## Isabel Henriques

List of Publications by Year in descending order

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Version: 2024-02-01

76294 95218 5,468 128 40 68 citations h-index g-index papers 128 128 128 6436 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	INTEGRALL: a database and search engine for integrons, integrases and gene cassettes. Bioinformatics, 2009, 25, 1096-1098.	1.8	578
2	Antibiotic resistance in European wastewater treatment plants mirrors the pattern of clinical antibiotic resistance prevalence. Science Advances, 2019, 5, eaau9124.	4.7	346
3	Antibiotic residues in final effluents of European wastewater treatment plants and their impact on the aquatic environment. Environment International, 2020, 140, 105733.	4.8	338
4	Wavelength dependence of biological damage induced by UV radiation on bacteria. Archives of Microbiology, 2013, 195, 63-74.	1.0	205
5	Occurrence and diversity of integrons and $\hat{l}^2$ -lactamase genes among ampicillin-resistant isolates from estuarine waters. Research in Microbiology, 2006, 157, 938-947.	1.0	177
6	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
7	Prevalence and characterization of integrons from bacteria isolated from a slaughterhouse wastewater treatment plant. Journal of Antimicrobial Chemotherapy, 2007, 60, 1243-1250.	1.3	141
8	Changes in the bacterial community structure in two-stage constructed wetlands with different plants for industrial wastewater treatment. Bioresource Technology, 2009, 100, 3228-3235.	4.8	125
9	Co-resistance to different classes of antibiotics among ESBL-producers from aquatic systems. Water Research, 2014, 48, 100-107.	5.3	110
10	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
11	Seasonal and spatial variability of free-living bacterial community composition along an estuarine gradient (Ria de Aveiro, Portugal). Estuarine, Coastal and Shelf Science, 2006, 68, 139-148.	0.9	93
12	Bacterial lineages putatively associated with the dissemination of antibiotic resistance genes in a full-scale urban wastewater treatment plant. Environment International, 2018, 118, 179-188.	4.8	93
13	Wastewater bacterial communities bring together broad-host range plasmids, integrons and a wide diversity of uncharacterized gene cassettes. Research in Microbiology, 2010, 161, 58-66.	1.0	89
14	Substrate effect on bacterial communities from constructed wetlands planted with Typha latifolia treating industrial wastewater. Ecological Engineering, 2009, 35, 744-753.	1.6	82
15	Novel gene cassettes and integrons in antibiotic-resistant bacteria isolated from urban wastewaters. Research in Microbiology, 2012, 163, 92-100.	1.0	77
16	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
17	Seawater is a reservoir of multi-resistant Escherichia coli, including strains hosting plasmid-mediated quinolones resistance and extended-spectrum beta-lactamases genes. Frontiers in Microbiology, 2014, 5, 426.	1.5	74
18	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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19	Sfh-I, a Subclass B2 Metallo- $\hat{l}^2$ -Lactamase from a Serratia fonticola Environmental Isolate. Antimicrobial Agents and Chemotherapy, 2003, 47, 2330-2333.	1.4	71
20	Contribution of reactive oxygen species to UV-B-induced damage in bacteria. Journal of Photochemistry and Photobiology B: Biology, 2012, 117, 40-46.	1.7	70
21	Long-term effects of oxytetracycline exposure in zebrafish: A multi-level perspective. Chemosphere, 2019, 222, 333-344.	4.2	65
22	Molecular Characterization of a Carbapenem-Hydrolyzing Class A $\hat{l}^2$ -Lactamase, SFC-1, from Serratia fonticola UTAD54. Antimicrobial Agents and Chemotherapy, 2004, 48, 2321-2324.	1.4	59
23	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
24	Rapid differentiation of species of Botryosphaeriaceae by PCR fingerprinting. Research in Microbiology, 2007, 158, 112-121.	1.0	58
25	Analysing diversity among β-lactamase encoding genes in aquatic environments. FEMS Microbiology Ecology, 2006, 56, 418-429.	1.3	57
26	Molecular sequence analysis of prokaryotic diversity in the middle and outer sections of the Portuguese estuary Ria de Aveiro. FEMS Microbiology Ecology, 2004, 49, 269-279.	1.3	56
27	Effects of UV Radiation on the Lipids and Proteins of Bacteria Studied by Mid-Infrared Spectroscopy. Environmental Science & E	4.6	55
28	A global multinational survey of cefotaxime-resistant coliforms in urban wastewater treatment plants. Environment International, 2020, 144, 106035.	4.8	55
29	Functional annotation of hypothetical proteins from the Exiguobacterium antarcticum strain B7 reveals proteins involved in adaptation to extreme environments, including high arsenic resistance. PLoS ONE, 2018, 13, e0198965.	1.1	52
30	Evaluation of amplified ribosomal DNA restriction analysis as a method for the identification of Botryosphaeria species. FEMS Microbiology Letters, 2005, 245, 221-229.	0.7	51
31	Bacterial community dynamics within an aerobic granular sludge reactor treating wastewater loaded with pharmaceuticals. Ecotoxicology and Environmental Safety, 2018, 147, 905-912.	2.9	49
32	Effects of UV-B Radiation on the Structural and Physiological Diversity of Bacterioneuston and Bacterioplankton. Applied and Environmental Microbiology, 2012, 78, 2066-2069.	1.4	48
33	The impact of antibiotic exposure in water and zebrafish gut microbiomes: A 16S rRNA gene-based metagenomic analysis. Ecotoxicology and Environmental Safety, 2019, 186, 109771.	2.9	48
34	Gulls identified as major source of fecal pollution in coastal waters: A microbial source tracking study. Science of the Total Environment, 2014, 470-471, 84-91.	3.9	46
35	<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
36	Occurrence of carbapenemase-producing Enterobacteriaceae in a Portuguese river: blaNDM, blaKPC and blaGES among the detected genes. Environmental Pollution, 2020, 260, 113913.	3.7	45

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37	Metal(loid)-Contaminated Soils as a Source of Culturable Heterotrophic Aerobic Bacteria for Remediation Applications. Geomicrobiology Journal, 2017, 34, 760-768.	1.0	44
38	Bacterial community composition over a dry winter in meso- and eutrophic Portuguese water bodies. FEMS Microbiology Ecology, 2007, 59, 638-650.	1.3	43
39	Broad diversity of conjugative plasmids in integron-carrying bacteria from wastewater environments. FEMS Microbiology Letters, 2012, 330, 157-164.	0.7	43
40	Antibiotic and metal resistance in a ST395 Pseudomonas aeruginosa environmental isolate: A genomics approach. Marine Pollution Bulletin, 2016, 110, 75-81.	2.3	43
41	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
42	Characterization of microbial population of â€~Alheira' (a traditional Portuguese fermented sausage) by PCR-DGGE and traditional cultural microbiological methods. Journal of Applied Microbiology, 2008, 105, 2187-2194.	1.4	40
43	Long-term effects of Cu(OH)2 nanopesticide exposure on soil microbial communities. Environmental Pollution, 2021, 269, 116113.	3.7	39
44	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
45	Extended Spectrum Beta-Lactamase-Producing Gram-Negative Bacteria Recovered From an Amazonian Lake Near the City of Belém, Brazil. Frontiers in Microbiology, 2019, 10, 364.	1.5	38
46	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
47	Microbacterium diaminobutyricum sp. nov., isolated from Halimione portulacoides, which contains diaminobutyric acid in its cell wall, and emended description of the genus Microbacterium. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 4492-4500.	0.8	37
48	Bacterial community associated to the pine wilt disease insect vectors Monochamus galloprovincialis and Monochamus alternatus. Scientific Reports, 2016, 6, 23908.	1.6	36
49	Occurrence of IMP-8, IMP-10, and IMP-13 metallo- $\hat{l}^2$ -lactamases located on class 1 integrons and other extended-spectrum $\hat{l}^2$ -lactamases in bacterial isolates from Tunisian rivers. Scandinavian Journal of Infectious Diseases, 2013, 45, 95-103.	1.5	33
50	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
51	Short-term variability of abundance, diversity and activity of estuarine bacterioneuston and bacterioplankton. Journal of Plankton Research, 2009, 31, 1545-1555.	0.8	30
52	The role of bacteria in pine wilt disease: insights from microbiome analysis. FEMS Microbiology Ecology, 2018, 94, .	1.3	30
53	Tetracycline-resistance genes in Gram-negative isolates from estuarine waters. Letters in Applied Microbiology, 2008, 47, 526-533.	1.0	29
54	Prevalence and Diversity of Carbapenem-Resistant Bacteria in Untreated Drinking Water in Portugal. Microbial Drug Resistance, 2012, 18, 531-537.	0.9	28

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55	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
56	The contribution of Escherichia coli from human and animal sources to the integron gene pool in coastal waters. Frontiers in Microbiology, 2014, 5, 419.	1.5	27
57	Salivary peptidomic as a tool to disclose new potential antimicrobial peptides. Journal of Proteomics, 2015, 115, 49-57.	1.2	26
58	Selection of antibiotic resistance by metals in a riverine bacterial community. Chemosphere, 2021, 263, 127936.	4.2	26
59	Zebrafish and water microbiome recovery after oxytetracycline exposure. Environmental Pollution, 2021, 272, 116371.	3.7	25
60	Altererythrobacter halimionae sp. nov. and Altererythrobacter endophyticus sp. nov., two endophytes from the salt marsh plant Halimione portulacoides. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3057-3062.	0.8	25
61	The endosphere of the salt marsh plant Halimione portulacoides is a diversity hotspot for the genus Salinicola: description of five novel species Salinicola halimionae sp. nov., Salinicola aestuarinus sp. nov., Salinicola endophyticus sp. nov., Salinicola halophyticus sp. nov. and Salinicola lusitanus sp. nov., International lournal of Systematic and Evolutionary Microbiology, 2019, 69, 46-62.	0.8	25
62	Biochemical Characterization of SFC-1, a Class A Carbapenem-Hydrolyzing Î <sup>2</sup> -Lactamase. Antimicrobial Agents and Chemotherapy, 2007, 51, 4512-4514.	1.4	23
63	Diversity in UV sensitivity and recovery potential among bacterioneuston and bacterioplankton isolates. Letters in Applied Microbiology, 2011, 52, 360-366.	1.0	23
64	Endophytic Lifestyle of Global Clones of Extended-Spectrum $\hat{l}^2$ -Lactamase-Producing Priority Pathogens in Fresh Vegetables: a Trojan Horse Strategy Favoring Human Colonization?. MSystems, 2021, 6, .	1.7	23
65	Antibacterial activity of oxytetracycline photoproducts in marine aquaculture's water. Environmental Pollution, 2017, 220, 644-649.	3.7	22
66	Evaluation of 16S rDNA- andgyrB-DGGE for typing members of the genusAeromonas. FEMS Microbiology Letters, 2005, 246, 11-18.	0.7	21
67	The UV responses of bacterioneuston and bacterioplankton isolates depend on the physiological condition and involve a metabolic shift. FEMS Microbiology Ecology, 2012, 80, 646-658.	1.3	21
68	Phylogenetic diversity and functional characterization of the Manila clam microbiota: a culture-based approach. Environmental Science and Pollution Research, 2017, 24, 21721-21732.	2.7	21
69	Applicability of rep-PCR genomic fingerprinting to molecular discrimination of members of the genera Phaeoacremonium and Phaeomoniella. Plant Pathology, 2004, 53, 629-634.	1.2	20
70	Diversity of Gene Cassette Promoters in Class 1 Integrons from Wastewater Environments. Applied and Environmental Microbiology, 2012, 78, 5413-5416.	1.4	20
71	Chemical composition and antimicrobial activity of Satureja montana byproducts essential oils. Industrial Crops and Products, 2019, 137, 541-548.	2.5	20
72	Bacterial Diversity and Geochemical Profiles in Sediments from Eutrophic Azorean Lakes. Geomicrobiology Journal, 2012, 29, 704-715.	1.0	19

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73	Resistome in Lake Bolonha, Brazilian Amazon: Identification of Genes Related to Resistance to Broad-Spectrum Antibiotics. Frontiers in Microbiology, 2020, $11,67$ .	1.5	19
74	Molecular analysis of the diversity of genus <i>Psychrobacter</i> present within a temperate estuary. FEMS Microbiology Ecology, 2013, 84, 451-460.	1.3	18
75	Basagran $\hat{A}^{\otimes}$ induces developmental malformations and changes the bacterial community of zebrafish embryos. Environmental Pollution, 2017, 221, 52-63.	3.7	18
76	Carbapenem-resistant bacteria over a wastewater treatment process: Carbapenem-resistant Enterobacteriaceae in untreated wastewater and intrinsically-resistant bacteria in final effluent. Science of the Total Environment, 2021, 782, 146892.	3.9	18
77	Common and distinctive genomic features of Klebsiella pneumoniae thriving in the natural environment or in clinical settings. Scientific Reports, 2022, $12$ , .	1.6	18
78	A microcosm approach to evaluate the degradation of tributyltin (TBT) by Aeromonas molluscorum Av27 in estuarine sediments. Environmental Research, 2014, 132, 430-437.	3.7	17
79	Impact of sampling depth and plant species on local environmental conditions, microbiological parameters and bacterial composition in a mercury contaminated salt marsh. Marine Pollution Bulletin, 2012, 64, 263-271.	2.3	16
80	Long-term performance and microbial dynamics of an up-flow fixed bed reactor established for the biodegradation of fluorobenzene. Applied Microbiology and Biotechnology, 2006, 71, 555-562.	1.7	15
81	Inorganic nitrate prevents the loss of tight junction proteins and modulates inflammatory events induced by broad-spectrum antibiotics: A role for intestinal microbiota?. Nitric Oxide - Biology and Chemistry, 2019, 88, 27-34.	1.2	15
82	Impact of Ag2S NPs on soil bacterial community $\hat{a} \in$ A terrestrial mesocosm approach. Ecotoxicology and Environmental Safety, 2020, 206, 111405.	2.9	15
83	Occurrence, antibiotic-resistance and virulence of E. coli strains isolated from mangrove oysters (Crassostrea gasar) farmed in estuaries of Amazonia. Marine Pollution Bulletin, 2020, 157, 111302.	2.3	15
84	Effects of ultraviolet radiation on the abundance, diversity and activity of bacterioneuston and bacterioplankton: insights from microcosm studies. Aquatic Sciences, 2011, 73, 63-77.	0.6	14
85	Biodegradation of 2-fluorobenzoate in upflow fixed bed bioreactors operated with different growth support materials. Journal of Chemical Technology and Biotechnology, 2006, 81, 1577-1585.	1.6	13
86	Spatial and temporal analysis of estuarine bacterioneuston and bacterioplankton using culture-dependent and culture-independent methodologies. Antonie Van Leeuwenhoek, 2012, 101, 819-835.	0.7	13
87	Genotypic and phenotypic traits of blaCTX-M-carrying Escherichia coli strains from an UV-C-treated wastewater effluent. Water Research, 2020, 184, 116079.	5.3	13
88	Saccharospirillum correiae sp. nov., an endophytic bacterium isolated from the halophyte Halimione portulacoides. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 2026-2030.	0.8	13
89	Genetic Characterization of a New Thermotolerant Bacillus licheniformis Strain. Current Microbiology, 2000, 40, 137-139.	1.0	12
90	New molecular variants of epsilon and beta IncP-1 plasmids are present in estuarine waters. Plasmid, 2012, 67, 252-258.	0.4	12

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91	Comparative genomics of IncP-1Î $\mu$ plasmids from water environments reveals diverse and unique accessory genetic elements. Plasmid, 2013, 70, 412-419.	0.4	12
92	Assessment of rhizospheric culturable bacteria of <i>Phragmites australis</i> and <i>Juncus effusus</i> from polluted sites. Journal of Basic Microbiology, 2015, 55, 1179-1190.	1.8	12
93	Zunongwangia endophytica sp. nov., an endophyte isolated from the salt marsh plant, Halimione portulacoides, and emended description of the genus Zunongwangia. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3004-3009.	0.8	12
94	Third generation cephalosporin-resistant Klebsiella pneumoniae thriving in patients and in wastewater: what do they have in common?. BMC Genomics, 2022, 23, 72.	1.2	12
95	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
96	A molecular and multivariate approach to the microbial community of a commercial shallow raceway marine recirculation system operating with a Moving Bed Biofilter. Aquaculture Research, 2011, 42, 1308-1322.	0.9	10
97	Analysis of Antibiotic Resistance in Bacteria Isolated from the Surface Microlayer and Underlying Water of an Estuarine Environment. Microbial Drug Resistance, 2013, 19, 64-71.	0.9	9
98	Role of Transition Metals in <scp>UV</scp> â€Bâ€Induced Damage to Bacteria. Photochemistry and Photobiology, 2013, 89, 640-648.	1.3	9
99	Food Ingredients Derived from Lemongrass Byproduct Hydrodistillation: Essential Oil, Hydrolate, and Decoction. Molecules, 2022, 27, 2493.	1.7	9
100	Contribution of chemical water properties to the differential responses of bacterioneuston and bacterioplankton to ultraviolet-B radiation. FEMS Microbiology Ecology, 2014, 87, 517-535.	1.3	8
101	Combined effect of temperature and copper pollution on soil bacterial community: Climate change and regional variation aspects. Ecotoxicology and Environmental Safety, 2015, 111, 153-159.	2.9	8
102	Exploring antibiotic resistance in environmental integron-cassettes through intl-attC amplicons deep sequencing. Brazilian Journal of Microbiology, 2021, 52, 363-372.	0.8	8
103	Draft Genome Sequence of Serratia fonticola UTAD54, a Carbapenem-Resistant Strain Isolated from Drinking Water. Genome Announcements, $2013,1,.$	0.8	7
104	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
105	Genomic analysis of Chromobacterium haemolyticum: insights into the species resistome, virulence determinants and genome plasticity. Molecular Genetics and Genomics, 2020, 295, 1001-1012.	1.0	7
106	Occurrence and distribution of Carbapenem-resistant Enterobacterales and carbapenemase genes along a highly polluted hydrographic basin. Environmental Pollution, 2022, 300, 118958.	3.7	7
107	Tetracycline-Resistant Bacteria Selected from Water and Zebrafish after Antibiotic Exposure. International Journal of Environmental Research and Public Health, 2021, 18, 3218.	1.2	6
108	Genome analysis of two multidrug-resistant Escherichia coli O8:H9-ST48 strains isolated from lettuce. Gene, 2021, 785, 145603.	1.0	6

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109	The impact of silver sulfide nanoparticles and silver ions in soil microbiome. Journal of Hazardous Materials, 2022, 422, 126793.	6.5	6
110	KPC-3-, GES-5-, and VIM-1-Producing Enterobacterales Isolated from Urban Ponds. International Journal of Environmental Research and Public Health, 2022, 19, 5848.	1.2	5
111	Short-Term Responses of Soil Microbial Communities to Changes in Air Temperature, Soil Moisture and UV Radiation. Genes, 2022, 13, 850.	1.0	5
112	New insights into the role of constitutive bacterial rhizobiome and phenolic compounds in two Pinus spp. with contrasting susceptibility to pine pitch canker. Tree Physiology, 2021, , .	1.4	4
113	PCR–DGGE-based methodologies to assess diversity and dynamics ofAeromonascommunities. Journal of Applied Microbiology, 2010, 108, 611-623.	1.4	3
114	Growth conditions influence UVB sensitivity and oxidative damage in an estuarine bacterial isolate. Photochemical and Photobiological Sciences, 2013, 12, 974-986.	1.6	3
115	Draft Genome Sequence of Serratia fonticola LMG 7882 T Isolated from Freshwater. Genome Announcements, 2013, 1, .	0.8	3
116	Using flow cytometry for bacterioplankton community analysis as a complementary tool to Water Framework Directive to signal putatively impacted sites. Science of the Total Environment, 2019, 695, 133754.	3.9	3
117	Effects of Long-Term Exposure to Increased Salinity on the Amphibian Skin Bacterium Erwinia toletana. Archives of Environmental Contamination and Toxicology, 2021, 80, 779-788.	2.1	3
118	Pollution- induced community tolerance framework - disc diffusion method to assess the impact of silver nanoparticles in soils: Potential relevance for risk assessment. Applied Soil Ecology, 2022, 169, 104185.	2.1	3
119	Microbial Associations of Abyssal Gorgonians and Anemones (>4,000 m Depth) at the Clarion-Clipperton Fracture Zone. Frontiers in Microbiology, 2022, 13, 828469.	1.5	3
120	qnrA gene diversity in Shewanella spp Microbiology (United Kingdom), 2021, 167, .	0.7	3
121	<i>Pseudomonas</i> associated with <i>Bursaphelenchus xylophilus,</i> its insect vector and the host tree: A role in pine wilt disease?. Forest Pathology, 2019, 49, e12564.	0.5	2
122	Gut and faecal bacterial community of the terrestrial isopod Porcellionides pruinosus: potential use for monitoring exposure scenarios. Ecotoxicology, 2021, 30, 2096-2108.	1.1	1
123	Evaluation of methods for molecular typing and identification of members of the genus Brevibacterium and other related species. FEMS Microbiology Letters, 2002, 213, 205-211.	0.7	1
124	Draft genome sequence of Psychrobacter sp. ENNN9_III, a strain isolated from water in a polluted temperate estuarine system (Ria de Aveiro, Portugal). Genomics Data, 2016, 8, 21-24.	1.3	0
125	Linking the Environmental Microbial Diversity and Antibiotic Resistance. , 2019, , 451-457.		0
126	Involvement of oxidative stress in UV-induced impairment of bacterial activity and culturability. , 2010, , .		0

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127	Epidemiology of carbapenemases-producing bacteria in Centro Hospitalar Baixo Vouga. International Journal of Infectious Diseases, 2020, 101, 18.	1.5	o
128	Surveillance of plasmid-mediated mcr-1, mcr-3, mcr-4 and mcr-5 genes in human isolates, in Aveiro, Portugal. International Journal of Infectious Diseases, 2020, 101, 343.	1.5	0