

Per Halkjær Nielsen

List of Publications by Year in descending order

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314
papers

33,813
citations

3334

91
h-index

4885

168
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336
all docs

336
docs citations

336
times ranked

20574
citing authors

#	ARTICLE	IF	CITATIONS
1	Monitoring antibiotic resistance genes in wastewater environments: The challenges of filling a gap in the One-Health cycle. <i>Journal of Hazardous Materials</i> , 2022, 424, 127407.	12.4	60
2	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. <i>ISME Journal</i> , 2022, 16, 1605-1616.	9.8	41
3	Microbial communities across activated sludge plants show recurring species-level seasonal patterns. <i>ISME Communications</i> , 2022, 2, .	4.2	18
4	Quantification of Biologically and Chemically Bound Phosphorus in Activated Sludge from Full-Scale Plants with Biological P-Removal. <i>Environmental Science & Technology</i> , 2022, 56, 5132-5140.	10.0	15
5	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
6	Seasonal microbial community dynamics complicates the evaluation of filamentous bulking mitigation strategies in full-scale WRRFs. <i>Water Research</i> , 2022, 216, 118340.	11.3	14
7	Global warming readiness: Feasibility of enhanced biological phosphorus removal at 35°C. <i>Water Research</i> , 2022, 216, 118301.	11.3	25
8	Reevaluation of the Phylogenetic Diversity and Global Distribution of the Genus <i>Candidatus</i> Accumulibacter. <i>MSystems</i> , 2022, 7, e0001622.	3.8	22
9	Exploring the microbial influence on seasonal nitrous oxide concentration in a full-scale wastewater treatment plant using metagenome assembled genomes. <i>Water Research</i> , 2022, 219, 118563.	11.3	5
10	Fouling of membranes in membrane bioreactors for wastewater treatment: Planktonic bacteria can have a significant contribution. <i>Water Environment Research</i> , 2021, 93, 207-216.	2.7	10
11	Flow-through stable isotope probing (Flow-SIP) minimizes cross-feeding in complex microbial communities. <i>ISME Journal</i> , 2021, 15, 348-353.	9.8	14
12	Identification of microorganisms responsible for foam formation in mesophilic anaerobic digesters treating surplus activated sludge. <i>Water Research</i> , 2021, 191, 116779.	11.3	18
13	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
14	High Diversity and Functional Potential of Undescribed <i>Acidobacteriota</i> in Danish Wastewater Treatment Plants. <i>Frontiers in Microbiology</i> , 2021, 12, 643950.	3.5	56
15	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. <i>Water Research</i> , 2021, 193, 116871.	11.3	51
16	Parasitic bacteria control foam formation. <i>Nature Microbiology</i> , 2021, 6, 701-702.	13.3	1
17	Low Global Diversity of <i>Candidatus</i> Microthrix, a Troublesome Filamentous Organism in Full-Scale WWTPs. <i>Frontiers in Microbiology</i> , 2021, 12, 690251.	3.5	18
18	Mass-immigration determines the assembly of activated sludge microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48

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19	âœ€ <i>Candidatus</i> Dechloromonas phosphoritrophaâœ€ and âœ€ <i>Ca</i> . D. phosphorivoransâœ€, novel polyphosphate accumulating organisms abundant in wastewater treatment systems. ISME Journal, 2021, 15, 3605-3614.	9.8	80
20	Long-term operation assessment of a full-scale membrane-aerated biofilm reactor under Nordic conditions. Science of the Total Environment, 2021, 779, 146366.	8.0	32
21	Prospects for multi-omics in the microbial ecology of water engineering. Water Research, 2021, 205, 117608.	11.3	26
22	Elucidating performance failures in use of granular sludge for nutrient removal from domestic wastewater in a warm coastal climate region. Environmental Technology (United Kingdom), 2020, 41, 1896-1911.	2.2	22
23	Novel syntrophic bacteria in full-scale anaerobic digesters revealed by genome-centric metatranscriptomics. ISME Journal, 2020, 14, 906-918.	9.8	117
24	Metabolic Traits of <i>Candidatus</i> Accumulibacter clade IIF Strain SCElse-1 Using Amino Acids As Carbon Sources for Enhanced Biological Phosphorus Removal. Environmental Science & Technology, 2020, 54, 2448-2458.	10.0	41
25	A refined set of rRNA-targeted oligonucleotide probes for in situ detection and quantification of ammonia-oxidizing bacteria. Water Research, 2020, 186, 116372.	11.3	19
26	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
27	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
28	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. Water Research, 2020, 182, 115955.	11.3	175
29	<i>Candidatus</i> Amarolinea and <i>Candidatus</i> Microthrix Are Mainly Responsible for Filamentous Bulking in Danish Municipal Wastewater Treatment Plants. Frontiers in Microbiology, 2020, 11, 1214.	3.5	37
30	âœ€ <i>Candidatus</i> Galacturonibacter soehngeniâœ€ Shows Acetogenic Catabolism of Galacturonic Acid but Lacks a Canonical Carbon Monoxide Dehydrogenase/Acetyl-CoA Synthase Complex. Frontiers in Microbiology, 2020, 11, 63.	3.5	6
31	Bacteria from the Genus <i>Arcobacter</i> Are Abundant in Effluent from Wastewater Treatment Plants. Applied and Environmental Microbiology, 2020, 86, .	3.1	65
32	On the evolution and physiology of cable bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19116-19125.	7.1	127
33	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>Ianthella basta</i> . Environmental Microbiology, 2019, 21, 3831-3854.	3.8	50
34	New Training to Meet the Global Phosphorus Challenge. Environmental Science & Technology, 2019, 53, 8479-8481.	10.0	29
35	Editorial overview: Integrating biotechnology and microbial ecology in urban water infrastructure through a microbiome continuum viewpoint. Current Opinion in Biotechnology, 2019, 57, iii-vi.	6.6	6
36	âœ€ <i>Candidatus</i> Accumulibacter delftensisâœ€. A clade IC novel polyphosphate-accumulating organism without denitrifying activity on nitrate. Water Research, 2019, 161, 136-151.	11.3	74

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37	Global diversity and biogeography of bacterial communities in wastewater treatment plants. <i>Nature Microbiology</i> , 2019, 4, 1183-1195.	13.3	491
38	The Proteome of <i>Tetrasphaera elongata</i> is adapted to Changing Conditions in Wastewater Treatment Plants. <i>Proteomes</i> , 2019, 7, 16.	3.5	21
39	Proteogenomic Refinement of the <i>Neomegalonema perideroedes</i> Genome Annotation. <i>Proteomics</i> , 2019, 19, e1800330.	2.2	4
40	Re-evaluating the microbiology of the enhanced biological phosphorus removal process. <i>Current Opinion in Biotechnology</i> , 2019, 57, 111-118.	6.6	180
41	Resolving the individual contribution of key microbial populations to enhanced biological phosphorus removal with Raman- ¹³ C-FISH. <i>ISME Journal</i> , 2019, 13, 1933-1946.	9.8	130
42	Extraction and quantification of polyphosphates in activated sludge from waste water treatment plants by ³¹ P NMR spectroscopy. <i>Water Research</i> , 2019, 157, 346-355.	11.3	32
43	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.	2.8	58
44	The Composition and Implications of Polyphosphate-Metal in Enhanced Biological Phosphorus Removal Systems. <i>Environmental Science & Technology</i> , 2019, 53, 1536-1544.	10.0	26
45	Polyphosphate-accumulating organisms in full-scale tropical wastewater treatment plants use diverse carbon sources. <i>Water Research</i> , 2019, 149, 496-510.	11.3	129
46	The morphology and metabolic potential of the Chloroflexi in full-scale activated sludge wastewater treatment plants. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	100
47	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	9.8	168
48	Monitoring foaming potential in anaerobic digesters. <i>Waste Management</i> , 2018, 75, 280-288.	7.4	13
49	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
50	Functional redundancy ensures performance robustness in 3-stage PHA-producing mixed cultures under variable feed operation. <i>New Biotechnology</i> , 2018, 40, 207-217.	4.4	28
51	Sludge fractionation as a method to study and predict fouling in MBR systems. <i>Separation and Purification Technology</i> , 2018, 194, 329-337.	7.9	30
52	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.	1.1	52
53	In situ visualisation of the abundant Chloroflexi populations in full-scale anaerobic digesters and the fate of immigrating species. <i>PLoS ONE</i> , 2018, 13, e0206255.	2.5	37
54	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

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55	Denitrification activity of polyphosphate accumulating organisms (PAOs) in full-scale wastewater treatment plants. <i>Water Science and Technology</i> , 2018, 78, 2449-2458.	2.5	17
56	Toward Better Understanding of EBPR Systems via Linking Raman-Based Phenotypic Profiling with Phylogenetic Diversity. <i>Environmental Science & Technology</i> , 2018, 52, 8596-8606.	10.0	28
57	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
58	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, .	4.1	112
59	Novel prosthecate bacteria from the candidate phylum Acetothermia. <i>ISME Journal</i> , 2018, 12, 2225-2237.	9.8	75
60	Linking Raman-Based Phenotypic Profiling and Phylogenetic Diversity to Reveal EBPR Physiological Characteristics. <i>Proceedings of the Water Environment Federation</i> , 2018, 2018, 320-327.	0.0	0
61	Non-denitrifying polyphosphate accumulating organisms obviate requirement for anaerobic condition. <i>Water Research</i> , 2017, 111, 393-403.	11.3	35
62	Cultivation and characterization of <i>Candidatus</i> Nitrosocosmicus exaquare, an ammonia-oxidizing archaeon from a municipal wastewater treatment system. <i>ISME Journal</i> , 2017, 11, 1142-1157.	9.8	182
63	Metabolism and ecological niche of <i>Tetrasphaera</i> and <i>Ca. Accumilibacter</i> in enhanced biological phosphorus removal. <i>Water Research</i> , 2017, 122, 159-171.	11.3	124
64	Unified understanding of physico-chemical properties of activated sludge and fouling propensity. <i>Water Research</i> , 2017, 120, 117-132.	11.3	48
65	Long-term effects of sulphide on the enhanced biological removal of phosphorus: The symbiotic role of <i>Thiothrix caldifontis</i> . <i>Water Research</i> , 2017, 116, 53-64.	11.3	92
66	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
67	Microbial biotechnology and circular economy in wastewater treatment. <i>Microbial Biotechnology</i> , 2017, 10, 1102-1105.	4.2	59
68	The impact of immigration on microbial community composition in full-scale anaerobic digesters. <i>Scientific Reports</i> , 2017, 7, 9343.	3.3	127
69	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, .	3.0	124
70	Diversity of microbial carbohydrate-active enzymes in Danish anaerobic digesters fed with wastewater treatment sludge. <i>Biotechnology for Biofuels</i> , 2017, 10, 158.	6.2	35
71	Direct Identification of Functional Amyloid Proteins by Label-Free Quantitative Mass Spectrometry. <i>Biomolecules</i> , 2017, 7, 58.	4.0	13
72	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.	3.5	212

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73	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
74	A new class of hybrid secretion system is employed in <i>Pseudomonas amyloid</i> biogenesis. <i>Nature Communications</i> , 2017, 8, 263.	12.8	56
75	Membrane filtration device for studying compression of fouling layers in membrane bioreactors. <i>PLoS ONE</i> , 2017, 12, e0181652.	2.5	6
76	Experimental Methods in Wastewater Treatment. <i>Water Intelligence Online</i> , 2016, 15, 9781780404752-9781780404752.	0.3	80
77	“ <i>Candidatus Propionivibrio aalborgensis</i> ”: A Novel Glycogen Accumulating Organism Abundant in Full-Scale Enhanced Biological Phosphorus Removal Plants. <i>Frontiers in Microbiology</i> , 2016, 7, 1033.	3.5	97
78	Dynamics of the Fouling Layer Microbial Community in a Membrane Bioreactor. <i>PLoS ONE</i> , 2016, 11, e0158811.	2.5	42
79	Enhancing metaproteomics—The value of models and defined environmental microbial systems. <i>Proteomics</i> , 2016, 16, 783-798.	2.2	62
80	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
81	Genomic insights into members of the candidate phylum Hyd24-12 common in mesophilic anaerobic digesters. <i>ISME Journal</i> , 2016, 10, 2352-2364.	9.8	62
82	Identification of active denitrifiers in full-scale nutrient removal wastewater treatment systems. <i>Environmental Microbiology</i> , 2016, 18, 50-64.	3.8	226
83	Phylogenetic diversity and ecophysiology of Candidate phylum Saccharibacteria in activated sludge. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw078.	2.7	155
84	In vivo gene expression in a <i>Staphylococcus aureus</i> prosthetic joint infection characterized by RNA sequencing and metabolomics: a pilot study. <i>BMC Microbiology</i> , 2016, 16, 80.	3.3	44
85	Comparing culture and molecular methods for the identification of microorganisms involved in necrotizing soft tissue infections. <i>BMC Infectious Diseases</i> , 2016, 16, 652.	2.9	41
86	Integrative microbial community analysis reveals full-scale enhanced biological phosphorus removal under tropical conditions. <i>Scientific Reports</i> , 2016, 6, 25719.	3.3	61
87	Impact of sludge retention time on the fine composition of the microbial community and extracellular polymeric substances in a membrane bioreactor. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8507-8521.	3.6	18
88	Proteomic dataset of the organohalide-respiring bacterium <i>Dehalococcoides mccartyi</i> strain CBDB1 grown on hexachlorobenzene as electron acceptor. <i>Data in Brief</i> , 2016, 7, 253-256.	1.0	10
89	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
90	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

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91	The activated sludge ecosystem contains a core community of abundant organisms. ISME Journal, 2016, 10, 11-20.	9.8	416
92	Back to Basics – The Influence of DNA Extraction and Primer Choice on Phylogenetic Analysis of Activated Sludge Communities. PLoS ONE, 2015, 10, e0132783.	2.5	437
93	Stabilization and De-Stabilization of (Membrane-)Proteins by Microbial Glycolipid and Lipopeptide Biosurfactants - in-vivo Relevance and Industrial Applications. Biophysical Journal, 2015, 108, 521a-522a.	0.5	0
94	MIDAS: the field guide to the microbes of activated sludge. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav062.	3.0	213
95	Label-free quantification reveals major proteomic changes in <i>Pseudomonas putida</i> F1 during the exponential growth phase. Proteomics, 2015, 15, 3244-3252.	2.2	17
96	Functional bacterial amyloid increases <i>Pseudomonas</i> biofilm hydrophobicity and stiffness. Frontiers in Microbiology, 2015, 6, 1099.	3.5	133
97	Characterization of the In Situ Ecophysiology of Novel Phylotypes in Nutrient Removal Activated Sludge Treatment Plants. PLoS ONE, 2015, 10, e0136424.	2.5	8
98	Dewatering in biological wastewater treatment: A review. Water Research, 2015, 82, 14-24.	11.3	231
99	Complete Genome Sequence of the Bacterium Aalborg_AAW-1, Representing a Novel Family within the Candidate Phylum SR1. Genome Announcements, 2015, 3, .	0.8	5
100	The Tubular Sheaths Encasing <i>Methanosaeta thermophila</i> Filaments Are Functional Amyloids. Journal of Biological Chemistry, 2015, 290, 20590-20600.	3.4	36
101	Ammonia and temperature determine potential clustering in the anaerobic digestion microbiome. Water Research, 2015, 75, 312-323.	11.3	276
102	Functional Amyloids Keep Quorum-sensing Molecules in Check. Journal of Biological Chemistry, 2015, 290, 6457-6469.	3.4	70
103	Intracellular Accumulation of Glycine in Polyphosphate-Accumulating Organisms in Activated Sludge, a Novel Storage Mechanism under Dynamic Anaerobic-Aerobic Conditions. Applied and Environmental Microbiology, 2015, 81, 4809-4818.	3.1	58
104	Survival and activity of individual bioaugmentation strains. Bioresource Technology, 2015, 186, 192-199.	9.6	53
105	High quality draft genome sequence of <i>Meganema perideroedes</i> str. Gr1T and a proposal for its reclassification to the family Meganemaceae fam. nov.. Standards in Genomic Sciences, 2015, 10, 23.	1.5	15
106	Limited dissemination of the wastewater treatment plant core resistome. Nature Communications, 2015, 6, 8452.	12.8	173
107	Complete nitrification by a single microorganism. Nature, 2015, 528, 555-559.	27.8	1,336
108	Complete nitrification by <i>Nitrospira</i> bacteria. Nature, 2015, 528, 504-509.	27.8	1,878

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109	Expanded metabolic versatility of ubiquitous nitrite-oxidizing bacteria from the genus <i>Nitrospira</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11371-11376.	7.1	439
110	Reappraisal of the phylogeny and fluorescence <i>in situ</i> hybridization probes for the analysis of the <i>Competibacteraceae</i> in wastewater treatment systems. Environmental Microbiology Reports, 2015, 7, 166-174.	2.4	28
111	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
112	Complete Genome of <i>Rhodococcus pyridinivorans</i> SB3094, a Methyl-Ethyl-Ketone-Degrading Bacterium Used for Bioaugmentation. Genome Announcements, 2014, 2, .	0.8	17
113	Complete Genome Sequences of <i>Pseudomonas monteilii</i> SB3078 and SB3101, Two Benzene-, Toluene-, and Ethylbenzene-Degrading Bacteria Used for Bioaugmentation. Genome Announcements, 2014, 2, .	0.8	12
114	<i>Candidatus</i> <i>Competibacter</i> TM -lineage genomes retrieved from metagenomes reveal functional metabolic diversity. ISME Journal, 2014, 8, 613-624.	9.8	203
115	Irreversible fouling of membrane bioreactors due to formation of a non-biofilm gel layer. Water Science and Technology, 2014, 69, 1641-1647.	2.5	5
116	Complete Genome Sequence of <i>Actinobaculum schaalii</i> Strain CCUG 27420. Genome Announcements, 2014, 2, .	0.8	9
117	Complete Genome Sequence of <i>Pseudomonas</i> sp. UK4, a Model Organism for Studies of Functional Amyloids in <i>Pseudomonas</i> . Genome Announcements, 2014, 2, .	0.8	20
118	Influence of shear on nitrification rates in a membrane bioreactor. Water Science and Technology, 2014, 69, 1705-1711.	2.5	1
119	Proteome profile and proteogenomics of the organohalide-respiring bacterium <i>Dehalococcoides mccartyi</i> strain CBDB1 grown on hexachlorobenzene as electron acceptor. Journal of Proteomics, 2014, 98, 59-64.	2.4	49
120	Comparison of targeted peptide quantification assays for reductive dehalogenases by selective reaction monitoring (SRM) and precursor reaction monitoring (PRM). Analytical and Bioanalytical Chemistry, 2014, 406, 283-291.	3.7	41
121	Application of Ozone in Full-Scale to Reduce Filamentous Bulking Sludge at Åresundsverket WWTP. Ozone: Science and Engineering, 2014, 36, 238-243.	2.5	7
122	Growth of nitrite-oxidizing bacteria by aerobic hydrogen oxidation. Science, 2014, 345, 1052-1054.	12.6	166
123	Metaproteomics: Evaluation of protein extraction from activated sludge. Proteomics, 2014, 14, 2535-2539.	2.2	41
124	Low Temperature Partial Nitritation/Anammox in a Moving Bed Biofilm Reactor Treating Low Strength Wastewater. Environmental Science & Technology, 2014, 48, 8784-8792.	10.0	319
125	Metabolic modelling of full-scale enhanced biological phosphorus removal sludge. Water Research, 2014, 66, 283-295.	11.3	41
126	The Family Saprospiraceae. , 2014, , 863-889.		91

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127	Metabolic versatility in full-scale wastewater treatment plants performing enhanced biological phosphorus removal. <i>Water Research</i> , 2013, 47, 7032-7041.	11.3	84
128	Filtration properties of activated sludge in municipal MBR wastewater treatment plants are related to microbial community structure. <i>Water Research</i> , 2013, 47, 6719-6730.	11.3	25
129	Population dynamics of bacteria involved in enhanced biological phosphorus removal in Danish wastewater treatment plants. <i>Water Research</i> , 2013, 47, 1529-1544.	11.3	153
130	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.	2.5	22
131	A metabolic model for members of the genus <i>Tetrasphaera</i> involved in enhanced biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 543-554.	9.8	188
132	Editorial: Microbial ecology. <i>Water Research</i> , 2013, 47, 6957.	11.3	0
133	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.	2.5	14
134	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.	2.5	22
135	Bioinformatic progress and applications in metaproteogenomics for bridging the gap between genomic sequences and metabolic functions in microbial communities. <i>Proteomics</i> , 2013, 13, 2786-2804.	2.2	46
136	Metabolic model for the filamentous <i>Candidatus</i> <i>Microthrix parvicella</i> ™ based on genomic and metagenomic analyses. <i>ISME Journal</i> , 2013, 7, 1161-1172.	9.8	93
137	Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. <i>Nature Biotechnology</i> , 2013, 31, 533-538.	17.5	1,176
138	Link between microbial composition and carbon substrate-uptake preferences in a PHA-storing community. <i>ISME Journal</i> , 2013, 7, 1-12.	9.8	138
139	Comparison of nutrient-removing microbial communities in activated sludge from full-scale MBRs and conventional plants. <i>Water Science and Technology</i> , 2013, 68, 366-371.	2.5	31
140	High and stable substrate specificities of microorganisms in enhanced biological phosphorus removal plants. <i>Environmental Microbiology</i> , 2013, 15, 1821-1831.	3.8	36
141	Expression of Fap amyloids in <i>Pseudomonas aeruginosa</i> and <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
142	Evolutionary Insight into the Functional Amyloids of the Pseudomonads. <i>PLoS ONE</i> , 2013, 8, e76630.	2.5	56
143	Culture-Dependent and -Independent Investigations of Microbial Diversity on Urinary Catheters. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3901-3908.	3.9	38
144	Microbial communities involved in enhanced biological phosphorus removal from wastewater – a model system in environmental biotechnology. <i>Current Opinion in Biotechnology</i> , 2012, 23, 452-459.	6.6	167

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145	Population dynamics of filamentous bacteria in Danish wastewater treatment plants with nutrient removal. <i>Water Research</i> , 2012, 46, 3781-3795.	11.3	110
146	A metagenome of a full-scale microbial community carrying out enhanced biological phosphorus removal. <i>ISME Journal</i> , 2012, 6, 1094-1106.	9.8	218
147	Identification of glucose-fermenting bacteria in a full-scale enhanced biological phosphorus removal plant by stable isotope probing. <i>Microbiology (United Kingdom)</i> , 2012, 158, 1818-1825.	1.8	53
148	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
149	Community structure of bacteria and fungi in aerosols of a pig confinement building. <i>FEMS Microbiology Ecology</i> , 2012, 80, 390-401.	2.7	35
150	The microorganisms in chronically infected end-stage and non-end-stage cystic fibrosis patients. <i>FEMS Immunology and Medical Microbiology</i> , 2012, 65, 236-244.	2.7	61
151	Bacterial diversity in suspected prosthetic joint infections: an exploratory study using 16S rRNA gene analysis. <i>FEMS Immunology and Medical Microbiology</i> , 2012, 65, 291-304.	2.7	35
152	<i>Candidatus</i> Halomonas phosphatis TM , a novel polyphosphate-accumulating organism in full-scale enhanced biological phosphorus removal plants. <i>Environmental Microbiology</i> , 2012, 14, 2826-2837.	3.8	76
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314	Diversity and Ecophysiology of the Genus <i>OLB8</i> and Other Abundant Uncultured <i>Saprospiraceae</i> Genera in Global Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	32