

Hanno Teeling

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

4,842
citations

236925

25
h-index

414414

32
g-index

33
all docs

33
docs citations

33
times ranked

4843
citing authors

#	ARTICLE	IF	CITATIONS
1	Glycoside hydrolase from the GH76 family indicates that marine <i>Salegendibacter</i> sp. Hel_I_6 consumes alpha-mannan from fungi. <i>ISME Journal</i> , 2022, 16, 1818-1830.	9.8	8
2	Diatom fucan polysaccharide precipitates carbon during algal blooms. <i>Nature Communications</i> , 2021, 12, 1150.	12.8	58
3	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. <i>ISME Journal</i> , 2021, 15, 2336-2350.	9.8	42
4	North Sea spring bloom-associated Gammaproteobacteria fill diverse heterotrophic niches. <i>Environmental Microbiomes</i> , 2021, 16, 15.	5.0	32
5	Polysaccharide niche partitioning of distinct <i>Polaribacter</i> clades during North Sea spring algal blooms. <i>ISME Journal</i> , 2020, 14, 1369-1383.	9.8	50
6	Ancestry and adaptive radiation of Bacteroidetes as assessed by comparative genomics. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126065.	2.8	17
7	Polysaccharide utilization loci of North Sea <i>Flavobacteriia</i> as basis for using SusC/D-protein expression for predicting major phytoplankton glycans. <i>ISME Journal</i> , 2019, 13, 76-91.	9.8	139
8	In marine Bacteroidetes the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. <i>ISME Journal</i> , 2019, 13, 2800-2816.	9.8	125
9	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. <i>ISME Journal</i> , 2019, 13, 3024-3036.	9.8	41
10	Candidatus <i>Prosiliicoccus vernus</i> , a spring phytoplankton bloom associated member of the Flavobacteriaceae. <i>Systematic and Applied Microbiology</i> , 2019, 42, 41-53.	2.8	39
11	Recurrent patterns of microdiversity in a temperate coastal marine environment. <i>ISME Journal</i> , 2018, 12, 237-252.	9.8	135
12	Proteogenomic Analysis of Epibacterium Mobile BBCC367, a Relevant Marine Bacterium Isolated From the South Pacific Ocean. <i>Frontiers in Microbiology</i> , 2018, 9, 3125.	3.5	4
13	Alpha- and beta-mannan utilization by marine Bacteroidetes. <i>Environmental Microbiology</i> , 2018, 20, 4127-4140.	3.8	31
14	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. <i>ISME Journal</i> , 2018, 12, 2894-2906.	9.8	84
15	Genomic and physiological analyses of <i>Reinekea forsetii</i> reveal a versatile opportunistic lifestyle during spring algae blooms. <i>Environmental Microbiology</i> , 2017, 19, 1209-1221.	3.8	13
16	Recurring patterns in bacterioplankton dynamics during coastal spring algae blooms. <i>ELife</i> , 2016, 5, e11888.	6.0	414
17	Polysaccharide utilisation loci of Bacteroidetes from two contrasting open ocean sites in the North Atlantic. <i>Environmental Microbiology</i> , 2016, 18, 4456-4470.	3.8	56
18	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsij ^T . <i>Environmental Microbiology</i> , 2016, 18, 4610-4627.	3.8	131

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19	Annual dynamics of North Sea bacterioplankton: seasonal variability superimposes short-term variation. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv099.	2.7	45
20	Niches of two polysaccharide-degrading <i>Polaribacter</i> isolates from the North Sea during a spring diatom bloom. <i>ISME Journal</i> , 2015, 9, 1410-1422.	9.8	182
21	Dilution cultivation of marine heterotrophic bacteria abundant after a spring phytoplankton bloom in the North Sea. <i>Environmental Microbiology</i> , 2015, 17, 3515-3526.	3.8	56
22	Functional characterization of polysaccharide utilization loci in the marine <i>Bacteroidetes</i> <i>Gramella forsetii</i> KTO803. <i>ISME Journal</i> , 2014, 8, 1492-1502.	9.8	177
23	Diversity and activity of marine bacterioplankton during a diatom bloom in the North Sea assessed by total RNA and pyrotag sequencing. <i>Marine Genomics</i> , 2014, 18, 185-192.	1.1	84
24	The Genome of the Alga-Associated Marine Flavobacterium <i>Formosa agariphila</i> KMM 3901 Reveals a Broad Potential for Degradation of Algal Polysaccharides. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6813-6822.	3.1	222
25	Current opportunities and challenges in microbial metagenome analysis—a bioinformatic perspective. <i>Briefings in Bioinformatics</i> , 2012, 13, 728-742.	6.5	193
26	Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom. <i>Science</i> , 2012, 336, 608-611.	12.6	1,304
27	Genomic content of uncultured <i>Bacteroidetes</i> from contrasting oceanic provinces in the North Atlantic Ocean. <i>Environmental Microbiology</i> , 2012, 14, 52-66.	3.8	137
28	Whole genome analysis of the marine <i>Bacteroidetes</i> ' <i>Gramella forsetii</i> ' reveals adaptations to degradation of polymeric organic matter. <i>Environmental Microbiology</i> , 2006, 8, 2201-2213.	3.8	334
29	RibAlign: a software tool and database for eubacterial phylogeny based on concatenated ribosomal protein subunits. <i>BMC Bioinformatics</i> , 2006, 7, 66.	2.6	20
30	Application of tetranucleotide frequencies for the assignment of genomic fragments. <i>Environmental Microbiology</i> , 2004, 6, 938-947.	3.8	319
31	TETRA: a web-service and a stand-alone program for the analysis and comparison of tetranucleotide usage patterns in DNA sequences. <i>BMC Bioinformatics</i> , 2004, 5, 163.	2.6	309
32	Evaluation of the phylogenetic position of the planctomycete <i>Rhodopirellula baltica</i> SH 1 by means of concatenated ribosomal protein sequences, DNA-directed RNA polymerase subunit sequences and whole genome trees. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 791-801.	1.7	41