

Melline F Noronha

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

654
citations

759233

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996975

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times ranked

1121
citing authors

#	ARTICLE	IF	CITATIONS
1	Conventional and ohmic heating pasteurization of fresh and thawed sheep milk: Energy consumption and assessment of bacterial microbiota during refrigerated storage. <i>Innovative Food Science and Emerging Technologies</i> , 2022, 76, 102947.	5.6	17
2	Wheat-durum pasta added of inactivated <i>Bifidobacterium animalis</i> decreases glucose and total cholesterol levels and modulates gut microbiota in healthy rats. <i>International Journal of Food Sciences and Nutrition</i> , 2021, 72, 781-793.	2.8	12
3	Paraprobiotics obtained by six different inactivation processes: impacts on the biochemical parameters and intestinal microbiota of Wistar male rats. <i>International Journal of Food Sciences and Nutrition</i> , 2021, 72, 1057-1070.	2.8	10
4	Exploring the genetic potential of a fosmid metagenomic library from an oil-impacted mangrove sediment for metabolism of aromatic compounds. <i>Ecotoxicology and Environmental Safety</i> , 2020, 189, 109974.	6.0	16
5	Amplicon sequencing reveals the bacterial diversity in milk, dairy premises and Serra da Canastra artisanal cheeses produced by three different farms. <i>Food Microbiology</i> , 2020, 89, 103453.	4.2	38
6	Land Use and Seasonal Effects on the Soil Microbiome of a Brazilian Dry Forest. <i>Frontiers in Microbiology</i> , 2019, 10, 648.	3.5	61
7	The metagenomic landscape of xenobiotics biodegradation in mangrove sediments. <i>Ecotoxicology and Environmental Safety</i> , 2019, 179, 232-240.	6.0	17
8	Microbiota of eggs revealed by 16S rRNA-based sequencing: From raw materials produced by different suppliers to chilled pasteurized liquid products. <i>Food Control</i> , 2019, 96, 194-204.	5.5	17
9	Microbial diversity of a full-scale UASB reactor applied to poultry slaughterhouse wastewater treatment: integration of 16S rRNA gene amplicon and shotgun metagenomic sequencing. <i>MicrobiologyOpen</i> , 2017, 6, e00443.	3.0	43
10	Potential of semiarid soil from Caatinga biome as a novel source for mining lignocellulose-degrading enzymes. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw248.	2.7	15
11	Taxonomic and functional patterns across soil microbial communities of global biomes. <i>Science of the Total Environment</i> , 2017, 609, 1064-1074.	8.0	32
12	Effect of Pre-weaning Diet on the Ruminal Archaeal, Bacterial, and Fungal Communities of Dairy Calves. <i>Frontiers in Microbiology</i> , 2017, 8, 1553.	3.5	83
13	<i>Saccharomyces cerevisiae</i> transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. <i>Microbial Cell Factories</i> , 2015, 14, 13.	4.0	51
14	Genome structure of a <i>Saccharomyces cerevisiae</i> strain widely used in bioethanol production. <i>Genome Research</i> , 2009, 19, 2258-2270.	5.5	237