies. Microbial Genomics, 2024, 10, .	2.0	0
534	Benchmarking informatics approaches for virus discovery: caution is needed when combining <i>in silico</i> identification methods. MSystems, 2024, 9, .	3.8	0
535	Biogeographic patterns and drivers of soil viromes. Nature Ecology and Evolution, 2024, 8, 717-728.	7.8	0
536	Viral potential to modulate microbial methane metabolism varies by habitat. Nature Communications, 2024, 15, .	12.8	0
537	Phages in different habitats and their ability to carry antibiotic resistance genes. Journal of Hazardous Materials, 2024, 469, 133941.	12.4	0
538	The multi-kingdom microbiome catalog of the chicken gastrointestinal tract. Biosafety and Health, 2024, 6, 101-115.	2.7	0
539	The bacteriome-coupled phage communities continuously contract and shift to orchestrate the traditional rice vinegar fermentation. Food Research International, 2024, 184, 114244.	6.2	0