Rising to the challenge: accelerated pace of discovery tr

Nature Reviews Microbiology 13, 147-159 DOI: 10.1038/nrmicro3404

Citation Report

#	Δρτισι σ	IF	CITATION
π		п	CHAHON
1	A New Fractionation and Recovery Method of Viral Genomes Based on Nucleic Acid Composition and Structure Using Tandem Column Chromatography. Microbes and Environments, 2015, 30, 199-203.	1.6	18
2	Variably lytic infection dynamics of large <scp><i>B</i></scp> <i>acteroidetes</i> podovirus phi38:1 against two <scp><i>C</i></scp> <i>ellulophaga baltica</i> host strains. Environmental Microbiology, 2015, 17, 4659-4671.	3.8	32
3	Viral dark matter and virus–host interactions resolved from publicly available microbial genomes. ELife, 2015, 4, .	6.0	400
4	Patterns and ecological drivers of ocean viral communities. Science, 2015, 348, 1261498.	12.6	617
5	First Insights into the Viral Communities of the Deep-sea Anoxic Brines of the Red Sea. Genomics, Proteomics and Bioinformatics, 2015, 13, 304-309.	6.9	33
6	Viromes, Not Gene Markers, for Studying Double-Stranded DNA Virus Communities. Journal of Virology, 2015, 89, 2459-2461.	3.4	59
7	VirSorter: mining viral signal from microbial genomic data. PeerJ, 2015, 3, e985.	2.0	949
8	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. Frontiers in Microbiology, 2015, 6, 199.	3.5	24
9	Set Phages to Stun: Reducing the Virulence ofStaphylococcus aureusin Diabetic Foot Ulcers: Figure 1. Diabetes, 2015, 64, 2701-2703.	0.6	0
10	Biogeography of Viruses in the Sea. Annual Review of Virology, 2015, 2, 41-66.	6.7	96
11	Metagenomic Analysis of Virioplankton of the Subtropical Jiulong River Estuary, China. Viruses, 2016, 8, 35.	3.3	55
12	Composition and Interactions among Bacterial, Microeukaryotic, and T4-like Viral Assemblages in Lakes from Both Polar Zones. Frontiers in Microbiology, 2016, 7, 337.	3.5	12
13	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. Frontiers in Microbiology, 2016, 7, 822.	3.5	49
14	Biogeographic Variation in Host Range Phenotypes and Taxonomic Composition of Marine Cyanophage Isolates. Frontiers in Microbiology, 2016, 7, 983.	3.5	26
15	Abundance of Two Pelagibacter ubique Bacteriophage Genotypes along a Latitudinal Transect in the North and South Atlantic Oceans. Frontiers in Microbiology, 2016, 7, 1534.	3.5	16
16	Largeâ€scale maps of variable infection efficiencies in aquatic <i>Bacteroidetes</i> phageâ€host model systems. Environmental Microbiology, 2016, 18, 3949-3961.	3.8	22
17	Novel viral genomes identified from six metagenomes reveal wide distribution of archaeal viruses and high viral diversity in terrestrial hot springs. Environmental Microbiology, 2016, 18, 863-874.	3.8	53
18	Inferring phage–bacteria infection networks from time-series data. Royal Society Open Science, 2016, 3, 160654.	2.4	10

ATION RED

#	Article	IF	CITATIONS
19	Viral metabolic reprogramming in marine ecosystems. Current Opinion in Microbiology, 2016, 31, 161-168.	5.1	192
20	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. Current Opinion in Biotechnology, 2016, 39, 174-181.	6.6	30
21	Uncovering Earth's virome. Nature, 2016, 536, 425-430.	27.8	880
22	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, 2016, 537, 689-693.	27.8	629
23	Viruses as Winners in the Game of Life. Annual Review of Virology, 2016, 3, 197-214.	6.7	215
24	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. Nucleic Acids Research, 2016, 45, D457-D465.	14.5	177
25	An assessment of US microbiome research. Nature Microbiology, 2016, 1, 15015.	13.3	101
26	Re-examination of the relationship between marine virus and microbial cell abundances. Nature Microbiology, 2016, 1, 15024.	13.3	264
27	Assessing viral taxonomic composition in benthic marine ecosystems: reliability and efficiency of different bioinformatic tools for viral metagenomic analyses. Scientific Reports, 2016, 6, 28428.	3.3	36
28	Marine Viruses. , 2016, , 155-183.		7
29	Marine phage genomics: the tip of the iceberg. FEMS Microbiology Letters, 2016, 363, fnw158.	1.8	48
30	Illuminating structural proteins in viral "dark matter―with metaproteomics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2436-2441.	7.1	95
31	Ecophysiological Distinctions of Haloarchaea from a Hypersaline Antarctic Lake as Determined by Metaproteomics. Applied and Environmental Microbiology, 2016, 82, 3165-3173.	3.1	24
32	Acidianus Tailed Spindle Virus: a New Archaeal Large Tailed Spindle Virus Discovered by Culture-Independent Methods. Journal of Virology, 2016, 90, 3458-3468.	3.4	27
33	Seasonal time bombs: dominant temperate viruses affect Southern Ocean microbial dynamics. ISME Journal, 2016, 10, 437-449.	9.8	257
34	VirusSeeker, a computational pipeline for virus discovery and virome composition analysis. Virology, 2017, 503, 21-30.	2.4	115
35	Temperature is a key factor in <i>Micromonas</i> –virus interactions. ISME Journal, 2017, 11, 601-612.	9.8	56
36	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. Microbiome, 2017, 5, 10.	11.1	901

		CITATION REPORT		
#	Article		IF	CITATIONS
37	Modelling plankton ecosystems in the meta-omics era. Are we ready?. Marine Genomics	, 2017, 32, 1-17.	1.1	29
38	Viruses comprise an extensive pool of mobile genetic elements in eukaryote cell culture clinical samples. FASEB Journal, 2017, 31, 1987-2000.	s and human	0.5	69
39	Genomic exploration of individual giant ocean viruses. ISME Journal, 2017, 11, 1736-17	45.	9.8	40
40	Visualizing Adsorption of Cyanophage P-SSP7 onto Marine Prochlorococcus. Scientific I 7, 44176.	Reports, 2017,	3.3	24
41	Marine Microbial Community Adaptation and Resiliency to Anthropogenic Stresses Thro Horizontal Gene Transfer. , 2017, , 109-131.	ough		0
42	Biotic interactions as drivers of algal origin and evolution. New Phytologist, 2017, 216,	670-681.	7.3	25
43	Genome characteristics and environmental distribution of the first phage that infects th aÂfreshwater methylotrophic bacterial group. Environmental Microbiology, 2017, 19, 4	ie LD28 clade, 714-4727.	3.8	26
44	A novel inducible prophage from the mycosphere inhabitant Paraburkholderia terrae BS Reports, 2017, 7, 9156.	437. Scientific	3.3	19
45	Unveiling the role and life strategies of viruses from the surface to the dark ocean. Scien 2017, 3, e1602565.	nce Advances,	10.3	113
46	Genomic, proteomic and bioinformatic analysis of two temperate phages in Roseobacte isolated from the deep-sea water. BMC Genomics, 2017, 18, 485.	r clade bacteria	2.8	10
47	Membrane vesicles in sea water: heterogeneous DNA content and implications for viral estimates. ISME Journal, 2017, 11, 394-404.	abundance	9.8	96
48	Viral ecology comes of age. Environmental Microbiology Reports, 2017, 9, 33-35.		2.4	81
49	Metagenomic Approaches to Assess Bacteriophages in Various Environmental Niches. V 127.	'iruses, 2017, 9,	3.3	98
50	The Human Gut Phage Community and Its Implications for Health and Disease. Viruses,	2017, 9, 141.	3.3	206
51	Marine Viruses: Key Players in Marine Ecosystems. Viruses, 2017, 9, 302.		3.3	78
52	Distribution and Inferred Evolutionary Characteristics of a Chimeric ssDNA Virus Associa Intertidal Marine Isopods. Viruses, 2017, 9, 361.	ited with	3.3	9
53	Bridging the Gap between Knowing and Modeling Viruses in Marine Systems—An Upc Frontiers in Marine Science, 2017, 3, .	oming Frontier.	2.5	31
54	Comparative Omics and Trait Analyses of Marine Pseudoalteromonas Phages Advance t Concept. Frontiers in Microbiology, 2017, 8, 1241.	he Phage OTU	3.5	34

#	Article	IF	CITATIONS
55	Inevitability of the emergence and persistence of genetic parasites caused by evolutionary instability of parasite-free states. Biology Direct, 2017, 12, 31.	4.6	59
56	Differentiation and Structure in Sulfolobus islandicus Rod-Shaped Virus Populations. Viruses, 2017, 9, 120.	3.3	26
57	A virus or more in (nearly) every cell: ubiquitous networks of virus–host interactions in extreme environments. ISME Journal, 2018, 12, 1706-1714.	9.8	94
58	Abundance and observations of thermophilic microbial and viral communities in submarine and terrestrial hot fluid systems of the French Southern and Antarctic Lands. Polar Biology, 2018, 41, 1335-1352.	1.2	5
59	Contemporary Phage Biology: From Classic Models to New Insights. Cell, 2018, 172, 1260-1270.	28.9	176
60	Does the microbiome and virome contribute to myalgic encephalomyelitis/chronic fatigue syndrome?. Clinical Science, 2018, 132, 523-542.	4.3	38
61	Viral Metagenomics Approaches for High-Resolution Screening of Multiplexed Arthropod and Plant Viral Communities. Methods in Molecular Biology, 2018, 1746, 77-95.	0.9	25
62	Lowâ€ŧemperature chemotaxis, halotaxis and chemohalotaxis by the psychrophilic marine bacterium <i>Colwellia psychrerythraea</i> 34H. Environmental Microbiology Reports, 2018, 10, 92-101.	2.4	12
63	Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. ISME Journal, 2018, 12, 1287-1295.	9.8	44
64	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. Nature, 2018, 554, 118-122.	27.8	160
65	The â€~Neglected' Soil Virome – Potential Role and Impact. Trends in Microbiology, 2018, 26, 649-662.	7.7	152
66	Quantification of diverse virus populations in the environment using the polony method. Nature Microbiology, 2018, 3, 62-72.	13.3	53
67	Prasinovirus Attack of Ostreococcus Is Furtive by Day but Savage by Night. Journal of Virology, 2018, 92, .	3.4	42
68	Interrogating marine virusâ€host interactions and elemental transfer with BONCAT and nanoSIMSâ€based methods. Environmental Microbiology, 2018, 20, 671-692.	3.8	53
69	Metagenomics reshapes the concepts of RNA virus evolution by revealing extensive horizontal virus transfer. Virus Research, 2018, 244, 36-52.	2.2	190
70	Iron Chloride Flocculation of Bacteriophages from Seawater. Methods in Molecular Biology, 2018, 1681, 49-57.	0.9	16
71	Increase in taxonomic assignment efficiency of viral reads in metagenomic studies. Virus Research, 2018, 244, 230-234.	2.2	10
72	Prochlorococcus viruses—From biodiversity to biogeochemical cycles. Science China Earth Sciences, 2018, 61, 1728-1736.	5.2	4

	CITATION	Report	
#	Article	IF	CITATIONS
73	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. MSystems, 2018, 3, .	3.8	189
74	Freshwater Viromes: From Sampling to Evaluation. Methods in Molecular Biology, 2018, 1849, 17-27.	0.9	0
75	Smoking is associated with quantifiable differences in the human lung DNA virome and metabolome. Respiratory Research, 2018, 19, 174.	3.6	28
76	Bacteriophage research – What we have learnt and what still needs to be addressed. Research in Microbiology, 2018, 169, 481-487.	2.1	22
77	Metavirome Sequencing of the Termite Gut Reveals the Presence of an Unexplored Bacteriophage Community. Frontiers in Microbiology, 2017, 8, 2548.	3.5	34
78	Quantitative Viral Community DNA Analysis Reveals the Dominance of Single-Stranded DNA Viruses in Offshore Upper Bathyal Sediment from Tohoku, Japan. Frontiers in Microbiology, 2018, 9, 75.	3.5	23
79	Host-linked soil viral ecology along a permafrost thaw gradient. Nature Microbiology, 2018, 3, 870-880.	13.3	372
80	Phage puppet masters of the marine microbial realm. Nature Microbiology, 2018, 3, 754-766.	13.3	438
81	Eco-evolutionary Dynamics Linked to Horizontal Gene Transfer in Vibrios. Annual Review of Microbiology, 2018, 72, 89-110.	7.3	89
82	Water-Mediated Transmission of Plant, Animal, and Human Viruses. Advances in Virus Research, 2018, 101, 85-128.	2.1	23
83	Viruses in Marine Ecosystems: From Open Waters to Coral Reefs. Advances in Virus Research, 2018, 101, 1-38.	2.1	20
84	Implication of Viral Infections for Greenhouse Gas Dynamics in Freshwater Wetlands: Challenges and Perspectives. Frontiers in Microbiology, 2019, 10, 1962.	3.5	14
85	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. Nature Microbiology, 2019, 4, 1895-1906.	13.3	206
86	Absolute quantification of infecting viral particles by chipâ€based digital polymerase chain reaction. Environmental Microbiology Reports, 2019, 11, 855-860.	2.4	4
87	Genomeâ€resolved viral and cellular metagenomes revealed potential key virusâ€host interactions in a deep freshwater lake. Environmental Microbiology, 2019, 21, 4740-4754.	3.8	49
88	Metagenomic Analysis of the Diversity of DNA Viruses in the Surface and Deep Sea of the South China Sea. Frontiers in Microbiology, 2019, 10, 1951.	3.5	34
89	Assessing the viral content of uncultured picoeukaryotes in the globalâ€ocean by single cell genomics. Molecular Ecology, 2019, 28, 4272-4289.	3.9	25
90	Metagenomic Analysis of Virus Diversity and Relative Abundance in a Eutrophic Freshwater Harbour. Viruses, 2019, 11, 792.	3.3	24

#	Article	IF	CITATIONS
91	Targeted metagenomic recovery of four divergent viruses reveals shared and distinctive characteristics of giant viruses of marine eukaryotes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190086.	4.0	22
92	Metagenomic Characterization of the Viral Community of the South Scotia Ridge. Viruses, 2019, 11, 95.	3.3	22
93	virMine: automated detection of viral sequences from complex metagenomic samples. PeerJ, 2019, 7, e6695.	2.0	48
94	Microbial ecology of the Namib Desert. , 2019, , 113-143.		0
95	Soil Viruses: A New Hope. MSystems, 2019, 4, .	3.8	71
96	Overview of Virus Infection and Tumorigenesis. , 2019, , 1-23.		0
97	Soil Aggregate Microbial Communities: Towards Understanding Microbiome Interactions at Biologically Relevant Scales. Applied and Environmental Microbiology, 2019, 85, .	3.1	233
98	Roles of Microbial Metabolites in Bacteriophage-Microbe Interactions. , 2019, , 175-207.		1
99	Viral invasion fitness across a continuum from lysis to latencyâ€. Virus Evolution, 2019, 5, vez006.	4.9	57
100	Estimate of the diversity of viral and bacterial assemblage in the coastal water of Lake Baikal. FEMS Microbiology Letters, 2019, 366, .	1.8	13
101	Autochthonous Bacteriophages in the Microbial Loop Structure of Different Biotopes of Lake Baikal. Contemporary Problems of Ecology, 2019, 12, 143-154.	0.7	5
102	The genera of bacteriophages and their receptors are the major determinants of host range. Environmental Microbiology, 2019, 21, 2095-2111.	3.8	45
103	A Needle in A Haystack: Tracing Bivalve-Associated Viruses in High-Throughput Transcriptomic Data. Viruses, 2019, 11, 205.	3.3	28
104	Host Taxon Predictor - A Tool for Predicting Taxon of the Host of a Newly Discovered Virus. Scientific Reports, 2019, 9, 3436.	3.3	30
105	Dynamic marine viral infections and major contribution to photosynthetic processes shown by spatiotemporal picoplankton metatranscriptomes. Nature Communications, 2019, 10, 1169.	12.8	62
106	Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. Environmental Microbiology, 2019, 21, 2148-2170.	3.8	15
108	Bacteria–Virus Interactions. , 2019, , 95-108.		6
109	Host-hijacking and planktonic piracy: how phages command the microbial high seas. Virology Journal, 2019, 16, 15.	3.4	99

#	Article	IF	CITATIONS
110	Novel marine diatom ssRNA virus NitRevRNAV infecting Nitzschia reversa. Plant Ecology and Evolution, 2019, 152, 178-187.	0.7	7
111	VFM: Identification of Bacteriophages From Metagenomic Bins and Contigs Based on Features Related to Gene and Genome Composition. IEEE Access, 2019, 7, 177529-177538.	4.2	7
113	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25900-25908.	7.1	165
114	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	17.5	414
115	IMC/VR v.2.0: an integrated data management and analysis system for cultivated and environmental viral genomes. Nucleic Acids Research, 2019, 47, D678-D686.	14.5	174
116	Coupled virus - bacteria interactions and ecosystem function in an engineered microbial system. Water Research, 2019, 152, 264-273.	11.3	31
117	A viral reckoning: viruses emerge as essential manipulators of global ecosystems. Environmental Microbiology Reports, 2019, 11, 3-8.	2.4	5
118	Metabolic and biogeochemical consequences of viral infection in aquatic ecosystems. Nature Reviews Microbiology, 2020, 18, 21-34.	28.6	222
119	Single-virus genomics and beyond. Nature Reviews Microbiology, 2020, 18, 705-716.	28.6	18
120	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. Nature Microbiology, 2020, 5, 1262-1270.	13.3	156
121	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
122	Viral Metagenomic Content Reflects Seawater Ecological Quality in the Coastal Zone. Viruses, 2020, 12, 806.	3.3	10
123	DRAM for distilling microbial metabolism to automate the curation of microbiome function. Nucleic Acids Research, 2020, 48, 8883-8900.	14.5	410
124	Genomic analysis of Synechococcus phage S-B43 and its adaption to the coastal environment. Virus Research, 2020, 289, 198155.	2.2	5
125	Lysogeny in the oceans: Lessons from cultivated model systems and a reanalysis of its prevalence. Environmental Microbiology, 2020, 22, 4919-4933.	3.8	25
126	Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. Nature Ecology and Evolution, 2020, 4, 1639-1649.	7.8	78
127	The International Virus Bioinformatics Meeting 2020. Viruses, 2020, 12, 1398.	3.3	3
128	Resurrection of inactive microbes and resistome present in the natural frozen world: Reality or myth?. Science of the Total Environment, 2020, 735, 139275.	8.0	21

# 129	ARTICLE Tara Oceans: towards global ocean ecosystems biology. Nature Reviews Microbiology, 2020, 18, 428-445.	IF 28.6	CITATIONS 227
130	In silico Prediction of Virus-Host Interactions for Marine Bacteroidetes With the Use of Metagenome-Assembled Genomes. Frontiers in Microbiology, 2020, 11, 738.	3.5	20
131	<i>Alteromonas</i> Myovirus V22 Represents a New Genus of Marine Bacteriophages Requiring a Tail Fiber Chaperone for Host Recognition. MSystems, 2020, 5, .	3.8	15
132	Quantification of T4-Like and T7-Like Cyanophages Using the Polony Method Show They Are Significant Members of the Virioplankton in the North Pacific Subtropical Gyre. Frontiers in Microbiology, 2020, 11, 1210.	3.5	16
133	The Ecology of Predation at the Microscale. , 2020, , .		8
134	Viral Ecogenomics of Arctic Cryopeg Brine and Sea Ice. MSystems, 2020, 5, .	3.8	23
135	Temporal Dynamics of Soil Virus and Bacterial Populations in Agricultural and Early Plant Successional Soils. Frontiers in Microbiology, 2020, 11, 1494.	3.5	42
136	Diverse and unique viruses discovered in the surface water of the East China Sea. BMC Genomics, 2020, 21, 441.	2.8	20
137	Diversity and potential biogeochemical impacts of viruses in bulk and rhizosphere soils. Environmental Microbiology, 2021, 23, 588-599.	3.8	62
138	Extraordinary diversity of viruses in deepâ€sea sediments as revealed by metagenomics without prior virion separation. Environmental Microbiology, 2021, 23, 728-743.	3.8	27
139	Bacteriophage Diversity. , 2021, , 265-275.		0
140	The communities and functional profiles of virioplankton along a salinity gradient in a subtropical estuary. Science of the Total Environment, 2021, 759, 143499.	8.0	16
141	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
142	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
143	Ecology and Global Impacts of Viruses. , 2021, , 621-626.		0
145	Bacteriophage Discovery and Genomics. , 2021, , 219-230.		0
146	Single-Virus Genomics: Studying Uncultured Viruses, One at a Time. , 2021, , 184-190.		3
147	Viromes outperform total metagenomes in revealing the spatiotemporal patterns of agricultural soil viral communities. ISME Journal, 2021, 15, 1956-1970.	9.8	101

#	Article	IF	CITATIONS
149	VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. Microbiome, 2021, 9, 37.	11.1	441
150	Deep sea sediments associated with cold seeps are a subsurface reservoir of viral diversity. ISME Journal, 2021, 15, 2366-2378.	9.8	93
151	VirION2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature. PeerJ, 2021, 9, e11088.	2.0	25
152	Streamlining CRISPR spacer-based bacterial host predictions to decipher the viral dark matter. Nucleic Acids Research, 2021, 49, 3127-3138.	14.5	72
153	Analysis of Different Size Fractions Provides a More Complete Perspective of Viral Diversity in a Freshwater Embayment. Applied and Environmental Microbiology, 2021, 87, .	3.1	9
154	A Novel Broad Host Range Phage Infecting Alteromonas. Viruses, 2021, 13, 987.	3.3	9
158	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. MSystems, 2021, 6, e0053721.	3.8	8
160	A Review of Marine Viruses in Coral Ecosystem. Journal of Marine Science and Engineering, 2021, 9, 711.	2.6	7
161	The genetic and ecophysiological diversity of <i>Microcystis</i> . Environmental Microbiology, 2021, 23, 7278-7313.	3.8	56
162	Glacier ice archives nearly 15,000-year-old microbes and phages. Microbiome, 2021, 9, 160.	11.1	59
163	Gut dsDNA virome shows diversity and richness alterations associated with childhood obesity and metabolic syndrome. IScience, 2021, 24, 102900.	4.1	26
164	DNase Treatment Improves Viral Enrichment in Agricultural Soil Viromes. MSystems, 2021, 6, e0061421.	3.8	12
165	Viral Characteristics of the Warm Atlantic and Cold Arctic Water Masses in the Nordic Seas. Applied and Environmental Microbiology, 2021, 87, e0116021.	3.1	12
166	High-throughput identification of viral termini and packaging mechanisms in virome datasets using PhageTermVirome. Scientific Reports, 2021, 11, 18319.	3.3	6
168	Incomplete tricarboxylic acid cycle and proton gradient in <i>Pandoravirus massiliensis</i> : is it still a virus?. ISME Journal, 2022, 16, 695-704.	9.8	16
169	Viral Community and Virus-Associated Antibiotic Resistance Genes in Soils Amended with Organic Fertilizers. Environmental Science & Technology, 2021, 55, 13881-13890.	10.0	49
171	Efficient dilution-to-extinction isolation of novel virus–host model systems for fastidious heterotrophic bacteria. ISME Journal, 2021, 15, 1585-1598.	9.8	26
172	Intraguild Predation: Predatory Networks at the Microbial Scale. , 2020, , 65-87.		3

		CITATION REPORT		
#	Article		IF	Citations
173	Phage diversity, genomics and phylogeny. Nature Reviews Microbiology, 2020, 18, 125	5-138.	28.6	455
186	Genome diversity of marine phages recovered from Mediterranean metagenomes: Size Genetics, 2017, 13, e1007018.	matters. PLoS	3.5	82
187	Water column stratification structures viral community composition in the Sargasso S Microbial Ecology, 2015, 76, 85-94.	ea. Aquatic	1.8	16
188	Optimization of viral resuspension methods for carbon-rich soils along a permafrost th PeerJ, 2016, 4, e1999.	aw gradient.	2.0	51
189	Towards quantitative viromics for both double-stranded and single-stranded DNA virus 4, e2777.	es. PeerJ, 2016,	2.0	185
190	Putative archaeal viruses from the mesopelagic ocean. PeerJ, 2017, 5, e3428.		2.0	46
191	Benchmarking viromics: an <i>in silico</i> evaluation of metagenome-enabled estimat community composition and diversity. PeerJ, 2017, 5, e3817.	es of viral	2.0	235
192	Bioreactor virome metagenomics sequencing using DNA spike-ins. PeerJ, 2018, 6, e43	51.	2.0	3
193	Towards optimized viral metagenomes for double-stranded and single-stranded DNA v challenging soils. PeerJ, 2019, 7, e7265.	iruses from	2.0	48
194	Benchmarking protocols for the metagenomic analysis of stream biofilm viromes. Peer	J, 2019, 7, e8187.	2.0	9
195	Virus diversity in metagenomes of a lichen symbiosis (<i>Umbilicaria phaea</i>): comp genomes, putative hosts and elevational distributions. Environmental Microbiology, 20 6637-6650.	lete viral)21, 23,	3.8	11
196	Active virus-host interactions at sub-freezing temperatures in Arctic peat soil. Microbic 208.	me, 2021, 9,	11.1	52
197	Bacteriophages in Biological Wastewater Treatment Systems: Occurrence, Characteriz Function. Frontiers in Microbiology, 2021, 12, 730071.	ation, and	3.5	16
198	Marine Microbial Diversity. , 2016, , 57-85.			0
199	Method-centered digital communities on protocols.io for fast-paced scientific innovati F1000Research, 2016, 5, 2271.	on.	1.6	0
200	Bacteriophage Discovery and Genomics. , 2017, , 1-13.			0
201	Method-centered digital communities on protocols.io for fast-paced scientific innovati F1000Research, 2016, 5, 2271.	on.	1.6	0
205	Marine Viruses. , 2019, , 25-62.			1

#	Article	IF	CITATIONS
208	Phage Communication and the Ecological Implications on Microbial Interactions, Diversity, and Function. , 2020, , 71-86.		1
210	Viral community analysis in a marine oxygen minimum zone indicates increased potential for viral manipulation of microbial physiological state. ISME Journal, 2022, 16, 972-982.	9.8	17
212	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. Microbiome, 2021, 9, 233.	11.1	53
213	Saline lakes on the Qinghai-Tibet Plateau harbor unique viral assemblages mediating microbial environmental adaption. IScience, 2021, 24, 103439.	4.1	13
214	Unravelling the ecological complexity of soil viromes: Challenges and opportunities. Science of the Total Environment, 2022, 812, 152217.	8.0	10
215	Organochlorine contamination enriches virus-encoded metabolism and pesticide degradation associated auxiliary genes in soil microbiomes. ISME Journal, 2022, 16, 1397-1408.	9.8	45
217	Viral tag and grow: a scalable approach to capture and characterize infectious virus–host pairs. ISME Communications, 2022, 2, .	4.2	4
220	Experimental evidence for the impact of soil viruses on carbon cycling during surface plant litter decomposition. ISME Communications, 2022, 2, .	4.2	26
221	Heterogeneity of soil bacterial and bacteriophage communities in three rice agroecosystems and potential impacts of bacteriophage on nutrient cycling. Environmental Microbiomes, 2022, 17, 17.	5.0	11
222	Distribution Characteristics of Soil Viruses Under Different Precipitation Gradients on the Qinghai-Tibet Plateau. Frontiers in Microbiology, 2022, 13, 848305.	3.5	5
223	Year-round dynamics of amplicon sequence variant communities differ among eukaryotes, <i>Imitervirales</i> and prokaryotes in a coastal ecosystem. FEMS Microbiology Ecology, 2022, 97, .	2.7	3
224	iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. ISME Communications, 2021, 1, .	4.2	13
240	Predators of Soil Bacteria in Plant and Human Health. Phytobiomes Journal, 2022, 6, 184-200.	2.7	7
241	Virus-Host Interactions and Genetic Diversity of Antarctic Sea Ice Bacteriophages. MBio, 2022, 13, e0065122.	4.1	8
242	Patterns and ecological drivers of viral communities in acid mine drainage sediments across Southern China. Nature Communications, 2022, 13, 2389.	12.8	25
243	Consecutive monoculture regimes differently affected the diversity of the rhizosphere soil viral community and accumulated soil-borne plant viruses. Agriculture, Ecosystems and Environment, 2022, 337, 108076.	5.3	5
244	Virioplankton assemblages from challenger deep, the deepest place in the oceans. IScience, 2022, 25, 104680.	4.1	7
245	Metabolic arsenal of giant viruses: Host hijack or self-use?. ELife, 0, 11, .	6.0	12

#	Article	IF	Citations
246	Phageâ€bacterium interactions and nutrient availability can shape C and N retention in microbial biomass. European Journal of Soil Science, 2022, 73, .	3.9	8
247	Recent insights into aquatic viruses: Emerging and reemerging pathogens, molecular features, biological effects, and novel investigative approaches. , 2022, 1, 100062.		11
251	Research in ecosystem services provided by bacteria, archaea, and viruses from inland waters: synthesis of main topics and trends over the last ca. 40Âyears. Hydrobiologia, 0, , .	2.0	1
252	Over two decades of research on the marine RNA virosphere. , 2022, 1, .		3
253	Soil viral diversity, ecology and climate change. Nature Reviews Microbiology, 2023, 21, 296-311.	28.6	41
254	Agricultural Land Use Influences Bacteriophage Community Diversity, Richness, and Heterogeneity. Current Microbiology, 2023, 80, .	2.2	0
255	FastViromeExplorer-Novel: Recovering Draft Genomes of Novel Viruses and Phages in Metagenomic Data. Journal of Computational Biology, 0, , .	1.6	0
256	What Lies Beneath? Taking the Plunge into the Murky Waters of Phage Biology. MSystems, 2023, 8, .	3.8	3
257	Ecological drivers and potential functions of viral communities in flooded arsenic-contaminated paddy soils. Science of the Total Environment, 2023, 872, 162289.	8.0	3
258	Prevalence of Viral Frequency-Dependent Infection in Coastal Marine Prokaryotes Revealed Using Monthly Time Series Virome Analysis. MSystems, 2023, 8, .	3.8	3
261	Viral and Bacterial Communities Collaborate through Complementary Assembly Processes in Soil to Survive Organochlorine Contamination. Applied and Environmental Microbiology, 2023, 89, .	3.1	5
263	Environmental vibrio phage–bacteria interaction networks reflect the genetic structure of host populations. Environmental Microbiology, 2023, 25, 1424-1438.	3.8	4
264	Potential Auxiliary Metabolic Capabilities and Activities Reveal Biochemical Impacts of Viruses in Municipal Wastewater Treatment Plants. Environmental Science & Technology, 2023, 57, 5485-5498.	10.0	9
265	Environmental viromes reveal the global distribution signatures of deep-sea DNA viruses. Journal of Advanced Research, 2024, 57, 107-117.	9.5	1
266	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
267	The Post-Antibiotic Era: A New Dawn for Bacteriophages. Biology, 2023, 12, 681.	2.8	0
268	Metatranscriptomic analysis uncovers prevalent viral ORFs compatible with mitochondrial translation. MSystems, 2023, 8, .	3.8	1
269	How Well do Earth System Models Capture Apparent Relationships Between Phytoplankton Biomass and Environmental Variables?. Global Biogeochemical Cycles, 2023, 37, .	4.9	1

#	Article	IF	CITATIONS
271	Lower viral evolutionary pressure under stable versus fluctuating conditions in subzero Arctic brines. Microbiome, 2023, 11, .	11.1	3
272	Characterization of Parageobacillus Bacteriophage vB_PtoS_NIIg3.2—A Representative of a New Genus within Thermophilic Siphoviruses. International Journal of Molecular Sciences, 2023, 24, 13980.	4.1	1
273	Viral but not bacterial community successional patterns reflect extreme turnover shortly after rewetting dry soils. Nature Ecology and Evolution, 2023, 7, 1809-1822.	7.8	6
274	Counting dots or counting reads? Complementary approaches to estimate virus-to-microbe ratios. ISME Journal, 2023, 17, 1521-1522.	9.8	2
275	MArVD2: a machine learning enhanced tool to discriminate between archaeal and bacterial viruses in viral datasets. ISME Communications, 2023, 3, .	4.2	1
280	With a pinch of salt: metagenomic insights into Namib Desert salt pan microbial mats and halites reveal functionally adapted and competitive communities. Applied and Environmental Microbiology, 2023, 89, .	3.1	1
281	Viruses under the Antarctic Ice Shelf are active and potentially involved in global nutrient cycles. Nature Communications, 2023, 14, .	12.8	1
283	Revealing viral diversity in the Napahai plateau wetland based on metagenomics. Antonie Van Leeuwenhoek, 2024, 117, .	1.7	0
284	The insights into the phage communities of fermented foods in the age of viral metagenomics. Critical Reviews in Food Science and Nutrition, 0, , 1-13.	10.3	0
286	The role of phages for microdiverse bacterial communities in proglacial stream biofilms. , 0, 2, .		0
287	Cyanophages: interacting mechanism and evolutionary significance. , 2024, , 255-282.		0