

Sabine Marie Podmirseg

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8031063/publications.pdf>

Version: 2024-02-01

43
papers

1,301
citations

471061
17
h-index

414034
32
g-index

43
all docs

43
docs citations

43
times ranked

1828
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial response on the first full-scale DEMONÂ® biomass transfer for mainstream deammonification. Water Research, 2022, 218, 118517.	5.3	12
2	Why <scp>eDNA</scp> fractions need consideration in biomonitoring. Molecular Ecology Resources, 2022, 22, 2458-2470.	2.2	16
3	The masking effect of extracellular DNA and robustness of intracellular DNA in anaerobic digester NGS studies: A discriminatory study of the total DNA pool. Molecular Ecology, 2021, 30, 438-450.	2.0	17
4	The Effect of a High-Grain Diet on the Rumen Microbiome of Goats with a Special Focus on Anaerobic Fungi. Microorganisms, 2021, 9, 157.	1.6	17
5	Enhanced solid-state biomethanisation of oil palm empty fruit bunches following fungal pretreatment. Industrial Crops and Products, 2020, 145, 112099.	2.5	24
6	Biomethanation at 45Â°C offers high process efficiency and supports hygienisation. Bioresource Technology, 2020, 300, 122671.	4.8	17
7	Employing anaerobic fungi in biogas production: challenges & opportunities. Bioresource Technology, 2020, 300, 122687.	4.8	34
8	Quantities of Intra- and Extracellular DNA Reveal Information About Activity and Physiological State of Methanogenic Archaea. Frontiers in Microbiology, 2020, 11, 1894.	1.5	5
9	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. PLoS ONE, 2020, 15, e0243241.	1.1	15
10	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
11	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
12	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
13	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
14	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
15	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
16	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
17	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0
18	CoMA â€œ an intuitive and user-friendly pipeline for amplicon-sequencing data analysis. , 2020, 15, e0243241.		0

#	ARTICLE	IF	CITATIONS
19	Microbiota in anaerobic digestion of sewage sludge with and without co-substrates. Water and Environment Journal, 2019, 33, 214-222.	1.0	34
20	Robustness of the autochthonous microbial soil community after amendment of cattle manure or its digestate. Biology and Fertility of Soils, 2019, 55, 565-576.	2.3	18
21	Simple yet effective: Microbial and biotechnological benefits of rumen liquid addition to lignocellulose-degrading biogas plants. Journal of Biotechnology, 2019, 300, 1-10.	1.9	29
22	Trace metals supplementation enhanced microbiota and biohydrogen production by two-stage thermophilic fermentation. International Journal of Hydrogen Energy, 2019, 44, 3325-3338.	3.8	17
23	The use of extracellular DNA as a proxy for specific microbial activity. Applied Microbiology and Biotechnology, 2018, 102, 2885-2898.	1.7	45
24	Temperature shapes the microbiota in anaerobic digestion and drives efficiency to a maximum at 45°C. Bioresource Technology, 2018, 269, 309-318.	4.8	43
25	Soil microbiota along Ayoloco glacier retreat area of Iztaccíhuatl volcano, Mexico. Catena, 2017, 153, 83-88.	2.2	8
26	Prokaryotic Community Dynamics during the Start-Up of a Full-Scale BIO4GAS Digester. Journal of Environmental Engineering, ASCE, 2016, 142, .	0.7	4
27	Expanding DEMON Sidestream Deammonification Technology Towards Mainstream Application. Water Environment Research, 2015, 87, 2084-2089.	1.3	93
28	A novel fixed fibre biofilm membrane process for on-site greywater reclamation requiring no fouling control. Biotechnology and Bioengineering, 2015, 112, 484-493.	1.7	41
29	Anaerobic Fungi and Their Potential for Biogas Production. Advances in Biochemical Engineering/Biotechnology, 2015, 151, 41-61.	0.6	35
30	Comparative evaluation of multiple methods to quantify and characterise granular anammox biomass. Water Research, 2015, 68, 194-205.	5.3	37
31	Finding a robust strain for biomethanation: Anaerobic fungi (Neocallimastigomycota) from the Alpine ibex (Capra ibex) and their associated methanogens. Anaerobe, 2014, 29, 34-43.	1.0	44
32	No oxygen-still vigorous: 8th International Symposium on Anaerobic Microbiology (ISAM 8) Innsbruck, Austria. Anaerobe, 2014, 29, 1-2.	1.0	0
33	Wood ash amendment to biogas reactors as an alternative to landfilling? A preliminary study on changes in process chemistry and biology. Waste Management and Research, 2013, 31, 829-842.	2.2	20
34	The dynamic bacterial communities of a melting High Arctic glacier snowpack. ISME Journal, 2013, 7, 1814-1826.	4.4	132
35	Going for mainstream deammonification from bench to full scale for maximized resource efficiency. Water Science and Technology, 2013, 68, 283-289.	1.2	181
36	Biological waste treatment. Waste Management and Research, 2013, 31, 773-774.	2.2	7

#	ARTICLE	IF	CITATIONS
37	The effect of maize silage as co-substrate for swine manure on the bacterial community structure in biogas plants. <i>Folia Microbiologica</i> , 2012, 57, 281-284.	1.1	4
38	Pathogenic bacteria and mineral N in soils following the land spreading of biogas digestates and fresh manure. <i>Applied Soil Ecology</i> , 2011, 49, 18-25.	2.1	112
39	Quantitative and qualitative effects of bioaugmentation on ammonia oxidisers at a two-step WWTP. <i>Water Science and Technology</i> , 2010, 61, 1003-1009.	1.2	10
40	Diet-related composition of the gut microbiota of <i>Lumbricus rubellus</i> as revealed by a molecular fingerprinting technique and cloning. <i>Soil Biology and Biochemistry</i> , 2009, 41, 2299-2307.	4.2	92
41	Molecular fingerprinting analysis of the gut microbiota of <i>Cylindroiulus fulviceps</i> (Diplopoda). <i>Pedobiologia</i> , 2009, 52, 325-336.	0.5	22
42	Application of denaturing gradient gel electrophoresis for analysing the gut microflora of <i>Lumbricus rubellus</i> Hoffmeister under different feeding conditions. <i>Bulletin of Entomological Research</i> , 2008, 98, 271-279.	0.5	21
43	<i>Buwchfawromyces eastonii</i> gen. nov., sp. nov.: a new anaerobic fungus (Neocallimastigomycota) isolated from buffalo faeces. <i>MycKeys</i> , 0, 9, 11-28.	0.8	95