

Lars Schreiber

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,485
citations

430442
18
h-index

476904
29
g-index

33
all docs

33
docs citations

33
times ranked

3077
citing authors

#	ARTICLE	IF	CITATIONS
1	Predominant archaea in marine sediments degrade detrital proteins. <i>Nature</i> , 2013, 496, 215-218.	13.7	526
2	Filamentous bacteria transport electrons over centimetre distances. <i>Nature</i> , 2012, 491, 218-221.	13.7	475
3	Microbial community assembly and evolution in subseafloor sediment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2940-2945.	3.3	194
4	Genome sequencing of a single cell of the widely distributed marine subsurface <i>Dehalococcoidia</i> phylum <i>Chloroflexi</i> . <i>ISME Journal</i> , 2014, 8, 383-397.	4.4	172
5	Identification of the dominant sulfate-reducing bacterial partner of anaerobic methanotrophs of the ANME-2 clade. <i>Environmental Microbiology</i> , 2010, 12, 2327-2340.	1.8	153
6	A taxonomic framework for cable bacteria and proposal of the candidate genera <i>Electrothrix</i> and <i>Electronema</i> . <i>Systematic and Applied Microbiology</i> , 2016, 39, 297-306.	1.2	151
7	On the evolution and physiology of cable bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19116-19125.	3.3	127
8	Disguised as a Sulfate Reducer: Growth of the Deltaproteobacterium <i>Desulfurivibrio alkaliphilus</i> by Sulfide Oxidation with Nitrate. <i>MBio</i> , 2017, 8, .	1.8	122
9	Cable Bacteria in Freshwater Sediments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6003-6011.	1.4	112
10	Single-Cell Genome and Group-Specific <i>dsrAB</i> Sequencing Implicate Marine Members of the Class <i>Dehalococcoidia</i> (Phylum <i>Chloroflexi</i>) in Sulfur Cycling. <i>MBio</i> , 2016, 7, .	1.8	78
11	Complete genome sequence of <i>Desulfocapsa sulfexigens</i> , a marine deltaproteobacterium specialized in disproportionating inorganic sulfur compounds. <i>Standards in Genomic Sciences</i> , 2013, 8, 58-68.	1.5	69
12	Single-Cell Genomics Reveals a Diverse Metabolic Potential of Uncultivated <i>Desulfatiglans</i> -Related Deltaproteobacteria Widely Distributed in Marine Sediment. <i>Frontiers in Microbiology</i> , 2018, 9, 2038.	1.5	69
13	<i>Endozoicomonas</i> Are Specific, Facultative Symbionts of Sea Squirts. <i>Frontiers in Microbiology</i> , 2016, 7, 1042.	1.5	43
14	Biofilm formation by marine bacteria is impacted by concentration and surface functionalization of polystyrene nanoparticles in a species-specific manner. <i>Environmental Microbiology Reports</i> , 2020, 12, 203-213.	1.0	36
15	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
16	Description of <i>Endozoicomonas ascidiicola</i> sp. nov., isolated from Scandinavian ascidians. <i>Systematic and Applied Microbiology</i> , 2016, 39, 313-318.	1.2	27
17	Potential for Microbially Mediated Natural Attenuation of Diluted Bitumen on the Coast of British Columbia (Canada). <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	25
18	Ammonia-oxidizing Bacteria of the Nitrosospirilla cluster 1 dominate over ammonia-oxidizing Archaea in oligotrophic surface sediments near the South Atlantic Gyre. <i>Environmental Microbiology Reports</i> , 2015, 7, 404-413.	1.0	22

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19	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
20	Complete genome sequence of <i>Desulfobacter hydrogenophilus</i> AcRS1. <i>Marine Genomics</i> , 2020, 50, 100691.	0.4	7
21	<i>In situ</i> microcosms deployed at the coast of British Columbia (Canada) to study dilbit weathering and associated microbial communities under marine conditions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	7
22	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
23	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
24	Draft genome sequence of <i>Bacillus azotoformans</i> MEV2011, a (Co-) denitrifying strain unable to grow with oxygen. <i>Standards in Genomic Sciences</i> , 2014, 9, 23.	1.5	4
25	Draft genome sequence of <i>Bacillus azotoformans</i> MEV2011, a (Co-) denitrifying strain unable to grow with oxygen. <i>Standards in Genomic Sciences</i> , 2015, 10, 4.	1.5	4
26	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
27	Draft Genome Sequence of <i>Pseudoruegeria</i> sp. SK021, a Representative of the Marine Roseobacter Group, Isolated from North Sea Sediment. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
28	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
29	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
30	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
31	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
32	Draft Genome Sequence of <i>Streptococcus caviae</i> Strain Cavy grass 6 ^T , Isolated from Domesticated Guinea Pig Fecal Samples. <i>Genome Announcements</i> , 2017, 5, .	0.8	0