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Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess

DOI: 10.1016/j.watres.2019.02.020 Water Research, 2019, 155, 275-287.

Source: https://exaly.com/paper-pdf/73662657/citation-report.pdf

Version: 2024-04-28

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#	Paper	IF	Citations
60	Characteristic and correlation analysis of influent and energy consumption of wastewater treatment plants in Taihu Basin. <i>Frontiers of Environmental Science and Engineering</i> , 2019 , 13, 1	5.8	12
59	Profiling population-level diversity and dynamics of Accumulibacter via high throughput sequencing of ppk1. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 9711-9722	5.7	7
58	Review in recent researches and applications of technology of environmental microbiology metagenomics in water treatment engineering. <i>IOP Conference Series: Earth and Environmental Science</i> , 2019 , 344, 012169	0.3	1
57	Impact of solid residence time (SRT) on functionally relevant microbial populations and performance in full-scale enhanced biological phosphorus removal (EBPR) systems. <i>Water Environment Research</i> , 2020 , 92, 389-402	2.8	15
56	Nutrient and pesticide remediation using a two-stage bioreactor-adsorptive system under two hydraulic retention times. <i>Water Research</i> , 2020 , 170, 115311	12.5	7
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53	Microbial community at transcription level in the synergy of GAOs and Candidatus Accumulibacter for saving carbon source in wastewater treatment. <i>Bioresource Technology</i> , 2020 , 297, 122454	11	5
52	N2O production using native nos-deficient denitrifying bacterial strains screened by a genome mining approach. <i>Bioresource Technology Reports</i> , 2020 , 11, 100529	4.1	1
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43	Identification of Genome Sequences of Polyphosphate-Accumulating Organisms by Machine Learning. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 626221	5.7		
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38	Integrated omics analyses reveal differential gene expression and potential for cooperation between denitrifying polyphosphate and glycogen accumulating organisms. <i>Environmental Microbiology</i> , 2021 , 23, 3274-3293	5.2	5	
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