

Sören M Karst

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

3,035
citations

361413

20
h-index

713466

21
g-index

29
all docs

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docs citations

29
times ranked

3702
citing authors

#	ARTICLE	IF	CITATIONS
1	Back to Basics â The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. PLoS ONE, 2015, 10, e0132783.	2.5	437
2	Cyanate as an energy source for nitrifiers. Nature, 2015, 524, 105-108.	27.8	231
3	MiDAS: the field guide to the microbes of activated sludge. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav062.	3.0	213
4	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	19.0	198
5	Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. Nature Communications, 2021, 12, 2009.	12.8	177
6	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. Nature Biotechnology, 2018, 36, 190-195.	17.5	165
7	Oxford Nanopore R10.4 long-read sequencing enables the generation of near-finished bacterial genomes from pure cultures and metagenomes without short-read or reference polishing. Nature Methods, 2022, 19, 823-826.	19.0	152
8	The impact of immigration on microbial community composition in full-scale anaerobic digesters. Scientific Reports, 2017, 7, 9343.	3.3	127
9	MiDAS 2.0: an ecosystem-specific taxonomy and online database for the organisms of wastewater treatment systems expanded for anaerobic digester groups. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	124
10	Characterization of the First â <i>Candidatus</i> Nitrotogaâ Isolate Reveals Metabolic Versatility and Separate Evolution of Widespread Nitrite-Oxidizing Bacteria. MBio, 2018, 9, .	4.1	112
11	â <i>Candidatus</i> Propionivibrio aalborgensisâ: A Novel Glycogen Accumulating Organism Abundant in Full-Scale Enhanced Biological Phosphorus Removal Plants. Frontiers in Microbiology, 2016, 7, 1033.	3.5	97
12	Genomic and <i>in situ</i> investigations of the novel uncultured Chloroflexi associated with 0092 morphotype filamentous bulking in activated sludge. ISME Journal, 2016, 10, 2223-2234.	9.8	88
13	Novel prosthecate bacteria from the candidate phylum Acetothermia. ISME Journal, 2018, 12, 2225-2237.	9.8	75
14	Generation of Comprehensive Ecosystem-Specific Reference Databases with Species-Level Resolution by High-Throughput Full-Length 16S rRNA Gene Sequencing and Automated Taxonomy Assignment (AutoTax). MBio, 2020, 11, .	4.1	66
15	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. ISME Journal, 2016, 10, 2352-2364.	9.8	62
16	Survival and activity of individual bioaugmentation strains. Bioresource Technology, 2015, 186, 192-199.	9.6	53
17	Metagenomes from deep Baltic Sea sediments reveal how past and present environmental conditions determine microbial community composition. Marine Genomics, 2018, 37, 58-68.	1.1	52
18	Exploring the upper pH limits of nitrite oxidation: diversity, ecophysiology, and adaptive traits of haloalkalitolerant <i>Nitrospira</i> . ISME Journal, 2020, 14, 2967-2979.	9.8	52

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19	Genomic and in Situ Analyses Reveal the <i>Micropruina</i> spp. as Abundant Fermentative Glycogen Accumulating Organisms in Enhanced Biological Phosphorus Removal Systems. <i>Frontiers in Microbiology</i> , 2018, 9, 1004.	3.5	45
20	The role of inoculum and reactor configuration for microbial community composition and dynamics in mainstream partial nitrification anammox reactors. <i>MicrobiologyOpen</i> , 2017, 6, e00456.	3.0	32
21	Complete Genome Sequence of the Bacterium Aalborg_AAW-1, Representing a Novel Family within the Candidate Phylum SR1. <i>Genome Announcements</i> , 2015, 3, .	0.8	5