

Rising to the challenge: accelerated pace of discovery tr

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A New Fractionation and Recovery Method of Viral Genomes Based on Nucleic Acid Composition and Structure Using Tandem Column Chromatography. <i>Microbes and Environments</i> , 2015, 30, 199-203.	0.7	18
2	Variably lytic infection dynamics of large <i>Bacteroidetes</i> podovirus phi38:1 against two <i>Cellulophaga baltica</i> host strains. <i>Environmental Microbiology</i> , 2015, 17, 4659-4671.	1.8	32
3	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>ELife</i> , 2015, 4, .	2.8	400
4	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261498.	6.0	617
5	First Insights into the Viral Communities of the Deep-sea Anoxic Brines of the Red Sea. <i>Genomics, Proteomics and Bioinformatics</i> , 2015, 13, 304-309.	3.0	33
6	Viromes, Not Gene Markers, for Studying Double-Stranded DNA Virus Communities. <i>Journal of Virology</i> , 2015, 89, 2459-2461.	1.5	59
7	VirSorter: mining viral signal from microbial genomic data. <i>PeerJ</i> , 2015, 3, e985.	0.9	949
8	Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. <i>Frontiers in Microbiology</i> , 2015, 6, 199.	1.5	24
9	Set Phages to Stun: Reducing the Virulence of <i>Staphylococcus aureus</i> in Diabetic Foot Ulcers: Figure 1. <i>Diabetes</i> , 2015, 64, 2701-2703.	0.3	0
10	Biogeography of Viruses in the Sea. <i>Annual Review of Virology</i> , 2015, 2, 41-66.	3.0	96
11	Metagenomic Analysis of Virioplankton of the Subtropical Jiulong River Estuary, China. <i>Viruses</i> , 2016, 8, 35.	1.5	55
12	Composition and Interactions among Bacterial, Microeukaryotic, and T4-like Viral Assemblages in Lakes from Both Polar Zones. <i>Frontiers in Microbiology</i> , 2016, 7, 337.	1.5	12
13	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. <i>Frontiers in Microbiology</i> , 2016, 7, 822.	1.5	49
14	Biogeographic Variation in Host Range Phenotypes and Taxonomic Composition of Marine Cyanophage Isolates. <i>Frontiers in Microbiology</i> , 2016, 7, 983.	1.5	26
15	Abundance of Two Pelagibacter ubiquitous Bacteriophage Genotypes along a Latitudinal Transect in the North and South Atlantic Oceans. <i>Frontiers in Microbiology</i> , 2016, 7, 1534.	1.5	16
16	Large-scale maps of variable infection efficiencies in aquatic <i>Bacteroidetes</i> phage-host model systems. <i>Environmental Microbiology</i> , 2016, 18, 3949-3961.	1.8	22
17	Novel viral genomes identified from six metagenomes reveal wide distribution of archaeal viruses and high viral diversity in terrestrial hot springs. <i>Environmental Microbiology</i> , 2016, 18, 863-874.	1.8	53
18	Inferring phage-bacteria infection networks from time-series data. <i>Royal Society Open Science</i> , 2016, 3, 160654.	1.1	10

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19	Viral metabolic reprogramming in marine ecosystems. <i>Current Opinion in Microbiology</i> , 2016, 31, 161-168.	2.3	192
20	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. <i>Current Opinion in Biotechnology</i> , 2016, 39, 174-181.	3.3	30
21	Uncovering Earth's virome. <i>Nature</i> , 2016, 536, 425-430.	13.7	880
22	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629
23	Viruses as Winners in the Game of Life. <i>Annual Review of Virology</i> , 2016, 3, 197-214.	3.0	215
24	IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2016, 45, D457-D465.	6.5	177
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30	Illuminating structural proteins in viral "dark matter" with metaproteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2436-2441.	3.3	95
31	Ecophysiological Distinctions of Haloarchaea from a Hypersaline Antarctic Lake as Determined by Metaproteomics. <i>Applied and Environmental Microbiology</i> , 2016, 82, 3165-3173.	1.4	24
32	Acidianus Tailed Spindle Virus: a New Archaeal Large Tailed Spindle Virus Discovered by Culture-Independent Methods. <i>Journal of Virology</i> , 2016, 90, 3458-3468.	1.5	27
33	Seasonal time bombs: dominant temperate viruses affect Southern Ocean microbial dynamics. <i>ISME Journal</i> , 2016, 10, 437-449.	4.4	257
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35	Temperature is a key factor in <i>Micromonas</i> virus interactions. <i>ISME Journal</i> , 2017, 11, 601-612.	4.4	56
36	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017, 5, 10.	4.9	901

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37	Modelling plankton ecosystems in the meta-omics era. Are we ready?. <i>Marine Genomics</i> , 2017, 32, 1-17.	0.4	29
38	Viruses comprise an extensive pool of mobile genetic elements in eukaryote cell cultures and human clinical samples. <i>FASEB Journal</i> , 2017, 31, 1987-2000.	0.2	69
39	Genomic exploration of individual giant ocean viruses. <i>ISME Journal</i> , 2017, 11, 1736-1745.	4.4	40
40	Visualizing Adsorption of Cyanophage P-SSP7 onto Marine <i>Prochlorococcus</i> . <i>Scientific Reports</i> , 2017, 7, 44176.	1.6	24
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42	Biotic interactions as drivers of algal origin and evolution. <i>New Phytologist</i> , 2017, 216, 670-681.	3.5	25
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49	Metagenomic Approaches to Assess Bacteriophages in Various Environmental Niches. <i>Viruses</i> , 2017, 9, 127.	1.5	98
50	The Human Gut Phage Community and Its Implications for Health and Disease. <i>Viruses</i> , 2017, 9, 141.	1.5	206
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56	Differentiation and Structure in <i>Sulfolobus islandicus</i> Rod-Shaped Virus Populations. <i>Viruses</i> , 2017, 9, 120.	1.5	26
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63	Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. <i>ISME Journal</i> , 2018, 12, 1287-1295.	4.4	44
64	A major lineage of non-tailed dsDNA viruses as unrecognized killers of marine bacteria. <i>Nature</i> , 2018, 554, 118-122.	13.7	160
65	The "Neglected" Soil Virome - Potential Role and Impact. <i>Trends in Microbiology</i> , 2018, 26, 649-662.	3.5	152
66	Quantification of diverse virus populations in the environment using the polony method. <i>Nature Microbiology</i> , 2018, 3, 62-72.	5.9	53
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68	Interrogating marine virus-host interactions and elemental transfer with BONCAT and nanoSIMS-based methods. <i>Environmental Microbiology</i> , 2018, 20, 671-692.	1.8	53
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71	Increase in taxonomic assignment efficiency of viral reads in metagenomic studies. <i>Virus Research</i> , 2018, 244, 230-234.	1.1	10
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74	Freshwater Viromes: From Sampling to Evaluation. <i>Methods in Molecular Biology</i> , 2018, 1849, 17-27.	0.4	0
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83	Viruses in Marine Ecosystems: From Open Waters to Coral Reefs. <i>Advances in Virus Research</i> , 2018, 101, 1-38.	0.9	20
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86	Absolute quantification of infecting viral particles by chipâ€based digital polymerase chain reaction. <i>Environmental Microbiology Reports</i> , 2019, 11, 855-860.	1.0	4
87	Genomeâ€resolved viral and cellular metagenomes revealed potential key virusâ€host interactions in a deep freshwater lake. <i>Environmental Microbiology</i> , 2019, 21, 4740-4754.	1.8	49
88	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.	1.5	34
89	Assessing the viral content of uncultured picoeukaryotes in the globalâ€ocean by single cell genomics. <i>Molecular Ecology</i> , 2019, 28, 4272-4289.	2.0	25
90	Metagenomic Analysis of Virus Diversity and Relative Abundance in a Eutrophic Freshwater Harbour. <i>Viruses</i> , 2019, 11, 792.	1.5	24

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114	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
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123	DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020, 48, 8883-8900.	6.5	410
124	Genomic analysis of <i>Synechococcus</i> phage S-B43 and its adaption to the coastal environment. <i>Virus Research</i> , 2020, 289, 198155.	1.1	5
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134	Viral Ecogenomics of Arctic Cryopeg Brine and Sea Ice. <i>MSystems</i> , 2020, 5, .	1.7	23
135	Temporal Dynamics of Soil Virus and Bacterial Populations in Agricultural and Early Plant Successional Soils. <i>Frontiers in Microbiology</i> , 2020, 11, 1494.	1.5	42
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137	Diversity and potential biogeochemical impacts of viruses in bulk and rhizosphere soils. <i>Environmental Microbiology</i> , 2021, 23, 588-599.	1.8	62
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164	DNase Treatment Improves Viral Enrichment in Agricultural Soil Viromes. <i>MSystems</i> , 2021, 6, e0061421.	1.7	12
165	Viral Characteristics of the Warm Atlantic and Cold Arctic Water Masses in the Nordic Seas. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0116021.	1.4	12
166	High-throughput identification of viral termini and packaging mechanisms in virome datasets using PhageTermVirome. <i>Scientific Reports</i> , 2021, 11, 18319.	1.6	6
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