

Ben Temperton

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4152039/publications.pdf>

Version: 2024-02-01

38
papers

4,889
citations

257450

24
h-index

315739

38
g-index

53
all docs

53
docs citations

53
times ranked

6375
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining seasonal marine microbial community dynamics. <i>ISME Journal</i> , 2012, 6, 298-308.	9.8	928
2	Implications of streamlining theory for microbial ecology. <i>ISME Journal</i> , 2014, 8, 1553-1565.	9.8	664
3	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541
4	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
5	Abundant SAR11 viruses in the ocean. <i>Nature</i> , 2013, 494, 357-360.	27.8	305
6	The Taxonomic and Functional Diversity of Microbes at a Temperate Coastal Site: A "Multi-Omic" Study of Seasonal and Diel Temporal Variation. <i>PLoS ONE</i> , 2010, 5, e15545.	2.5	219
7	High-resolution SAR11 ecotype dynamics at the Bermuda Atlantic Time-series Study site by phylogenetic placement of pyrosequences. <i>ISME Journal</i> , 2013, 7, 1322-1332.	9.8	191
8	Discovery of a SAR11 growth requirement for thiamin's pyrimidine precursor and its distribution in the Sargasso Sea. <i>ISME Journal</i> , 2014, 8, 1727-1738.	9.8	128
9	Single-cell enabled comparative genomics of a deep ocean SAR11 bathytype. <i>ISME Journal</i> , 2014, 8, 1440-1451.	9.8	119
10	Pyrosequencing of <i>Mytilus galloprovincialis</i> cDNAs: Tissue-Specific Expression Patterns. <i>PLoS ONE</i> , 2010, 5, e8875.	2.5	114
11	The abundant marine bacterium <i>Pelagibacter</i> simultaneously catabolizes dimethylsulfoniopropionate to the gases dimethyl sulfide and methanethiol. <i>Nature Microbiology</i> , 2016, 1, 16065.	13.3	110
12	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
13	Metagenomics: microbial diversity through a scratched lens. <i>Current Opinion in Microbiology</i> , 2012, 15, 605-612.	5.1	106
14	Host-hijacking and planktonic piracy: how phages command the microbial high seas. <i>Virology Journal</i> , 2019, 16, 15.	3.4	99
15	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. <i>FEBS Letters</i> , 2014, 588, 3770-3777.	2.8	92
16	Metabolic Roles of Uncultivated Bacterioplankton Lineages in the Northern Gulf of Mexico "Dead Zone". <i>MBio</i> , 2017, 8, .	4.1	80
17	Probiotics and competitive exclusion of pathogens in shrimp aquaculture. <i>Reviews in Aquaculture</i> , 2021, 13, 324-352.	9.0	74
18	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

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19	Average genome size: a potential source of bias in comparative metagenomics. <i>ISME Journal</i> , 2010, 4, 1075-1077.	9.8	64
20	Biogeochemical and Microbial Variation across 5500 km of Antarctic Surface Sediment Implicates Organic Matter as a Driver of Benthic Community Structure. <i>Frontiers in Microbiology</i> , 2016, 7, 284.	3.5	57
21	Novel Analysis of Oceanic Surface Water Metagenomes Suggests Importance of Polyphosphate Metabolism in Oligotrophic Environments. <i>PLoS ONE</i> , 2011, 6, e16499.	2.5	56
22	Discovery and ecogenomic context of a global <i>Caldiserica</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
23	Bias in assessments of marine microbial biodiversity in fosmid libraries as evaluated by pyrosequencing. <i>ISME Journal</i> , 2009, 3, 792-796.	9.8	35
24	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
25	Giovannoni et al. reply. <i>Nature</i> , 2013, 499, E4-E5.	27.8	31
26	Efficient dilution-to-extinction isolation of novel virusâ€œhost model systems for fastidious heterotrophic bacteria. <i>ISME Journal</i> , 2021, 15, 1585-1598.	9.8	26
27	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
28	A Parasitic Arsenic Cycle That Shuttles Energy from Phytoplankton to Heterotrophic Bacterioplankton. <i>MBio</i> , 2019, 10, .	4.1	24
29	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
30	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
31	Permanent draft genome sequence of <i>Vibrio tubiashii</i> strain NCIMB 1337 (ATCC19106). <i>Standards in Genomic Sciences</i> , 2011, 4, 183-190.	1.5	19
32	Metagenomic Assembly and Prokaryotic Metagenome-Assembled Genome Sequences from the Northern Gulf of Mexico â€œDead Zoneâ€œ. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	14
33	Day-length is central to maintaining consistent seasonal diversity in marine bacterioplankton. <i>Nature Precedings</i> , 2010, , .	0.1	8
34	Metagenomics. <i>Methods in Molecular Biology</i> , 2011, 733, 173-183.	0.9	8
35	Draft Genome Sequences of Pelagimyophage Mosig EXVC030M and Pelagipodophage Lederberg EXVC029P, Isolated from Devilâ€™s Hole, Bermuda. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	5
36	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

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37	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
38	Complete Genome Sequence of <i>Marinobacterium</i> sp. Strain LSUCC0821, Isolated from the Coastal Gulf of Mexico. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1