

Matthew B Sullivan

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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|--------------------|--------------------------|-----------------|-----------------|
| 177 papers | 18,234 citations | 69 h-index | 134 g-index |
| 199 ext. papers | 25,754 ext. citations | 13.9 avg, IF | 6.77 L-index |

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 177 | Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359 | 33.3 | 1261 |
| 176 | Community genomics among stratified microbial assemblages in the ocean's interior. <i>Science</i> , 2006 , 311, 496-503 | 33.3 | 1055 |
| 175 | Genome divergence in two <i>Prochlorococcus</i> ecotypes reflects oceanic niche differentiation. <i>Nature</i> , 2003 , 424, 1042-7 | 50.4 | 904 |
| 174 | Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017 , 5, 10 | 16.6 | 595 |
| 173 | VirSorter: mining viral signal from microbial genomic data. <i>PeerJ</i> , 2015 , 3, e985 | 3.1 | 563 |
| 172 | Scientists' warning to humanity: microorganisms and climate change. <i>Nature Reviews Microbiology</i> , 2019 , 17, 569-586 | 22.2 | 516 |
| 171 | Ocean plankton. Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015 , 348, 1262073 | 33.3 | 496 |
| 170 | Ocean plankton. Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015 , 348, 1261498 | 33.3 | 421 |
| 169 | Three <i>Prochlorococcus</i> cyanophage genomes: signature features and ecological interpretations. <i>PLoS Biology</i> , 2005 , 3, e144 | 9.7 | 411 |
| 168 | Transfer of photosynthesis genes to and from <i>Prochlorococcus</i> viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11013-8 | 11.5 | 406 |
| 167 | Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016 , 537, 689-693 | 50.4 | 400 |
| 166 | Cyanophages infecting the oceanic cyanobacterium <i>Prochlorococcus</i> . <i>Nature</i> , 2003 , 424, 1047-51 | 50.4 | 393 |
| 165 | Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016 , 532, 465-470 | 50.4 | 392 |
| 164 | Consensus statement: Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017 , 15, 161-168 | 22.2 | 375 |
| 163 | Genomic islands and the ecology and evolution of <i>Prochlorococcus</i> . <i>Science</i> , 2006 , 311, 1768-70 | 33.3 | 362 |
| 162 | Prevalence and evolution of core photosystem II genes in marine cyanobacterial viruses and their hosts. <i>PLoS Biology</i> , 2006 , 4, e234 | 9.7 | 326 |
| 161 | Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>eLife</i> , 2015 , 4, | 8.9 | 274 |

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|-----|---|------|-----|
| 160 | Lysogeny in nature: mechanisms, impact and ecology of temperate phages. <i>ISME Journal</i> , 2017 , 11, 1511-1520 | 11.9 | 272 |
| 159 | Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019 , 177, 1109-1123.e14 | 56.2 | 256 |
| 158 | The Pacific Ocean virome (POV): a marine viral metagenomic dataset and associated protein clusters for quantitative viral ecology. <i>PLoS ONE</i> , 2013 , 8, e57355 | 3.7 | 256 |
| 157 | Genome-wide expression dynamics of a marine virus and host reveal features of co-evolution. <i>Nature</i> , 2007 , 449, 83-6 | 50.4 | 248 |
| 156 | Abundant SAR11 viruses in the ocean. <i>Nature</i> , 2013 , 494, 357-60 | 50.4 | 238 |
| 155 | Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. <i>Environmental Microbiology</i> , 2010 , 12, 3035-56 | 5.2 | 237 |
| 154 | Rising to the challenge: accelerated pace of discovery transforms marine virology. <i>Nature Reviews Microbiology</i> , 2015 , 13, 147-59 | 22.2 | 205 |
| 153 | Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019 , 37, 632-639 | 44.5 | 201 |
| 152 | Phage-bacteria infection networks. <i>Trends in Microbiology</i> , 2013 , 21, 82-91 | 12.4 | 200 |
| 151 | Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. <i>ISME Journal</i> , 2017 , 11, 237-247 | 11.9 | 189 |
| 150 | Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , 2018 , 3, 870-880 | 26.6 | 182 |
| 149 | Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37 | 44.5 | 180 |
| 148 | A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , 2011 , 3, 195-202 | 3.7 | 176 |
| 147 | Seasonal time bombs: dominant temperate viruses affect Southern Ocean microbial dynamics. <i>ISME Journal</i> , 2016 , 10, 437-49 | 11.9 | 168 |
| 146 | A global ocean atlas of eukaryotic genes. <i>Nature Communications</i> , 2018 , 9, 373 | 17.4 | 168 |
| 145 | Single-cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. <i>ISME Journal</i> , 2015 , 9, 2386-99 | 11.9 | 153 |
| 144 | Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics. <i>ELife</i> , 2014 , 3, e03125 | 8.9 | 141 |
| 143 | Twelve previously unknown phage genera are ubiquitous in global oceans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12798-803 | 11.5 | 140 |

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|-----|---|------|-----|
| 142 | Viral tagging reveals discrete populations in <i>Synechococcus</i> viral genome sequence space. <i>Nature</i> , 2014 , 513, 242-5 | 50.4 | 137 |
| 141 | Metabolic reprogramming by viruses in the sunlit and dark ocean. <i>Genome Biology</i> , 2013 , 14, R123 | 18.3 | 137 |
| 140 | Efficient phage-mediated pigment biosynthesis in oceanic cyanobacteria. <i>Current Biology</i> , 2008 , 18, 442-8.3 | 128 | |
| 139 | vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect and. <i>PeerJ</i> , 2017 , 5, e3243 | 3.1 | 128 |
| 138 | Soil Aggregate Microbial Communities: Towards Understanding Microbiome Interactions at Biologically Relevant Scales. <i>Applied and Environmental Microbiology</i> , 2019 , 85, | 4.8 | 126 |
| 137 | The Gut Virome Database Reveals Age-Dependent Patterns of Virome Diversity in the Human Gut. <i>Cell Host and Microbe</i> , 2020 , 28, 724-740.e8 | 23.4 | 125 |
| 136 | Depth-stratified functional and taxonomic niche specialization in the CoreTand FlexibleTPacific Ocean Virome. <i>ISME Journal</i> , 2015 , 9, 472-84 | 11.9 | 124 |
| 135 | Benchmarking viromics: an evaluation of metagenome-enabled estimates of viral community composition and diversity. <i>PeerJ</i> , 2017 , 5, e3817 | 3.1 | 124 |
| 134 | Towards quantitative metagenomics of wild viruses and other ultra-low concentration DNA samples: a rigorous assessment and optimization of the linker amplification method. <i>Environmental Microbiology</i> , 2012 , 14, 2526-37 | 5.2 | 122 |
| 133 | Evaluation of methods to concentrate and purify ocean virus communities through comparative, replicated metagenomics. <i>Environmental Microbiology</i> , 2013 , 15, 1428-40 | 5.2 | 122 |
| 132 | Structural changes in a marine podovirus associated with release of its genome into <i>Prochlorococcus</i> . <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 830-6 | 17.6 | 121 |
| 131 | IMG/VR: a database of cultured and uncultured DNA Viruses and retroviruses. <i>Nucleic Acids Research</i> , 2017 , 45, D457-D465 | 20.1 | 115 |
| 130 | Gene Expression Changes and Community Turnover Differentially Shape the Global Ocean Metatranscriptome. <i>Cell</i> , 2019 , 179, 1068-1083.e21 | 56.2 | 113 |
| 129 | Global Trends in Marine Plankton Diversity across Kingdoms of Life. <i>Cell</i> , 2019 , 179, 1084-1097.e21 | 56.2 | 108 |
| 128 | Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. <i>PeerJ</i> , 2016 , 4, e2777 | 3.1 | 108 |
| 127 | Global morphological analysis of marine viruses shows minimal regional variation and dominance of non-tailed viruses. <i>ISME Journal</i> , 2013 , 7, 1738-51 | 11.9 | 106 |
| 126 | Single-virus genomics reveals hidden cosmopolitan and abundant viruses. <i>Nature Communications</i> , 2017 , 8, 15892 | 17.4 | 104 |
| 125 | Ocean plankton. Environmental characteristics of Agulhas rings affect interocean plankton transport. <i>Science</i> , 2015 , 348, 1261447 | 33.3 | 100 |

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|-----|--|------|----|
| 124 | Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. <i>MSystems</i> , 2018 , 3, | 7.6 | 99 |
| 123 | The genome and structural proteome of an ocean siphovirus: a new window into the cyanobacterial TmobilomeT <i>Environmental Microbiology</i> , 2009 , 11, 2935-51 | 5.2 | 97 |
| 122 | Metabolic and biogeochemical consequences of viral infection in aquatic ecosystems. <i>Nature Reviews Microbiology</i> , 2020 , 18, 21-34 | 22.2 | 97 |
| 121 | Single-cell and population level viral infection dynamics revealed by phageFISH, a method to visualize intracellular and free viruses. <i>Environmental Microbiology</i> , 2013 , 15, 2306-18 | 5.2 | 95 |
| 120 | Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. <i>Scientific Data</i> , 2017 , 4, 170093 | 8.2 | 89 |
| 119 | Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , 2008 , 10, 2810-23 | 5.2 | 87 |
| 118 | Phylogenomics of T4 cyanophages: lateral gene transfer in the TcoreTand origins of host genes. <i>Environmental Microbiology</i> , 2012 , 14, 2113-26 | 5.2 | 84 |
| 117 | iVirus: facilitating new insights in viral ecology with software and community data sets imbedded in a cyberinfrastructure. <i>ISME Journal</i> , 2017 , 11, 7-14 | 11.9 | 80 |
| 116 | Modeling ecological drivers in marine viral communities using comparative metagenomics and network analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10714-9 | 11.5 | 79 |
| 115 | Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013 , 14, 320 | 4.5 | 77 |
| 114 | DRAM for distilling microbial metabolism to automate the curation of microbiome function. <i>Nucleic Acids Research</i> , 2020 , 48, 8883-8900 | 20.1 | 77 |
| 113 | Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. <i>BMC Genomics</i> , 2016 , 17, 930 | 4.5 | 75 |
| 112 | Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. <i>MSphere</i> , 2017 , 2, | 5 | 72 |
| 111 | Ocean viruses: rigorously evaluating the metagenomic sample-to-sequence pipeline. <i>Virology</i> , 2012 , 434, 181-6 | 3.6 | 72 |
| 110 | Contrasting life strategies of viruses that infect photo- and heterotrophic bacteria, as revealed by viral tagging. <i>MBio</i> , 2012 , 3, | 7.8 | 72 |
| 109 | Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. <i>Nature Microbiology</i> , 2018 , 3, 1274-1284 | 26.6 | 70 |
| 108 | VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. <i>Microbiome</i> , 2021 , 9, 37 | 16.6 | 69 |
| 107 | Long-read viral metagenomics captures abundant and microdiverse viral populations and their niche-defining genomic islands. <i>PeerJ</i> , 2019 , 7, e6800 | 3.1 | 68 |

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|-----|--|------|----|
| 106 | Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020 , 165, 1253-1260 | 2.6 | 66 |
| 105 | Discovery of several thousand highly diverse circular DNA viruses. <i>ELife</i> , 2020 , 9, | 8.9 | 65 |
| 104 | Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. <i>Nature Communications</i> , 2017 , 8, 858 | 17.4 | 62 |
| 103 | Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018 , 163, 1125-1129 | 2.6 | 62 |
| 102 | Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020 , 18, 428-445 | 22.2 | 60 |
| 101 | Phage-specific metabolic reprogramming of virocells. <i>ISME Journal</i> , 2020 , 14, 881-895 | 11.9 | 56 |
| 100 | Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020 , 69, 110-123 | 8.4 | 56 |
| 99 | Single-cell genomics of multiple uncultured stramenopiles reveals underestimated functional diversity across oceans. <i>Nature Communications</i> , 2018 , 9, 310 | 17.4 | 55 |
| 98 | The global virome: not as big as we thought?. <i>Current Opinion in Virology</i> , 2013 , 3, 566-71 | 7.5 | 51 |
| 97 | Numerous cultivated and uncultivated viruses encode ribosomal proteins. <i>Nature Communications</i> , 2019 , 10, 752 | 17.4 | 49 |
| 96 | 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, 2436-41 | 11.5 | 49 |
| 95 | Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , 2019 , 4, 352-361 | 26.6 | 49 |
| 94 | Viral ecology comes of age. <i>Environmental Microbiology Reports</i> , 2017 , 9, 33-35 | 3.7 | 45 |
| 93 | Community-Level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019 , 33, 391-419 | 5.9 | 42 |
| 92 | Viromes, not gene markers, for studying double-stranded DNA virus communities. <i>Journal of Virology</i> , 2015 , 89, 2459-61 | 6.6 | 41 |
| 91 | Dietary energy drives the dynamic response of bovine rumen viral communities. <i>Microbiome</i> , 2017 , 5, 155 | 16.6 | 38 |
| 90 | Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017 , 162, 1153-1157 | 2.6 | 38 |
| 89 | Putative archaeal viruses from the mesopelagic ocean. <i>PeerJ</i> , 2017 , 5, e3428 | 3.1 | 36 |

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|----|--|------|----|
| 88 | On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017 , 8, | 7.8 | 34 |
| 87 | Regulation of infection efficiency in a globally abundant marine Bacterioidetes virus. <i>ISME Journal</i> , 2017 , 11, 284-295 | 11.9 | 33 |
| 86 | Optimization of viral resuspension methods for carbon-rich soils along a permafrost thaw gradient. <i>PeerJ</i> , 2016 , 4, e1999 | 3.1 | 32 |
| 85 | Multiple mechanisms drive phage infection efficiency in nearly identical hosts. <i>ISME Journal</i> , 2018 , 12, 1605-1618 | 11.9 | 28 |
| 84 | Emerging methods to study bacteriophage infection at the single-cell level. <i>Frontiers in Microbiology</i> , 2014 , 5, 724 | 5.7 | 28 |
| 83 | Contrasting genomic patterns and infection strategies of two co-existing Bacterioidetes podovirus genera. <i>Environmental Microbiology</i> , 2014 , 16, 2501-13 | 5.2 | 28 |
| 82 | Comparative Omics and Trait Analyses of Marine Phages Advance the Phage OTU Concept. <i>Frontiers in Microbiology</i> , 2017 , 8, 1241 | 5.7 | 27 |
| 81 | The human gut virome database | | 27 |
| 80 | Preparation of metagenomic libraries from naturally occurring marine viruses. <i>Methods in Enzymology</i> , 2013 , 531, 143-65 | 1.7 | 26 |
| 79 | Towards optimized viral metagenomes for double-stranded and single-stranded DNA viruses from challenging soils. <i>PeerJ</i> , 2019 , 7, e7265 | 3.1 | 26 |
| 78 | The spinal cord-gut-immune axis as a master regulator of health and neurological function after spinal cord injury. <i>Experimental Neurology</i> , 2020 , 323, 113085 | 5.7 | 26 |
| 77 | Biogeography of marine giant viruses reveals their interplay with eukaryotes and ecological functions. <i>Nature Ecology and Evolution</i> , 2020 , 4, 1639-1649 | 12.3 | 25 |
| 76 | Modelling plankton ecosystems in the meta-omics era. Are we ready?. <i>Marine Genomics</i> , 2017 , 32, 1-17 | 1.9 | 23 |
| 75 | Variably lytic infection dynamics of large Bacterioidetes podovirus phi38:1 against two Cellulophaga baltica host strains. <i>Environmental Microbiology</i> , 2015 , 17, 4659-71 | 5.2 | 20 |
| 74 | Genomic evidence for global ocean plankton biogeography shaped by large-scale current systems | | 20 |
| 73 | Smoking is associated with quantifiable differences in the human lung DNA virome and metabolome. <i>Respiratory Research</i> , 2018 , 19, 174 | 7.3 | 20 |
| 72 | Large-scale maps of variable infection efficiencies in aquatic Bacterioidetes phage-host model systems. <i>Environmental Microbiology</i> , 2016 , 18, 3949-3961 | 5.2 | 18 |
| 71 | Future Ocean Observations to Connect Climate, Fisheries and Marine Ecosystems. <i>Frontiers in Marine Science</i> , 2019 , 6, | 4.5 | 17 |

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|----|--|------|----|
| 70 | 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 | 9.7 | 17 |
| 69 | Metabolic Architecture of the Deep Ocean Microbiome | | 17 |
| 68 | Deep ocean metagenomes provide insight into the metabolic architecture of bathypelagic microbial communities. <i>Communications Biology</i> , 2021 , 4, 604 | 6.7 | 17 |
| 67 | Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean. <i>IScience</i> , 2021 , 24, 102002 | 6.1 | 17 |
| 66 | An inexpensive, accurate, and precise wet-mount method for enumerating aquatic viruses. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 2995-3000 | 4.8 | 16 |
| 65 | Visualizing Adsorption of Cyanophage P-SSP7 onto Marine Prochlorococcus. <i>Scientific Reports</i> , 2017 , 7, 44176 | 4.9 | 15 |
| 64 | Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. <i>Frontiers in Microbiology</i> , 2015 , 6, 199 | 5.7 | 15 |
| 63 | Optimizing genome assembly from PCR-amplified metagenomes. <i>PeerJ</i> , 2019 , 7, e6902 | 3.1 | 14 |
| 62 | Revisiting the rules of life for viruses of microorganisms. <i>Nature Reviews Microbiology</i> , 2021 , 19, 501-513 | 22.2 | 14 |
| 61 | Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. <i>ISME Journal</i> , 2021 , 15, 981-998 | 11.9 | 13 |
| 60 | Viral Ecogenomics of Arctic Cryopeg Brine and Sea Ice. <i>MSystems</i> , 2020 , 5, | 7.6 | 12 |
| 59 | Clean Low-Biomass Procedures and Their Application to Ancient Ice Core Microorganisms. <i>Frontiers in Microbiology</i> , 2018 , 9, 1094 | 5.7 | 12 |
| 58 | Viral elements and their potential influence on microbial processes along the permanently stratified Cariaco Basin redoxcline. <i>ISME Journal</i> , 2020 , 14, 3079-3092 | 11.9 | 12 |
| 57 | Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , 2021 , 12, 3503 | 17.4 | 12 |
| 56 | Closely related viruses of the marine picoeukaryotic alga <i>Ostreococcus lucimarinus</i> exhibit different ecological strategies. <i>Environmental Microbiology</i> , 2019 , 21, 2148-2170 | 5.2 | 11 |
| 55 | Iron Chloride Flocculation of Bacteriophages from Seawater. <i>Methods in Molecular Biology</i> , 2018 , 1681, 49-57 | 1.4 | 11 |
| 54 | Prevalence of viral photosynthesis genes along a freshwater to saltwater transect in Southeast USA. <i>Environmental Microbiology Reports</i> , 2019 , 11, 672-689 | 3.7 | 10 |
| 53 | Life-style and genome structure of marine <i>Pseudoalteromonas</i> siphovirus B8b isolated from the northwestern Mediterranean Sea. <i>PLoS ONE</i> , 2015 , 10, e0114829 | 3.7 | 10 |

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|----|---|------|----|
| 52 | Interaction dynamics and virus-host range for estuarine actinophages captured by epicPCR. <i>Nature Microbiology</i> , 2021 , 6, 630-642 | 26.6 | 10 |
| 51 | Life and death in the soil microbiome: how ecological processes influence biogeochemistry.. <i>Nature Reviews Microbiology</i> , 2022 , | 22.2 | 10 |
| 50 | Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021 , 6, 1561-1574 | 26.6 | 9 |
| 49 | Glacier ice archives fifteen-thousand-year-old viruses | | 9 |
| 48 | Gene sharing networks to automate genome-based prokaryotic viral taxonomy | | 9 |
| 47 | Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome.. <i>Science</i> , 2022 , 376, 156-162 | 33.3 | 9 |
| 46 | Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Bacteriophages | | 8 |
| 45 | 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 | 3.1 | 8 |
| 44 | Novel integrative elements and genomic plasticity in ocean ecosystems | | 7 |
| 43 | Expanding standards in viromics: in silico evaluation of dsDNA viral genome identification, classification, and auxiliary metabolic gene curation. <i>PeerJ</i> , 2021 , 9, e11447 | 3.1 | 7 |
| 42 | Glacier ice archives nearly 15,000-year-old microbes and phages. <i>Microbiome</i> , 2021 , 9, 160 | 16.6 | 7 |
| 41 | Fighting Fire with Fire: Phage Potential for the Treatment of O157 Infection. <i>Antibiotics</i> , 2018 , 7, | 4.9 | 7 |
| 40 | Six Pseudoalteromonas Strains Isolated from Surface Waters of Kabeltonne, Offshore Helgoland, North Sea. <i>Genome Announcements</i> , 2016 , 4, | | 6 |
| 39 | Closing the gaps on the viral photosystem-I psaDCAB gene organization. <i>Environmental Microbiology</i> , 2015 , 17, 5100-8 | 5.2 | 6 |
| 38 | DRAM for distilling microbial metabolism to automate the curation of microbiome function | | 6 |
| 37 | Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages | | 6 |
| 36 | Uncharted biosynthetic potential of the ocean microbiome | | 6 |
| 35 | Spinal Cord Injury Changes the Structure and Functional Potential of Gut Bacterial and Viral Communities. <i>MSystems</i> , 2021 , 6, | 7.6 | 6 |

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| 34 | efam: an expanded, metaproteome-supported HMM profile database of viral protein families. <i>Bioinformatics</i> , 2021 , | 7.2 | 6 |
| 33 | Functional repertoire convergence of distantly related eukaryotic plankton lineages abundant in the sunlit ocean. <i>Cell Genomics</i> , 2022 , 2, 100123 | | 6 |
| 32 | Biosynthetic potential of the global ocean microbiome. <i>Nature</i> , | 50.4 | 6 |
| 31 | A simple and efficient method for concentration of ocean viruses by chemical flocculation. <i>Environmental Microbiology Reports</i> , 2011 , 3, 809-809 | 3.7 | 5 |
| 30 | Perspective on taxonomic classification of uncultivated viruses. <i>Current Opinion in Virology</i> , 2021 , 51, 207-215 | 7.5 | 5 |
| 29 | Author response: Discovery of several thousand highly diverse circular DNA viruses 2020 , | | 5 |
| 28 | Discovery of several thousand highly diverse circular DNA viruses | | 5 |
| 27 | Eukaryotic virus composition can predict the efficiency of carbon export in the global ocean | | 5 |
| 26 | Improving Phage-Biofilm In Vitro Experimentation. <i>Viruses</i> , 2021 , 13, | 6.2 | 5 |
| 25 | Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021 , 166, 3239-3244 | 2.6 | 5 |
| 24 | Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021 , 7, | 14.3 | 5 |
| 23 | The IsoGenie database: an interdisciplinary data management solution for ecosystems biology and environmental research. <i>PeerJ</i> , 8, e9467 | 3.1 | 4 |
| 22 | Genome-resolved viral ecology in a marine oxygen minimum zone. <i>Environmental Microbiology</i> , 2021 , 23, 2858-2874 | 5.2 | 4 |
| 21 | Contrasting Life Strategies of Viruses That Infect Photo- and Heterotrophic Bacteria, as Revealed by Viral Tagging. <i>MBio</i> , 2013 , 4, | 7.8 | 3 |
| 20 | MetaPop: A pipeline for macro- and micro-diversity analyses and visualization of microbial and viral metagenome-derived populations | | 3 |
| 19 | Soil viruses are underexplored players in ecosystem carbon processing | | 3 |
| 18 | Long-read viral metagenomics enables capture of abundant and microdiverse viral populations and their niche-defining genomic islands | | 3 |
| 17 | Coupling plant litter quantity to a novel metric for litter quality explains C storage changes in a thawing permafrost peatland. <i>Global Change Biology</i> , 2021 , | 11.4 | 2 |

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|----|---|------|---|
| 16 | Viral community analysis in a marine oxygen minimum zone indicates increased potential for viral manipulation of microbial physiological state. <i>ISME Journal</i> , 2021 , | 11.9 | 2 |
| 15 | Friends or Foes? Rapid Determination of Dissimilar Colistin and Ciprofloxacin Antagonism of Phages. <i>Pharmaceuticals</i> , 2021 , 14, | 5.2 | 2 |
| 14 | VIRLON2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature | | 2 |
| 13 | 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 | 11.9 | 2 |
| 12 | Whole-Genome Sequences of Phages p000v and p000y, Which Infect the Bacterial Pathogen Shiga-Toxigenic <i>Escherichia coli</i> . <i>Microbiology Resource Announcements</i> , 2018 , 7, | 1.3 | 2 |
| 11 | Macroscale patterns of oceanic zooplankton composition and size structure. <i>Scientific Reports</i> , 2021 , 11, 15714 | 4.9 | 2 |
| 10 | Diel cycle of sea spray aerosol concentration. <i>Nature Communications</i> , 2021 , 12, 5476 | 17.4 | 2 |
| 9 | Microbial metabolites in the marine carbon cycle.. <i>Nature Microbiology</i> , 2022 , 7, 508-523 | 26.6 | 2 |
| 8 | In vitro analysis of colistin and ciprofloxacin antagonism of <i>Pseudomonas aeruginosa</i> phage PEV2 infection activities | | 1 |
| 7 | Genome-resolved viral ecology in a marine oxygen minimum zone (OMZ) | | 1 |
| 6 | Divergent Genomic Adaptations in the Microbiomes of Arctic Subzero Sea-Ice and Cryopeg Brines. <i>Frontiers in Microbiology</i> , 2021 , 12, 701186 | 5.7 | 1 |
| 5 | MetaPop: a pipeline for macro- and microdiversity analyses and visualization of microbial and viral metagenome-derived populations.. <i>Microbiome</i> , 2022 , 10, 49 | 16.6 | 1 |
| 4 | iVirus 2.0: Cyberinfrastructure-supported tools and data to power DNA virus ecology. <i>ISME Communications</i> , 2021 , 1, | | 1 |
| 3 | High-throughput identification of viral termini and packaging mechanisms in virome datasets using PhageTermVirome. <i>Scientific Reports</i> , 2021 , 11, 18319 | 4.9 | 0 |
| 2 | The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022 , 14, 973 | 6.2 | 0 |
| 1 | Unveiling Infection Strategies across Diverse Marine PhageHost Systems. <i>Proceedings (mdpi)</i> , 2020 , 50, 99 | 0.3 | |