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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Impact of Inoculation with Pseudomonas aestus CMAA 1215T on the Non-target Resident Bacterial Community in a Saline Rhizosphere Soil. Current Microbiology, 2021, 78, 218-228.	1.0	6
2	Application of extracellular polymers on soil communities exposed to oil and nickel contamination. Brazilian Journal of Microbiology, 2021, 52, 651-661.	0.8	1
3	Structure and diversity of bacterial community in semiarid soils cultivated with prickly-pear cactus (Opuntia ficus-indica (L.) Mill.). Anais Da Academia Brasileira De Ciencias, 2021, 93, e20190183.	0.3	3
4	Genomic analysis reveals the potential for hydrocarbon degradation of Rhodopirellula sp. MGV isolated from a polluted Brazilian mangrove. Brazilian Journal of Microbiology, 2021, 52, 1397-1404.	0.8	7
5	Land Management Legacy Affects Abundance and Function of the acdS Gene in Wheat Root Associated Pseudomonads. Frontiers in Microbiology, 2021, 12, 611339.	1.5	2
6	Editorial: Advancements in the Understanding of Anthropogenic Impacts on the Microbial Ecology and Function of Aquatic Environments. Frontiers in Microbiology, 2021, 12, 820697.	1.5	0
7	The unexplored bacterial lifestyle on leaf surface. Brazilian Journal of Microbiology, 2020, 51, 1233-1240.	0.8	3
8	Use of plant materials for the bioremediation of soil from an industrial site. Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering, 2020, 55, 650-660.	0.9	8
9	Effect of nickel in the degradation of oil in soils contaminated with petroleum and nickel. International Journal of Advanced Engineering Research and Science, 2020, 7, 511-521.	0.0	2
10	Intraspecific variation on epiphytic bacterial community from Laguncularia racemosa phylloplane. Brazilian Journal of Microbiology, 2019, 50, 1041-1050.	0.8	3
11	Application of surfactants and biosurfactants in the bioremediation of multi-contaminated soils: microcosms and bench scale bioreactor trials. International Journal of Advanced Engineering Research and Science, 2019, 6, 91-98.	0.0	0
12	Bacterial Succession Decreases Network Complexity During Plant Material Decomposition in Mangroves. Microbial Ecology, 2018, 76, 954-963.	1.4	20
13	The role of species turnover in structuring bacterial communities in a local scale in theÂcactus rhizosphere. Plant and Soil, 2018, 425, 101-112.	1.8	10
14	Higher phylogenetic diversity prevents loss of functional diversity caused by successive drying and rewetting cycles. Antonie Van Leeuwenhoek, 2018, 111, 1033-1045.	0.7	2
15	Draft Genome Sequence of Rhodopirellula baltica Strain BR-MGV, a Planctomycete Isolated from Brazilian Mangrove Soil. Microbiology Resource Announcements, 2018, 7, .	0.3	2
16	Co-occurrence patterns of litter decomposing communities in mangroves indicate a robust community resistant to disturbances. PeerJ, 2018, 6, e5710.	0.9	11
17	Draft Genome Sequence of Plant Growth-Promoting Drought-Tolerant <i>Bacillus</i> sp. Strain CMAA 1363 Isolated from the Brazilian Caatinga Biome. Genome Announcements, 2017, 5, .	0.8	4
18	Diversity and Technological Aspects of Microorganisms from Semiarid Environments. , 2017, , 3-19.		3

Diversity and Technological Aspects of Microorganisms from Semiarid Environments. , 2017, , 3-19. 18

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19	Dominance of Epsilonproteobacteria associated with a whale fall at a 4204 m depth – South Atlantic Ocean. Deep-Sea Research Part II: Topical Studies in Oceanography, 2017, 146, 53-58.	0.6	11
20	The drivers underlying biogeographical patterns of bacterial communities in soils under sugarcane cultivation. Applied Soil Ecology, 2017, 110, 12-20.	2.1	32
21	Dry Season Constrains Bacterial Phylogenetic Diversity in a Semi-Arid Rhizosphere System. Microbial Ecology, 2017, 73, 153-161.	1.4	86
22	Analysis of bacterial composition in marine sponges reveals the influence of host phylogeny and environment. FEMS Microbiology Ecology, 2017, 93, fiw204.	1.3	31
23	A Novel Multifunctional β-N-Acetylhexosaminidase Revealed through Metagenomics of an Oil-Spilled Mangrove. Bioengineering, 2017, 4, 62.	1.6	13
24	Genome Sequence of Streptomyces caatingaensis CMAA 1322, a New Abiotic Stress-Tolerant Actinomycete Isolated from Dried Lake Bed Sediment in the Brazilian Caatinga Biome. Genome Announcements, 2015, 3, .	0.8	2
25	Draft Genome Sequence of <i>Bacillus</i> sp. Strain CMAA 1185, a Cellullolytic Bacterium Isolated from Stain House Lake, Antarctic Peninsula. Genome Announcements, 2015, 3, .	0.8	2
26	Functional congruence of rhizosphere microbial communities associated to leguminous tree from <scp>B</scp> razilian semiarid region. Environmental Microbiology Reports, 2015, 7, 95-101.	1.0	20
27	Exploring the sheep rumen microbiome for carbohydrate-active enzymes. Antonie Van Leeuwenhoek, 2015, 108, 15-30.	0.7	55
28	The influence of nickel on the bioremediation of multi-component contaminated tropical soil: microcosm and batch bioreactor studies. World Journal of Microbiology and Biotechnology, 2015, 31, 1127-1135.	1.7	2
29	Draft Genome Sequence of Bacillus thuringiensis Strain BrMgv02-JM63, a Chitinolytic Bacterium Isolated from Oil-Contaminated Mangrove Soil in Brazil. Genome Announcements, 2014, 2, .	0.8	4
30	Bacterial community characterization in the soils of native and restored rainforest fragments. Antonie Van Leeuwenhoek, 2014, 106, 947-957.	0.7	2
31	Effect of ultraviolet-B (UV-B) radiation on bacterial community in the soybean phyllosphere. African Journal of Microbiology Research, 2014, 8, 2916-2923.	0.4	2
32	Screening of Brazilian cacti rhizobacteria for plant growth promotion under drought. Microbiological Research, 2013, 168, 183-191.	2.5	215
33	Microbial community biogeographic patterns in the rhizosphere of two Brazilian semi-arid leguminous trees. World Journal of Microbiology and Biotechnology, 2013, 29, 1233-1241.	1.7	18
34	Streptomyces araujoniae sp. nov.: an actinomycete isolated from a potato tubercle. Antonie Van Leeuwenhoek, 2013, 103, 1235-1244.	0.7	18
35	Bacterial community composition of anthropogenic biochar and Amazonian anthrosols assessed by 16S rRNA gene 454 pyrosequencing. Antonie Van Leeuwenhoek, 2013, 104, 233-242.	0.7	61
36	Whole-Genome Shotgun Sequencing of Rhodococcus erythropolis Strain P27, a Highly Radiation-Resistant Actinomycete from Antarctica. Genome Announcements, 2013, 1, .	0.8	6

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37	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain CMAA 1215, a Plant Growth-Promoting Bacterium Isolated from a Brazilian Mangrove. Genome Announcements, 2013, 1, .	0.8	5
38	Endo-and exoglucanase activities in bacteria from mangrove sediment. Brazilian Journal of Microbiology, 2013, 44, 969-976.	0.8	27
39	Water Regime Influences Bulk Soil and Rhizosphere of Cereus jamacaru Bacterial Communities in the Brazilian Caatinga Biome. PLoS ONE, 2013, 8, e73606.	1.1	90
40	Shifts in phylogenetic diversity of archaeal communities in mangrove sediments at different sites and depths in southeastern Brazil. Research in Microbiology, 2012, 163, 366-377.	1.0	35
41	The Microbiome of Brazilian Mangrove Sediments as Revealed by Metagenomics. PLoS ONE, 2012, 7, e38600.	1.1	222
42	Interspecific variation of the bacterial community structure in the phyllosphere of the three major plant components of mangrove forests. Brazilian Journal of Microbiology, 2012, 43, 653-660.	0.8	16
43	Land-use systems affect Archaeal community structure and functional diversity in western Amazon soils. Revista Brasileira De Ciencia Do Solo, 2011, 35, 1527-1540.	0.5	31
44	Archaeal communities in the sediments of three contrasting mangroves. Journal of Soils and Sediments, 2011, 11, 1466-1476.	1.5	50
45	A Molecular Survey of the Diversity of Microbial Communities in Different Amazonian Agricultural Model Systems. Diversity, 2010, 2, 787-809.	0.7	64
46	The Influence of Different Land Uses on the Structure of Archaeal Communities in Amazonian Anthrosols Based on 16S rRNA and amoA Genes. Microbial Ecology, 2010, 59, 734-743.	1.4	61
47	Diversity and identification of methanogenic archaea and sulphate-reducing bacteria in sediments from a pristine tropical mangrove. Antonie Van Leeuwenhoek, 2010, 97, 401-411.	0.7	80
48	Microbial community response to a simulated hydrocarbon spill in mangrove sediments. Journal of Microbiology, 2010, 48, 7-15.	1.3	72
49	Influence of the bacterioplankton community of a tropical eutrophic lagoon on the bacterial community of its neighbouring ocean. World Journal of Microbiology and Biotechnology, 2010, 26, 1865-1873.	1.7	2
50	Bacterial soil community in a Brazilian sugarcane field. Plant and Soil, 2010, 336, 337-349.	1.8	16
51	Characterisation of the effect of a simulated hydrocarbon spill on diazotrophs in mangrove sediment mesocosm. Antonie Van Leeuwenhoek, 2009, 96, 343-354.	0.7	30
52	Use of molecular approach to verify the influence of a eutrophic lagoon in the nearby ocean's bacterioplankton communities. Brazilian Journal of Microbiology, 0, 34, .	0.8	2