Ran Mei

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5489543/publications.pdf Version: 2024-02-01



RAN ME

| # | Article | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Meta-Omics-Supervised Characterization of Respiration Activities Associated with Microbial Immigrants in Anaerobic Sludge Digesters. Environmental Science & Technology, 2022, 56, 6689-6698. | 4.6 | 4 |
| 2 | Bacterial enrichment in highly-selective acetate-fed bioreactors and its application in rapid biofilm formation. Water Research, 2020, 170, 115359. | 5.3 | 5 |
| 3 | Catabolism and interactions of uncultured organisms shaped by eco-thermodynamics in methanogenic bioprocesses. Microbiome, 2020, 8, 111. | 4.9 | 48 |
| 4 | Metagenomic and Metatranscriptomic Analyses Revealed Uncultured Bacteroidales Populations as the Dominant Proteolytic Amino Acid Degraders in Anaerobic Digesters. Frontiers in Microbiology, 2020, 11, 593006. | 1,5 | 57 |
| 5 | Ecogenomics-Based Mass Balance Model Reveals the Effects of Fermentation Conditions on Microbial Activity. Frontiers in Microbiology, 2020, 11, 595036. | 1.5 | 8 |
| 6 | Identifying anaerobic amino acids degraders through the comparison of shortâ€ŧerm and longâ€ŧerm enrichments. Environmental Microbiology Reports, 2020, 12, 173-184. | 1.0 | 8 |
| 7 | Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. Microbiome, 2020, 8, 16. | 4.9 | 42 |
| 8 | Superior resolution characterisation of microbial diversity in anaerobic digesters using full-length 16S rRNA gene amplicon sequencing. Water Research, 2020, 178, 115815. | 5.3 | 40 |
| 9 | Nexus of Stochastic and Deterministic Processes on Microbial Community Assembly in Biological Systems. Frontiers in Microbiology, 2019, 10, 1536. | 1.5 | 37 |
| 10 | Quantifying the contribution of microbial immigration in engineered water systems. Microbiome, 2019, 7, 144. | 4.9 | 41 |
| 11 | Molecular microbial ecology of stable versus failing rice straw anaerobic digesters. Microbial Biotechnology, 2019, 12, 879-891. | 2.0 | 7 |
| 12 | Coupling growth kinetics modeling with machine learning reveals microbial immigration impacts and identifies key environmental parameters in a biological wastewater treatment process. Microbiome, 2019, 7, 65. | 4.9 | 27 |
| 13 | Novel Geobacter species and diverse methanogens contribute to enhanced methane production in media-added methanogenic reactors. Water Research, 2018, 147, 403-412. | 5.3 | 69 |
| 14 | Microbial community composition and diversity in rice straw digestion bioreactors with and without dairy manure. Applied Microbiology and Biotechnology, 2018, 102, 8599-8612. | 1.7 | 23 |
| 15 | Coâ€occurrence network analysis reveals thermodynamicsâ€driven microbial interactions in methanogenic bioreactors. Environmental Microbiology Reports, 2018, 10, 673-685. | 1.0 | 22 |
| 16 | Thermodynamically diverse syntrophic aromatic compound catabolism. Environmental Microbiology, 2017, 19, 4576-4586. | 1.8 | 32 |
| 17 | Operation-driven heterogeneity and overlooked feed-associated populations in global anaerobic digester microbiome. Water Research, 2017, 124, 77-84. | 5.3 | 82 |
| 18 | Effects of heat shocks on microbial community structure and microbial activity of a methanogenic enrichment degrading benzoate. Letters in Applied Microbiology, 2016, 63, 356-362. | 1.0 | 40 |

Ran Mei

| # | Article | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Evaluating digestion efficiency in full-scale anaerobic digesters by identifying active microbial populations through the lens of microbial activity. Scientific Reports, 2016, 6, 34090. | 1.6 | 87 |
| 20 | Chasing the elusive Euryarchaeota class WSA2: genomes reveal a uniquely fastidious methyl-reducing methanogen. ISME Journal, 2016, 10, 2478-2487. | 4.4 | 239 |
| 21 | A Single-Granule-Level Approach Reveals Ecological Heterogeneity in an Upflow Anaerobic Sludge Blanket Reactor. PLoS ONE, 2016, 11, e0167788. | 1.1 | 46 |
| 22 | Microbial Community Analysis of Anaerobic Reactors Treating Soft Drink Wastewater. PLoS ONE, 2015, 10, e0119131. | 1.1 | 27 |
| 23 | Glycocaulis alkaliphilus sp. nov., a dimorphic prosthecate bacterium isolated from crude oil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 838-844. | 0.8 | 17 |
| 24 | Paradevosia shaoguanensis gen. nov., sp. nov., Isolated from a Coking Wastewater. Current Microbiology, 2015, 70, 110-118. | 1.0 | 23 |
| 25 | Defluviimonas alba sp. nov., isolated from an oilfield. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 1805-1811. | 0.8 | 23 |
| 26 | Microbial Community Involved in Anaerobic Purified Terephthalic Acid Treatment Process. , 2015, , 31-48. | | 4 |
| 27 | Ottowia shaoguanensis sp. nov., Isolated From Coking Wastewater. Current Microbiology, 2014, 68, 324-329. | 1.0 | 28 |
| 28 | Nitratireductor shengliensis sp. nov., Isolated from an Oil-Polluted Saline Soil. Current Microbiology, 2014, 69, 561-566. | 1.0 | 18 |