

Morten S. Dueholm

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

3,809
citations

147801

31
h-index

182427

51
g-index

65
all docs

65
docs citations

65
times ranked

3938
citing authors

#	ARTICLE	IF	CITATIONS
1	Amyloid adhesins are abundant in natural biofilms. <i>Environmental Microbiology</i> , 2007, 9, 3077-3090.	3.8	291
2	Functional amyloid in <i>Pseudomonas</i> . <i>Molecular Microbiology</i> , 2010, 77, 1009-1020.	2.5	256
3	Extracellular polymeric substances of biofilms: Suffering from an identity crisis. <i>Water Research</i> , 2019, 151, 1-7.	11.3	228
4	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.	12.8	177
5	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.	11.3	175
6	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.	17.5	165
7	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.	3.5	158
8	Functional bacterial amyloid increases <i>Pseudomonas</i> biofilm hydrophobicity and stiffness. <i>Frontiers in Microbiology</i> , 2015, 6, 1099.	3.5	133
9	Expression of Fap amyloids in <i>Pseudomonas aeruginosa</i> , <i>Pseudomonas fluorescens</i> and <i>Pseudomonas putida</i> results in aggregation and increased biofilm formation. <i>MicrobiologyOpen</i> , 2013, 2, 365-382.	3.0	130
10	The impact of immigration on microbial community composition in full-scale anaerobic digesters. <i>Scientific Reports</i> , 2017, 7, 9343.	3.3	127
11	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.	7.1	127
12	Curli Functional Amyloid Systems Are Phylogenetically Widespread and Display Large Diversity in Operon and Protein Structure. <i>PLoS ONE</i> , 2012, 7, e51274.	2.5	124
13	Novel syntrophic bacteria in full-scale anaerobic digesters revealed by genome-centric metatranscriptomics. <i>ISME Journal</i> , 2020, 14, 906-918.	9.8	117
14	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.	12.8	114
15	Fibrillation of the Major Curli Subunit CsgA under a Wide Range of Conditions Implies a Robust Design of Aggregation. <i>Biochemistry</i> , 2011, 50, 8281-8290.	2.5	89
16	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.	9.8	88
17	Detection of Pathogenic Biofilms with Bacterial Amyloid Targeting Fluorescent Probe, CDy11. <i>Journal of the American Chemical Society</i> , 2016, 138, 402-407.	13.7	82
18	Epigallocatechin Gallate Remodels Overexpressed Functional Amyloids in <i>Pseudomonas aeruginosa</i> and Increases Biofilm Susceptibility to Antibiotic Treatment. <i>Journal of Biological Chemistry</i> , 2016, 291, 26540-26553.	3.4	75

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19	Novel prosthecate bacteria from the candidate phylum Acetothermia. ISME Journal, 2018, 12, 2225-2237.	9.8	75
20	Functional Amyloids Keep Quorum-sensing Molecules in Check. Journal of Biological Chemistry, 2015, 290, 6457-6469.	3.4	70
21	Widespread Abundance of Functional Bacterial Amyloid in Mycolata and Other Gram-Positive Bacteria. Applied and Environmental Microbiology, 2009, 75, 4101-4110.	3.1	66
22	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
23	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. ISME Journal, 2016, 10, 2352-2364.	9.8	62
24	Evolutionary Insight into the Functional Amyloids of the Pseudomonads. PLoS ONE, 2013, 8, e76630.	2.5	56
25	A new class of hybrid secretion system is employed in Pseudomonas amyloid biogenesis. Nature Communications, 2017, 8, 263.	12.8	56
26	Survival and activity of individual bioaugmentation strains. Bioresource Technology, 2015, 186, 192-199.	9.6	53
27	Characterizing the growing microorganisms at species level in 46 anaerobic digesters at Danish wastewater treatment plants: A six-year survey on microbial community structure and key drivers. Water Research, 2021, 193, 116871.	11.3	51
28	Ecology and Biogenesis of Functional Amyloids in Pseudomonas. Journal of Molecular Biology, 2018, 430, 3685-3695.	4.2	48
29	The fungal community changes over time in developing wheat heads. International Journal of Food Microbiology, 2016, 222, 30-39.	4.7	45
30	Genomic and in Situ Analyses Reveal the Micropruina spp. as Abundant Fermentative Glycogen Accumulating Organisms in Enhanced Biological Phosphorus Removal Systems. Frontiers in Microbiology, 2018, 9, 1004.	3.5	45
31	The novel genus, <i>Candidatus</i> Phosphoribacter TM , previously identified as <i>Tetrasphaera</i> , is the dominant polyphosphate accumulating lineage in EBPR wastewater treatment plants worldwide. ISME Journal, 2022, 16, 1605-1616.	9.8	41
32	The Tubular Sheaths Encasing Methanosaeta thermophila Filaments Are Functional Amyloids. Journal of Biological Chemistry, 2015, 290, 20590-20600.	3.4	36
33	Major Proteomic Changes Associated with Amyloid-Induced Biofilm Formation in <i>Pseudomonas aeruginosa</i> PAO1. Journal of Proteome Research, 2015, 14, 72-81.	3.7	34
34	Controlling the degree of esterification in lipase catalysed synthesis of xylitol fatty acid esters. Enzyme and Microbial Technology, 2007, 41, 346-352.	3.2	29
35	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus <i>Candidatus</i> Accumulibacter. MSystems, 2022, 7, e0001622.	3.8	22
36	The Proteome of Tetrasphaera elongata is adapted to Changing Conditions in Wastewater Treatment Plants. Proteomes, 2019, 7, 16.	3.5	21

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37	Complete Genome Sequence of <i>Pseudomonas</i> sp. UK4, a Model Organism for Studies of Functional Amyloids in <i>Pseudomonas</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	20
38	Low Global Diversity of <i>Candidatus Microthrix</i> , a Troublesome Filamentous Organism in Full-Scale WWTPs. <i>Frontiers in Microbiology</i> , 2021, 12, 690251.	3.5	18
39	Microbial communities across activated sludge plants show recurring species-level seasonal patterns. <i>ISME Communications</i> , 2022, 2, .	4.2	18
40	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
41	Label-free quantification reveals major proteomic changes in <i>Pseudomonas putida</i> F1 during the exponential growth phase. <i>Proteomics</i> , 2015, 15, 3244-3252.	2.2	17
42	Direct Identification of Functional Amyloid Proteins by Label-Free Quantitative Mass Spectrometry. <i>Biomolecules</i> , 2017, 7, 58.	4.0	13
43	The Sheaths of <i>Methanospirillum</i> Are Made of a New Type of Amyloid Protein. <i>Frontiers in Microbiology</i> , 2018, 9, 2729.	3.5	13
44	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
45	In situ Sub-cellular Identification of Functional Amyloids in Bacteria and Archaea by Infrared Nanospectroscopy. <i>Small Methods</i> , 2021, 5, e2001002.	8.6	11
46	Complete Genome Sequence of <i>Actinobaculum schaalii</i> Strain CCUG 27420. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
47	Functional Bacterial Amyloids in Biofilms. <i>Springer Series on Biofilms</i> , 2011, , 41-62.	0.1	9
48	<i>Candidatus Galacturonibacter soehngeni</i> Shows Acetogenic Catabolism of Galacturonic Acid but Lacks a Canonical Carbon Monoxide Dehydrogenase/Acetyl-CoA Synthase Complex. <i>Frontiers in Microbiology</i> , 2020, 11, 63.	3.5	6
49	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
50	Identification of amyloidogenic proteins in the microbiomes of a rat Parkinson's disease model and wild-type rats. <i>Protein Science</i> , 2021, 30, 1854-1870.	7.6	5
51	Stabilization and De-Stabilization of (Membrane-)Proteins by Microbial Glycolipid and Lipopeptide Biosurfactants - in-vivo Relevance and Industrial Applications. <i>Biophysical Journal</i> , 2015, 108, 521a-522a.	0.5	0
52	High-Quality Draft Genome Sequence of <i>Sphaerisporangium cinnabarinum</i> ATCC 31213. <i>Genome Announcements</i> , 2018, 6, .	0.8	0