Ian P G Marshall

List of Publications by Year
in descending order

41	1,041	430442 18	454577 30
papers	citations	h-index	g-index

42	42	42	1573
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Slow Microbial Life in the Seabed. Annual Review of Marine Science, 2016, 8, 311-332.	5.1	134
2	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated Desulfatiglans-Related Deltaproteobacteria Widely Distributed in Marine Sediment. Frontiers in Microbiology, 2018, 9, 2038.	1.5	69
3	A Single-Cell Genome for Thiovulum sp. Applied and Environmental Microbiology, 2012, 78, 8555-8563.	1.4	58
4	Influence of setup and carbon source on the bacterial community of biocathodes in microbial electrolysis cells. Enzyme and Microbial Technology, 2014, 61-62, 67-75.	1.6	58
5	Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. ISME Journal, 2013, 7, 817-829.	4.4	57
6	Comparison of lactate, formate, and propionate as hydrogen donors for the reductive dehalogenation of trichloroethene in a continuous-flow column. Journal of Contaminant Hydrology, 2010, 113, 77-92.	1.6	53
7	Metagenomes from deep Baltic Sea sediments reveal how past and present environmental conditions determine microbial community composition. Marine Genomics, 2018, 37, 58-68.	0.4	52
8	Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. MBio, 2019, 10, .	1.8	45
9	The Hydrogenase Chip: a tiling oligonucleotide DNA microarray technique for characterizing hydrogen-producing and -consuming microbes in microbial communities. ISME Journal, 2012, 6, 814-826.	4.4	44
10	Environmental filtering determines family-level structure of sulfate-reducing microbial communities in subsurface marine sediments. ISME Journal, 2019, 13, 1920-1932.	4.4	40
11	The novel bacterial phylum Calditrichaeota is diverse, widespread and abundant in marine sediments and has the capacity to degrade detrital proteins. Environmental Microbiology Reports, 2017, 9, 397-403.	1.0	39
12	Thriving or surviving? Evaluating active microbial guilds in Baltic Sea sediment. Environmental Microbiology Reports, 2017, 9, 528-536.	1.0	39
13	Effects of Sulfate Reduction on the Bacterial Community and Kinetic Parameters of a Dechlorinating Culture under Chemostat Growth Conditions. Environmental Science & Technology, 2013, 47, 1879-1886.	4.6	38
14	Pig Farmersâ€™ Homes Harbor More Diverse Airborne Bacterial Communities Than Pig Stables or Suburban Homes. Frontiers in Microbiology, 2018, 9, 870.	1.5	33
15	Cable bacteria at oxygenâ€releasing roots of aquatic plants: a widespread and diverse plantâ€“microbe association. New Phytologist, 2021, 232, 2138-2151.	3.5	32
16	Identification of <scp>D</scp>esulfobacterales as primary hydrogenotrophs in a complex microbial mat community. Geobiology, 2014, 12, 221-230.	1.1	30
17	High quality draft genome sequence of Janthinobacterium psychrotolerans sp. nov., isolated from a frozen freshwater pond. Standards in Genomic Sciences, 2017, 12, 8.	1.5	28
18	Labilibaculum manganireducens gen. nov., sp. nov. and Labilibaculum filiforme sp. nov., Novel Bacteroidetes Isolated from Subsurface Sediments of the Baltic Sea. Frontiers in Microbiology, 2017, 8, 2614.	1.5	25

#	Article	IF	Citations
19	Effect of salinity on cable bacteria species composition and diversity. Environmental Microbiology, 2021, 23, 2605-2616.	1.8	23
20	Cutting out the middle clam: lucinid endosymbiotic bacteria are also associated with seagrass roots worldwide. ISME Journal, 2020, 14, 2901-2905.	4.4	22
21	Subâ€seafloor biogeochemical processes and microbial life in the Baltic Sea. Environmental Microbiology, 2020, 22, 1688-1706.	1.8	22
22	Single-cell amplified genomes of two uncultivated members of the deltaproteobacterial SEEP-SRB1 clade, isolated from marine sediment. Marine Genomics, 2019, 46, 66-69.	0.4	14
23	Reduced TCA cycle rates at high hydrostatic pressure hinder hydrocarbon degradation and obligate oil degraders in natural, deep-sea microbial communities. ISME Journal, 2019, 13, 1004-1018.	4.4	14
24	Genomic insights into the Agromyces-like symbiont of earthworms and its distribution among host species. FEMS Microbiology Ecology, 2018, 94, .	1.3	9
25	Microbial biomass turnover times and clues to cellular protein repair in energy-limited deep Baltic Sea sediments. FEMS Microbiology Ecology, 2019, 95, .	1.3	9
26	Inferring community dynamics of organohalide-respiring bacteria in chemostats by covariance ofrdhAgene abundance. FEMS Microbiology Ecology, 2014, 87, 428-440.	1.3	8
27	Phyllobacterium calauticae sp. nov. isolated from a microaerophilic veil transversed by cable bacteria in freshwater sediment. Antonie Van Leeuwenhoek, 2021, 114, 1877-1887.	0.7	8
28	Complete genome sequence of Desulfobacter hydrogenophilus AcRS1. Marine Genomics, 2020, 50, 100691.	0.4	7
29	Cow Farmersâ€™ Homes Host More Diverse Airborne Bacterial Communities Than Pig Farmersâ€™ Homes and Suburban Homes. Frontiers in Microbiology, 0, 13, .	1.5	6
30	High-quality draft genome of the methanotroph Methylovulum psychrotolerans Str. HV10-M2 isolated from plant material at a high-altitude environment. Standards in Genomic Sciences, 2018, 13, 10.	1.5	5
31	Draft Genome Sequence of Streptococcus anginosus Strain CALM001, Isolated from the Gut of an Elderly Dane. Microbiology Resource Announcements, 2019, 8, .	0.3	5
32	High-Quality Draft Genome Sequence of Lactobacillus casei Strain Z11, Isolated from a Human Adult Intestinal Biopsy Sample. Genome Announcements, 2017, 5, .	0.8	3
33	Draft Genome Sequence of Megasphaera sp. Strain DJF_B143, an Isolate from Pig Hindgut Unable to Produce Skatole. Genome Announcements, 2016, 4, .	0.8	2
34	Properties relevant to atmospheric dispersal of the ice-nucleation active Pseudomonas syringae strain R10.79 isolated from rain water. Aerobiologia, 2021, 37, 225-241.	0.7	2
35	An antimicrobial Staphylococcus sciuri with broad temperature and salt spectrum isolated from the surface of the African social spider, Stegodyphus dumicola. Antonie Van Leeuwenhoek, 2021, 114, 325-335.	0.7	2
36	Genome Sequence of Staphylococcus epidermidis AUH4567, a Clinical Isolate from an Infected Central Venous Catheter. Microbiology Resource Announcements, 2021, 10, .	0.3	2

#	Article	IF	Citations
37	Corganiser: a web-based software tool for planning time-sensitive sampling of whole rounds during scientific drilling. Scientific Drilling, 2014, 18, 1-4.	1.0	1
38	Draft Genome Sequence of Sphingomonas sp. Strain Sph1(2015), Isolated from a Fouled Membrane Filter Used to Produce Drinking Water. Genome Announcements, 2017, 5, .	0.8	0
39	Draft Genome Sequence of Bacillus sp. FMQ74, a Dairy-Contaminating Isolate from Raw Milk. Genome Announcements, 2017, 5, .	0.8	0
40	Draft Genome Sequence of Streptococcus caviae Strain Cavy grass 6 ^T , Isolated from Domesticated Guinea Pig Fecal Samples. Genome Announcements, 2017, 5, .	0.8	0
41	Draft Genome Sequence of Bacillus subtilis SB-14, an Antimicrobially Active Isolate from Namibian Social Spiders (Stegodyphus dumicola). Microbiology Resource Announcements, 2019, 8, .	0.3	0