

# Ian P G Marshall

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2042784/publications.pdf>

Version: 2024-02-01

41  
papers

1,041  
citations

430442

18  
h-index

454577

30  
g-index

42  
all docs

42  
docs citations

42  
times ranked

1573  
citing authors

#	ARTICLE	IF	CITATIONS
1	Properties relevant to atmospheric dispersal of the ice-nucleation active <i>Pseudomonas syringae</i> strain R10.79 isolated from rain water. <i>Aerobiologia</i> , 2021, 37, 225-241.	0.7	2
2	An antimicrobial <i>Staphylococcus sciuri</i> with broad temperature and salt spectrum isolated from the surface of the African social spider, <i>Stegodyphus dumicola</i> . <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 325-335.	0.7	2
3	Genome Sequence of <i>Staphylococcus epidermidis</i> AUH4567, a Clinical Isolate from an Infected Central Venous Catheter. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
4	Cable bacteria at oxygen-releasing roots of aquatic plants: a widespread and diverse plant-microbe association. <i>New Phytologist</i> , 2021, 232, 2138-2151.	3.5	32
5	Effect of salinity on cable bacteria species composition and diversity. <i>Environmental Microbiology</i> , 2021, 23, 2605-2616.	1.8	23
6	<i>Phyllobacterium calauticae</i> sp. nov. isolated from a microaerophilic veil transversed by cable bacteria in freshwater sediment. <i>Antonie Van Leeuwenhoek</i> , 2021, 114, 1877-1887.	0.7	8
7	Complete genome sequence of <i>Desulfobacter hydrogenophilus</i> AcRS1. <i>Marine Genomics</i> , 2020, 50, 100691.	0.4	7
8	Cutting out the middle clam: lucinid endosymbiotic bacteria are also associated with seagrass roots worldwide. <i>ISME Journal</i> , 2020, 14, 2901-2905.	4.4	22
9	Sub-seafloor biogeochemical processes and microbial life in the Baltic Sea. <i>Environmental Microbiology</i> , 2020, 22, 1688-1706.	1.8	22
10	Draft Genome Sequence of <i>Streptococcus anginosus</i> Strain CALM001, Isolated from the Gut of an Elderly Dane. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
11	Single-cell amplified genomes of two uncultivated members of the deltaproteobacterial SEEP-SRB1 clade, isolated from marine sediment. <i>Marine Genomics</i> , 2019, 46, 66-69.	0.4	14
12	Draft Genome Sequence of <i>Bacillus subtilis</i> SB-14, an Antimicrobially Active Isolate from Namibian Social Spiders ( <i>Stegodyphus dumicola</i> ). <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
13	Microbial biomass turnover times and clues to cellular protein repair in energy-limited deep Baltic Sea sediments. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	9
14	Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. <i>MBio</i> , 2019, 10, .	1.8	45
15	Environmental filtering determines family-level structure of sulfate-reducing microbial communities in subsurface marine sediments. <i>ISME Journal</i> , 2019, 13, 1920-1932.	4.4	40
16	Reduced TCA cycle rates at high hydrostatic pressure hinder hydrocarbon degradation and obligate oil degraders in natural, deep-sea microbial communities. <i>ISME Journal</i> , 2019, 13, 1004-1018.	4.4	14
17	Genomic insights into the <i>Agromyces</i> -like symbiont of earthworms and its distribution among host species. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	9
18	Metagenomes from deep Baltic Sea sediments reveal how past and present environmental conditions determine microbial community composition. <i>Marine Genomics</i> , 2018, 37, 58-68.	0.4	52

#	ARTICLE	IF	CITATIONS
19	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated Desulfatiglans-Related Deltaproteobacteria Widely Distributed in Marine Sediment. <i>Frontiers in Microbiology</i> , 2018, 9, 2038.	1.5	69
20	Pig Farmersâ€™ Homes Harbor More Diverse Airborne Bacterial Communities Than Pig Stables or Suburban Homes. <i>Frontiers in Microbiology</i> , 2018, 9, 870.	1.5	33
21	High-quality draft genome of the methanotroph <i>Methylovulum psychrotolerans</i> Str. HV10-M2 isolated from plant material at a high-altitude environment. <i>Standards in Genomic Sciences</i> , 2018, 13, 10.	1.5	5
22	High quality draft genome sequence of <i>Janthinobacterium psychrotolerans</i> sp. nov., isolated from a frozen freshwater pond. <i>Standards in Genomic Sciences</i> , 2017, 12, 8.	1.5	28
23	The novel bacterial phylum <i>Calditrichaeota</i> is diverse, widespread and abundant in marine sediments and has the capacity to degrade detrital proteins. <i>Environmental Microbiology Reports</i> , 2017, 9, 397-403.	1.0	39
24	Thriving or surviving? Evaluating active microbial guilds in Baltic Sea sediment. <i>Environmental Microbiology Reports</i> , 2017, 9, 528-536.	1.0	39
25	High-Quality Draft Genome Sequence of <i>Lactobacillus casei</i> Strain Z11, Isolated from a Human Adult Intestinal Biopsy Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
26	Draft Genome Sequence of <i>Sphingomonas</i> sp. Strain Sph1(2015), Isolated from a Fouled Membrane Filter Used to Produce Drinking Water. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
27	Draft Genome Sequence of <i>Bacillus</i> sp. FMQ74, a Dairy-Contaminating Isolate from Raw Milk. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
28	Draft Genome Sequence of <i>Streptococcus caviae</i> Strain Cavy grass 6 <sup>T</sup> , Isolated from Domesticated Guinea Pig Fecal Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
29	<i>Labilibaculum manganireducens</i> gen. nov., sp. nov. and <i>Labilibaculum filiforme</i> sp. nov., Novel Bacteroidetes Isolated from Subsurface Sediments of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2017, 8, 2614.	1.5	25
30	Draft Genome Sequence of <i>Megasphaera</i> sp. Strain DJF_B143, an Isolate from Pig Hindgut Unable to Produce Skatole. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
31	Slow Microbial Life in the Seabed. <i>Annual Review of Marine Science</i> , 2016, 8, 311-332.	5.1	134
32	Corganiser: a web-based software tool for planning time-sensitive sampling of whole rounds during scientific drilling. <i>Scientific Drilling</i> , 2014, 18, 1-4.	1.0	1
33	Inferring community dynamics of organohalide-respiring bacteria in chemostats by covariance of <i>rdhA</i> gene abundance. <i>FEMS Microbiology Ecology</i> , 2014, 87, 428-440.	1.3	8
34	Influence of setup and carbon source on the bacterial community of biocathodes in microbial electrolysis cells. <i>Enzyme and Microbial Technology</i> , 2014, 61-62, 67-75.	1.6	58
35	Identification of <i>Desulfobacteriales</i> as primary hydrogenotrophs in a complex microbial mat community. <i>Geobiology</i> , 2014, 12, 221-230.	1.1	30
36	Effects of Sulfate Reduction on the Bacterial Community and Kinetic Parameters of a Dechlorinating Culture under Chemostat Growth Conditions. <i>Environmental Science &amp; Technology</i> , 2013, 47, 1879-1886.	4.6	38

#	ARTICLE	IF	CITATIONS
37	Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. ISME Journal, 2013, 7, 817-829.	4.4	57
38	A Single-Cell Genome for Thiovulum sp. Applied and Environmental Microbiology, 2012, 78, 8555-8563.	1.4	58
39	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
40	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
41	Cow Farmersâ€™ Homes Host More Diverse Airborne Bacterial Communities Than Pig Farmersâ€™ Homes and Suburban Homes. Frontiers in Microbiology, 0, 13, .	1.5	6