M: Managing microbial community

P001-M Dechloromonas: to be or not to be a PAO? That is the question!
Francesca Petriglieri, Aalborg University, Denmark

P002-M Problems in Detecting Methanogens in Anaerobic Reactors by 16S rRNA Gene Amplicon Sequencing: Which Method Is More Reliable?
Claudia Etchebéhère, Biological Research Institute Clemente Estable, Uruguay

P003-M Predictive Models of Microbial Bioprocesses Inhibition Can Be Built by Integrating Independent Studies
Olivier Chapleur, IRSTEA, France

P004-M Exploring Microbiomes in Arsenic-rich Aquatic Environments: Structure, Metabolic Potentials and As-related Functional Genes
Simona Crogna, IRSA-CNR, Italy

P005-M Correlation Between Dominant Filament Kouleothrix (type 1851), the Settleablity of Activated Sludge Biomass, and Other Operating Factors in a Domedstic A2O Plant in Japan
Tadashi Nittami, Yokohama National University, Japan

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P007-M Managing the Activated Sludge Community Through Real-time DNA Sequencing
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Dorothy S Wagnér, University of Bath, United Kingdom

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P020-M Predicting microbial communities in engineered biological systems using modern deep learning models
Kasper Skytte Andersen, Aalborg University, Denmark

P021-M Impact of microbial community composition on the start-up of PNA MABR: Activated sludge vs. DEMON® biomass
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P022-M Species richness or abundance in activated sludge vs. partial nitrification anammox systems? Primer selection as a critical determinant of community analysis at lower taxonomic ranks
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Morton Simonen Dueholm, Aalborg University, Denmark

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