

Mads Albertsen

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

12,424
citations

57631

44
h-index

88477

70
g-index

89
all docs

89
docs citations

89
times ranked

11299
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	13.7	1,878
2	Complete nitrification by a single microorganism. <i>Nature</i> , 2015, 528, 555-559.	13.7	1,336
3	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	9.4	1,176
4	Kinetic analysis of a complete nitrifier reveals an oligotrophic lifestyle. <i>Nature</i> , 2017, 549, 269-272.	13.7	588
5	Expanded metabolic versatility of ubiquitous nitrite-oxidizing bacteria from the genus <i>Nitrospira</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11371-11376.	3.3	439
6	Back to Basics – The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. <i>PLoS ONE</i> , 2015, 10, e0132783.	1.1	437
7	The activated sludge ecosystem contains a core community of abundant organisms. <i>ISME Journal</i> , 2016, 10, 11-20.	4.4	416
8	A metagenome of a full-scale microbial community carrying out enhanced biological phosphorus removal. <i>ISME Journal</i> , 2012, 6, 1094-1106.	4.4	218
9	MiDAS: the field guide to the microbes of activated sludge. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav062.	1.4	213
10	A Critical Assessment of the Microorganisms Proposed to be Important to Enhanced Biological Phosphorus Removal in Full-Scale Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 718.	1.5	212
11	<i>Candidatus</i> <i>Competibacter</i> TM -lineage genomes retrieved from metagenomes reveal functional metabolic diversity. <i>ISME Journal</i> , 2014, 8, 613-624.	4.4	203
12	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021, 18, 165-169.	9.0	198
13	Cultivation and characterization of <i>Candidatus</i> <i>Nitrosocosmicus</i> exaquare, an ammonia-oxidizing archaeon from a municipal wastewater treatment system. <i>ISME Journal</i> , 2017, 11, 1142-1157.	4.4	182
14	Re-evaluating the microbiology of the enhanced biological phosphorus removal process. <i>Current Opinion in Biotechnology</i> , 2019, 57, 111-118.	3.3	180
15	Connecting structure to function with the recovery of over 1000 high-quality metagenome-assembled genomes from activated sludge using long-read sequencing. <i>Nature Communications</i> , 2021, 12, 2009.	5.8	177
16	MiDAS 3: An ecosystem-specific reference database, taxonomy and knowledge platform for activated sludge and anaerobic digesters reveals species-level microbiome composition of activated sludge. <i>Water Research</i> , 2020, 182, 115955.	5.3	175
17	Limited dissemination of the wastewater treatment plant core resistome. <i>Nature Communications</i> , 2015, 6, 8452.	5.8	173
18	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	4.4	168

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19	Growth of nitrite-oxidizing bacteria by aerobic hydrogen oxidation. <i>Science</i> , 2014, 345, 1052-1054.	6.0	166
20	Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. <i>Nature Biotechnology</i> , 2018, 36, 190-195.	9.4	165
21	Culture-Independent Analyses Reveal Novel Anaerolineaceae as Abundant Primary Fermenters in Anaerobic Digesters Treating Waste Activated Sludge. <i>Frontiers in Microbiology</i> , 2017, 8, 1134.	1.5	158
22	Phylogenetic diversity and ecophysiology of Candidate phylum Saccharibacteria in activated sludge. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv078.	1.3	155
23	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. <i>Nature Methods</i> , 2022, 19, 823-826.	9.0	152
24	<i>Crenothrix</i> are major methane consumers in stratified lakes. <i>ISME Journal</i> , 2017, 11, 2124-2140.	4.4	146
25	Identification of syntrophic acetate-oxidizing bacteria in anaerobic digesters by combined protein-based stable isotope probing and metagenomics. <i>ISME Journal</i> , 2016, 10, 2405-2418.	4.4	135
26	Risk of hospitalisation associated with infection with SARS-CoV-2 lineage B.1.1.7 in Denmark: an observational cohort study. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 1507-1517.	4.6	129
27	The impact of immigration on microbial community composition in full-scale anaerobic digesters. <i>Scientific Reports</i> , 2017, 7, 9343.	1.6	127
28	Curl Functional Amyloid Systems Are Phylogenetically Widespread and Display Large Diversity in Operon and Protein Structure. <i>PLoS ONE</i> , 2012, 7, e51274.	1.1	124
29	MiDAS 2.0: an ecosystem-specific taxonomy and online database for the organisms of wastewater treatment systems expanded for anaerobic digester groups. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	124
30	Novel syntrophic bacteria in full-scale anaerobic digesters revealed by genome-centric metatranscriptomics. <i>ISME Journal</i> , 2020, 14, 906-918.	4.4	117
31	MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants. <i>Nature Communications</i> , 2022, 13, 1908.	5.8	114
32	Characterization of the First <i>Candidatus</i> Nitrotoga Isolate Reveals Metabolic Versatility and Separate Evolution of Widespread Nitrite-Oxidizing Bacteria. <i>MBio</i> , 2018, 9, .	1.8	112
33	<i>Candidatus</i> Propionivibrio aalborgensis: A Novel Glycogen Accumulating Organism Abundant in Full-Scale Enhanced Biological Phosphorus Removal Plants. <i>Frontiers in Microbiology</i> , 2016, 7, 1033.	1.5	97
34	Metabolic model for the filamentous <i>Candidatus</i> Microthrix parvicella™ based on genomic and metagenomic analyses. <i>ISME Journal</i> , 2013, 7, 1161-1172.	4.4	93
35	Genomic and <i>in situ</i> investigations of the novel uncultured Chloroflexi associated with 0092 morphotype filamentous bulking in activated sludge. <i>ISME Journal</i> , 2016, 10, 2223-2234.	4.4	88
36	Perspectives and Benefits of High-Throughput Long-Read Sequencing in Microbial Ecology. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0062621.	1.4	80

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37	Cultivation and Genomic Analysis of <i>Candidatus Nitrosocaldus islandicus</i> , an Obligately Thermophilic, Ammonia-Oxidizing Thaumarchaeon from a Hot Spring Biofilm in Graendalur Valley, Iceland. <i>Frontiers in Microbiology</i> , 2018, 9, 193.	1.5	76
38	Novel prosthecate bacteria from the candidate phylum Acetothermia. <i>ISME Journal</i> , 2018, 12, 2225-2237.	4.4	75
39	<i>Candidatus Accumulibacter delftensis</i> : A clade IC novel polyphosphate-accumulating organism without denitrifying activity on nitrate. <i>Water Research</i> , 2019, 161, 136-151.	5.3	74
40	Increased transmissibility of SARS-CoV-2 lineage B.1.1.7 by age and viral load. <i>Nature Communications</i> , 2021, 12, 7251.	5.8	67
41	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). <i>MBio</i> , 2020, 11, .	1.8	66
42	Bacteria from the Genus <i>Arcobacter</i> Are Abundant in Effluent from Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	65
43	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. <i>ISME Journal</i> , 2016, 10, 2352-2364.	4.4	62
44	Hospitalisation associated with SARS-CoV-2 delta variant in Denmark. <i>Lancet Infectious Diseases</i> , The, 2021, 21, 1351.	4.6	59
45	Genomic insights into <i>Candidatus Amarolinea aalborgensis</i> gen. nov., sp. nov., associated with settleability problems in wastewater treatment plants. <i>Systematic and Applied Microbiology</i> , 2019, 42, 77-84.	1.2	58
46	Exploring the upper pH limits of nitrite oxidation: diversity, ecophysiology, and adaptive traits of haloalkalitolerant <i>Nitrospira</i> . <i>ISME Journal</i> , 2020, 14, 2967-2979.	4.4	52
47	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>Ianthella basta</i> . <i>Environmental Microbiology</i> , 2019, 21, 3831-3854.	1.8	50
48	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019, 27, 670-677.	3.5	50
49	Investigation of Detection Limits and the Influence of DNA Extraction and Primer Choice on the Observed Microbial Communities in Drinking Water Samples Using 16S rRNA Gene Amplicon Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2140.	1.5	49
50	Dynamics of the Fouling Layer Microbial Community in a Membrane Bioreactor. <i>PLoS ONE</i> , 2016, 11, e0158811.	1.1	42
51	Comparative Genome-Centric Analysis of Freshwater and Marine ANAMMOX Cultures Suggests Functional Redundancy in Nitrogen Removal Processes. <i>Frontiers in Microbiology</i> , 2020, 11, 1637.	1.5	37
52	Increased Risk of Hospitalisation Associated with Infection with SARS-CoV-2 Lineage B.1.1.7 in Denmark. <i>SSRN Electronic Journal</i> , 0, , .	0.4	34
53	Unlinked rRNA genes are widespread among bacteria and archaea. <i>ISME Journal</i> , 2020, 14, 597-608.	4.4	30
54	The Microbial Database for Danish wastewater treatment plants with nutrient removal (MiDas-DK) – a tool for understanding activated sludge population dynamics and community stability. <i>Water Science and Technology</i> , 2013, 67, 2519-2526.	1.2	22

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55	Digging into the extracellular matrix of a complex microbial community using a combined metagenomic and metaproteomic approach. <i>Water Science and Technology</i> , 2013, 67, 1650-1656.	1.2	22
56	Clinical results and microbiota changes after faecal microbiota transplantation for chronic pouchitis: a pilot study. <i>Scandinavian Journal of Gastroenterology</i> , 2020, 55, 421-429.	0.6	19
57	Complete Genome of <i>Rhodococcus pyridinivorans</i> SB3094, a Methyl-Ethyl-Ketone-Degrading Bacterium Used for Bioaugmentation. <i>Genome Announcements</i> , 2014, 2, .	0.8	17
58	Spatial separation of ribosomes and DNA in Asgard archaeal cells. <i>ISME Journal</i> , 2022, 16, 606-610.	4.4	17
59	Metagenomes obtained by “deep sequencing”™ “ what do they tell about the enhanced biological phosphorus removal communities?. <i>Water Science and Technology</i> , 2013, 68, 1959-1968.	1.2	14
60	Introduction and transmission of SARS-CoV-2 lineage B.1.1.7, Alpha variant, in Denmark. <i>Genome Medicine</i> , 2022, 14, 47.	3.6	14
61	A B-cell-associated gene signature classification of diffuse large B-cell lymphoma by NanoString technology. <i>Blood Advances</i> , 2018, 2, 1542-1546.	2.5	13
62	Complete Genome Sequences of <i>Pseudomonas monteilii</i> SB3078 and SB3101, Two Benzene-, Toluene-, and Ethylbenzene-Degrading Bacteria Used for Bioaugmentation. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
63	Draft Genome Sequence of <i>Desulfuromonas acetexigens</i> Strain 2873, a Novel Anode-Respiring Bacterium. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
64	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
65	Characterization of the In Situ Ecophysiology of Novel Phylotypes in Nutrient Removal Activated Sludge Treatment Plants. <i>PLoS ONE</i> , 2015, 10, e0136424.	1.1	8
66	<i>In situ</i> metabolomic- and transcriptomic-profiling of the host-associated cyanobacteria <i>Prochloron</i> and <i>Acaryochloris marina</i> . <i>ISME Journal</i> , 2018, 12, 556-567.	4.4	7
67	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
68	The Microbiota Profile in Inflamed and Non-Inflamed Ileal Pouch-Anal Anastomosis. <i>Microorganisms</i> , 2020, 8, 1611.	1.6	3
69	The Signal and the Noise: Characteristics of Antisense RNA in Complex Microbial Communities. <i>MSystems</i> , 2020, 5, .	1.7	2