

# Marta Nierychlo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8021958/publications.pdf>

Version: 2024-02-01

31  
papers

2,598  
citations

257450

24  
h-index

434195

31  
g-index

40  
all docs

40  
docs citations

40  
times ranked

2073  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial communities across activated sludge plants show recurring species-level seasonal patterns. <i>ISME Communications</i> , 2022, 2, .	4.2	18
2	Quantification of Biologically and Chemically Bound Phosphorus in Activated Sludge from Full-Scale Plants with Biological P-Removal. <i>Environmental Science &amp; Technology</i> , 2022, 56, 5132-5140.	10.0	15
3	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
4	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
5	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
6	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
7	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
8	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
9	<i>Candidatus</i> <i>Dechloromonas phosphoritropha</i> and <i>Candidatus</i> <i>D. phosphorivorans</i> , novel polyphosphate accumulating organisms abundant in wastewater treatment systems. <i>ISME Journal</i> , 2021, 15, 3605-3614.	9.8	80
10	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
11	<i>Candidatus</i> <i>Amarolinea</i> and <i>Candidatus</i> <i>Microthrix</i> Are Mainly Responsible for Filamentous Bulking in Danish Municipal Wastewater Treatment Plants. <i>Frontiers in Microbiology</i> , 2020, 11, 1214.	3.5	37
12	Bacteria from the Genus <i>Arcobacter</i> Are Abundant in Effluent from Wastewater Treatment Plants. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	65
13	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
14	Re-evaluating the microbiology of the enhanced biological phosphorus removal process. <i>Current Opinion in Biotechnology</i> , 2019, 57, 111-118.	6.6	180
15	Resolving the individual contribution of key microbial populations to enhanced biological phosphorus removal with Raman "FISH. <i>ISME Journal</i> , 2019, 13, 1933-1946.	9.8	130
16	Genomic insights into <i>Candidatus</i> <i>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
17	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
18	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

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19	Genomic and in Situ Analyses Reveal the Micropruina 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	Unified understanding of physico-chemical properties of activated sludge and fouling propensity. <i>Water Research</i> , 2017, 120, 117-132.	11.3	48
21	The impact of immigration on microbial community composition in full-scale anaerobic digesters. <i>Scientific Reports</i> , 2017, 7, 9343.	3.3	127
22	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
23	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
24	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
25	Effects of relaxation time on fouling propensity in membrane bioreactors. <i>Journal of Membrane Science</i> , 2016, 504, 176-184.	8.2	28
26	Identification of active denitrifiers in full-scale nutrient removal wastewater treatment systems. <i>Environmental Microbiology</i> , 2016, 18, 50-64.	3.8	226
27	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
28	MiDAS: the field guide to the microbes of activated sludge. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav062.	3.0	213
29	Characterization of the In Situ Ecophysiology of Novel Phylotypes in Nutrient Removal Activated Sludge Treatment Plants. <i>PLoS ONE</i> , 2015, 10, e0136424.	2.5	8
30	High and stable substrate specificities of microorganisms in enhanced biological phosphorus removal plants. <i>Environmental Microbiology</i> , 2013, 15, 1821-1831.	3.8	36
31	Diversity and Ecophysiology of the Genus OLB8 and Other Abundant Uncultured Saprospiraceae Genera in Global Wastewater Treatment Systems. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	32