

# Marta Tacã£o

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

1,416  
citations

304368

22  
h-index

329751

37  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1941  
citing authors

#	ARTICLE	IF	CITATIONS
1	Occurrence and distribution of Carbapenem-resistant Enterobacterales and carbapenemase genes along a highly polluted hydrographic basin. <i>Environmental Pollution</i> , 2022, 300, 118958.	3.7	7
2	KPC-3-, GES-5-, and VIM-1-Producing Enterobacterales Isolated from Urban Ponds. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 5848.	1.2	5
3	Draft Genome Resources Sequences of Six <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Strains Isolated from <i>Actinidia chinensis</i> var. <i>deliciosa</i> Leaves in Portugal. <i>Phytopathology</i> , 2021, 111, 237-239.	1.1	5
4	Selection of antibiotic resistance by metals in a riverine bacterial community. <i>Chemosphere</i> , 2021, 263, 127936.	4.2	26
5	Tetracycline-Resistant Bacteria Selected from Water and Zebrafish after Antibiotic Exposure. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 3218.	1.2	6
6	Genome analysis of two multidrug-resistant <i>Escherichia coli</i> O8:H9-ST48 strains isolated from lettuce. <i>Gene</i> , 2021, 785, 145603.	1.0	6
7	Carbapenem-resistant bacteria over a wastewater treatment process: Carbapenem-resistant Enterobacteriaceae in untreated wastewater and intrinsically-resistant bacteria in final effluent. <i>Science of the Total Environment</i> , 2021, 782, 146892.	3.9	18
8	qnrA gene diversity in <i>Shewanella</i> spp.. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	3
9	Genome and Metabolome MS-Based Mining of a Marine Strain of <i>Aspergillus affinis</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 1091.	1.5	9
10	Occurrence of carbapenemase-producing Enterobacteriaceae in a Portuguese river: bla <sub>NDM</sub> , bla <sub>KPC</sub> and bla <sub>GES</sub> among the detected genes. <i>Environmental Pollution</i> , 2020, 260, 113913.	3.7	45
11	A global multinational survey of cefotaxime-resistant coliforms in urban wastewater treatment plants. <i>Environment International</i> , 2020, 144, 106035.	4.8	55
12	Genotypic and phenotypic traits of bla <sub>CTX-M</sub> -carrying <i>Escherichia coli</i> strains from an UV-C-treated wastewater effluent. <i>Water Research</i> , 2020, 184, 116079.	5.3	13
13	Occurrence, antibiotic-resistance and virulence of <i>E. coli</i> strains isolated from mangrove oysters ( <i>Crassostrea gasar</i> ) farmed in estuaries of Amazonia. <i>Marine Pollution Bulletin</i> , 2020, 157, 111302.	2.3	15
14	Genomic analysis of <i>Chromobacterium haemolyticum</i> : insights into the species resistome, virulence determinants and genome plasticity. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1001-1012.	1.0	7
15	Epidemiology of carbapenemases-producing bacteria in Centro Hospitalar Baixo Vouga. <i>International Journal of Infectious Diseases</i> , 2020, 101, 18.	1.5	0
16	Surveillance of plasmid-mediated mcr-1, mcr-3, mcr-4 and mcr-5 genes in human isolates, in Aveiro, Portugal. <i>International Journal of Infectious Diseases</i> , 2020, 101, 343.	1.5	0
17	Long-term effects of oxytetracycline exposure in zebrafish: A multi-level perspective. <i>Chemosphere</i> , 2019, 222, 333-344.	4.2	65
18	Extended Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria Recovered From an Amazonian Lake Near the City of Belém, Brazil. <i>Frontiers in Microbiology</i> , 2019, 10, 364.	1.5	38

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19	Shewanella species as the origin of blaOXA-48 genes: insights into gene diversity, associated phenotypes and possible transfer mechanisms. International Journal of Antimicrobial Agents, 2018, 51, 340-348.	1.1	37
20	Integrated Optical Mach-Zehnder Interferometer Based on Organic-Inorganic Hybrids for Photonics-on-a-Chip Biosensing Applications. Sensors, 2018, 18, 840.	2.1	24
21	Fate of cefotaxime-resistant Enterobacteriaceae and ESBL-producers over a full-scale wastewater treatment process with UV disinfection. Science of the Total Environment, 2018, 639, 1028-1037.	3.9	28
22	Culture-independent methods reveal high diversity of OXA-48-like genes in water environments. Journal of Water and Health, 2017, 15, 519-525.	1.1	7
23	Characterization of antibiotic resistant and pathogenic Escherichia coli in irrigation water and vegetables in household farms. International Journal of Food Microbiology, 2017, 257, 192-200.	2.1	95
24	<i>mcr-1</i> and <i>bla</i> <sub>KPC-3</sub> in <i>Escherichia coli</i> Sequence Type 744 after Meropenem and Colistin Therapy, Portugal. Emerging Infectious Diseases, 2017, 23, 1419-1421.	2.0	45
25	Diversity of endophytic Pseudomonas in Halimione portulacoides from metal(loid)-polluted salt marshes. Environmental Science and Pollution Research, 2016, 23, 13255-13267.	2.7	11
26	Co-selection of antibiotic and metal(loid) resistance in gram-negative epiphytic bacteria from contaminated salt marshes. Marine Pollution Bulletin, 2016, 109, 427-434.	2.3	38
27	Antibiotic and metal resistance in a ST395 Pseudomonas aeruginosa environmental isolate: A genomics approach. Marine Pollution Bulletin, 2016, 110, 75-81.	2.3	43
28	Culturable endophytic bacteria from the salt marsh plant Halimione portulacoides: phylogenetic diversity, functional characterization, and influence of metal(loid) contamination. Environmental Science and Pollution Research, 2016, 23, 10200-10214.	2.7	59
29	Low Prevalence of Carbapenem-Resistant Bacteria in River Water: Resistance Is Mostly Related to Intrinsic Mechanisms. Microbial Drug Resistance, 2015, 21, 497-506.	0.9	77
30	Co-resistance to different classes of antibiotics among ESBL-producers from aquatic systems. Water Research, 2014, 48, 100-107.	5.3	110
31	Genetic diversity and antimicrobial resistance of Escherichia coli from Tagus estuary (Portugal). Science of the Total Environment, 2013, 461-462, 65-71.	3.9	41
32	Environmental Shewanella xiamenensis Strains That Carry <i>bla</i> <sub>OXA-48</sub> or <i>bla</i> <sub>OXA-204</sub> Genes: Additional Proof for <i>bla</i> <sub>OXA-48-Like</sub> Gene Origin. Antimicrobial Agents and Chemotherapy, 2013, 57, 6399-6400.	1.4	32
33	Resistance to Broad-Spectrum Antibiotics in Aquatic Systems: Anthropogenic Activities Modulate the Dissemination of <i>bla</i> <sub>CTX-M</sub> -Like Genes. Applied and Environmental Microbiology, 2012, 78, 4134-4140.	1.4	148
34	Molecular assessment of microbiota structure and dynamics along mixed olive oil and winery wastewaters biotreatment. Biodegradation, 2011, 22, 773-795.	1.5	9
35	PCR-DGGE-based methodologies to assess diversity and dynamics of Aeromonas communities. Journal of Applied Microbiology, 2010, 108, 611-623.	1.4	3
36	Characterization of bacterial diversity in two aerated lagoons of a wastewater treatment plant using PCR-DGGE analysis. Microbiological Research, 2009, 164, 560-569.	2.5	73

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37	Seasonal and spatial variability of free-living bacterial community composition along an estuarine gradient (Ria de Aveiro, Portugal). <i>Estuarine, Coastal and Shelf Science</i> , 2006, 68, 139-148.	0.9	93
38	Evaluation of 16S rDNA- and gyrB-DGGE for typing members of the genus <i>Aeromonas</i> . <i>FEMS Microbiology Letters</i> , 2005, 246, 11-18.	0.7	21
39	BOX-PCR is an Adequate Tool for Typing <i>Aeromonas</i> spp.. <i>Antonie Van Leeuwenhoek</i> , 2005, 88, 173-179.	0.7	47
40	Resistance to beta-lactam antibiotics in <i>Aeromonas hydrophila</i> isolated from rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>International Microbiology</i> , 2004, 7, 207-11.	1.1	52