

Ben Temperton

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

4,889
citations

257450

24
h-index

315739

38
g-index

53
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53
docs citations

53
times ranked

6375
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Probiotics and competitive exclusion of pathogens in shrimp aquaculture. <i>Reviews in Aquaculture</i> , 2021, 13, 324-352.	9.0	74
4	Draft Genome Sequences of Pelagimyophage Mosig EXVC030M and Pelagipodophage Lederberg EXVC029P, Isolated from Devil's Hole, Bermuda. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	5
5	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
6	Efficient dilution-to-extinction isolation of novel virus-host model systems for fastidious heterotrophic bacteria. <i>ISME Journal</i> , 2021, 15, 1585-1598.	9.8	26
7	Contrasting impacts of a novel specialist vector on multihost viral pathogen epidemiology in wild and managed bees. <i>Molecular Ecology</i> , 2020, 29, 380-393.	3.9	20
8	Expanding the Diversity of Bacterioplankton Isolates and Modeling Isolation Efficacy with Large-Scale Dilution-to-Extinction Cultivation. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	34
9	Complete Genome Sequence of Marinobacterium sp. Strain LSUCC0821, Isolated from the Coastal Gulf of Mexico. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
10	Genome Sequences of Four <i>Vibrio parahaemolyticus</i> Strains Isolated from the English Channel and the River Thames. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
11	Knock-on community impacts of a novel vector: spillover of emerging DWV from <i>Varroa</i> -infested honeybees to wild bumblebees. <i>Ecology Letters</i> , 2019, 22, 1306-1315.	6.4	68
12	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
13	Discovery and ecogenomic context of a global <i>Candidatus Cryoserica</i> -related phylum active in thawing permafrost, <i>Candidatus Cryoserica</i> phylum nov., <i>Ca. Cryoserica</i> class nov., <i>Ca. Cryosericales</i> ord. nov., <i>Ca. Cryoseriaceae</i> fam. nov., comprising the four species <i>Cryosericum septentrionale</i> gen. nov. sp. nov., <i>Ca. C. hinesii</i> sp. nov., <i>Ca. C. odellii</i> sp. nov., <i>Ca. C. terrychapinii</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2019, 42, 54-66.	2.8	42
14	A Parasitic Arsenic Cycle That Shuttles Energy from Phytoplankton to Heterotrophic Bacterioplankton. <i>MBio</i> , 2019, 10, .	4.1	24
15	Host-hijacking and planktonic piracy: how phages command the microbial high seas. <i>Virology Journal</i> , 2019, 16, 15.	3.4	99
16	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
17	Long-read viral metagenomics captures abundant and microdiverse viral populations and their niche-defining genomic islands. <i>PeerJ</i> , 2019, 7, e6800.	2.0	109
18	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico "Dead Zone". <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	14

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19	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". MBio, 2017, 8, .	4.1	80
20	Biogeochemical and Microbial Variation across 5500 km of Antarctic Surface Sediment Implicates Organic Matter as a Driver of Benthic Community Structure. Frontiers in Microbiology, 2016, 7, 284.	3.5	57
21	The abundant marine bacterium <i>Pelagibacter</i> simultaneously catabolizes dimethylsulfoniopropionate to the gases dimethyl sulfide and methanethiol. Nature Microbiology, 2016, 1, 16065.	13.3	110
22	Implications of streamlining theory for microbial ecology. ISME Journal, 2014, 8, 1553-1565.	9.8	664
23	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. ISME Journal, 2014, 8, 1440-1451.	9.8	119
24	Chlorophyll <i>f</i> and chlorophyll <i>d</i> are produced in the cyanobacterium <i>Chlorogloeopsis fritschii</i> when cultured under natural light and near-infrared radiation. FEBS Letters, 2014, 588, 3770-3777.	2.8	92
25	Discovery of a SAR11 growth requirement for thiamin's pyrimidine precursor and its distribution in the Sargasso Sea. ISME Journal, 2014, 8, 1727-1738.	9.8	128
26	Giovannoni et al. reply. Nature, 2013, 499, E4-E5.	27.8	31
27	High-resolution SAR11 ecotype dynamics at the Bermuda Atlantic Time-series Study site by phylogenetic placement of pyrosequences. ISME Journal, 2013, 7, 1322-1332.	9.8	191
28	Abundant SAR11 viruses in the ocean. Nature, 2013, 494, 357-360.	27.8	305
29	Metagenomics: microbial diversity through a scratched lens. Current Opinion in Microbiology, 2012, 15, 605-612.	5.1	106
30	Defining seasonal marine microbial community dynamics. ISME Journal, 2012, 6, 298-308.	9.8	928
31	Metagenomics. Methods in Molecular Biology, 2011, 733, 173-183.	0.9	8
32	Novel Analysis of Oceanic Surface Water Metagenomes Suggests Importance of Polyphosphate Metabolism in Oligotrophic Environments. PLoS ONE, 2011, 6, e16499.	2.5	56
33	Permanent draft genome sequence of <i>Vibrio tubiashii</i> strain NCIMB 1337 (ATCC19106). Standards in Genomic Sciences, 2011, 4, 183-190.	1.5	19
34	Average genome size: a potential source of bias in comparative metagenomics. ISME Journal, 2010, 4, 1075-1077.	9.8	64
35	Day-length is central to maintaining consistent seasonal diversity in marine bacterioplankton. Nature Precedings, 2010, .	0.1	8
36	Pyrosequencing of <i>Mytilus galloprovincialis</i> cDNAs: Tissue-Specific Expression Patterns. PLoS ONE, 2010, 5, e8875.	2.5	114

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37	The Taxonomic and Functional Diversity of Microbes at a Temperate Coastal Site: A "Multi-Omic"™ Study of Seasonal and Diel Temporal Variation. PLoS ONE, 2010, 5, e15545.	2.5	219
38	Bias in assessments of marine microbial biodiversity in fosmid libraries as evaluated by pyrosequencing. ISME Journal, 2009, 3, 792-796.	9.8	35