## Sebastian Hupfauf

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3359458/publications.pdf

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188	1307594	1474206
citations	h-index	g-index
18	18	273
docs citations	times ranked	citing authors
	citations 18	188 7 citations h-index  18 18

#	Article	IF	CITATIONS
1	Biogas digestates affect crop P uptake and soil microbial community composition. Science of the Total Environment, 2016, 542, 1144-1154.	8.0	46
2	Temperature shapes the microbiota in anaerobic digestion and drives efficiency to a maximum at 45 °C. Bioresource Technology, 2018, 269, 309-318.	9.6	43
3	Microbiota in anaerobic digestion of sewage sludge with and without coâ€substrates. Water and Environment Journal, 2019, 33, 214-222.	2.2	34
4	Symbiotic Bacteroides and Clostridium-rich methanogenic consortium enhanced biogas production of high-solid anaerobic digestion systems. Bioresource Technology Reports, 2021, 14, 100685.	2.7	20
5	Biomethanation at $45 \hat{A} \hat{A}^{\circ} \text{C}$ offers high process efficiency and supports hygienisation. Bioresource Technology, 2020, 300, 122671.	9.6	17
6	CoMA $\hat{a} \in ``an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. PLoS ONE, 2020, 15, e0243241.$	2.5	15
7	Residual municipal solid waste as co-substrate at wastewater treatment plants: An assessment of methane yield, dewatering potential and microbial diversity. Science of the Total Environment, 2022, 804, 149936.	8.0	8
8	Can the addition of biochar improve the performance of biogas digesters operated at 45°C?. Environmental Engineering Research, 2022, 27, 200648-0.	2.5	3
9	Stability of the Anaerobic Digestion Process during Switch from Parallel to Serial Operation—A Microbiome Study. Sustainability, 2022, 14, 7161.	3.2	2
10	CoMA $\hat{a} \in ``an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.$		0
11	CoMA $\hat{a} \in \hat{a}$ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		O
12	CoMA $\hat{a} \in \hat{a}$ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
13	CoMA $\hat{a}\in$ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		O
14	CoMA $\hat{a} \in \hat{a}$ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
15	CoMA $\hat{a}\in$ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		O
16	CoMA $\hat{a} \in ``an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.$		0
17	CoMA $\hat{a}\in$ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		O
18	CoMA – an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0