Andrea Di Cesare

List of Publications by Year
in descending order

58 papers	2,669 citations	172207 29 h-index	189595 50 g-index
59 all docs	59 docs citations	59 times ranked	3323 citing authors

#	Article	IF	Citations
1	Contribution of plasmidome, metal resistome and integrases to the persistence of the antibiotic resistome in aquatic environments. Environmental Pollution, 2022, 297, 118774.	3.7	6
2	Zooplankton as a Transitional Host for Escherichia coli in Freshwater. Applied and Environmental Microbiology, 2022, 88, e0252221.	1.4	2
3	Frenemies: Interactions between Rhizospheric Bacteria and Fungi from Metalliferous Soils. Life, 2021, 11, 273.	1.1	3
4	Are microplastic particles a hotspot for the spread and the persistence of antibiotic resistance in aquatic systems?. Environmental Pollution, 2021, 279, 116896.	3.7	60
5	Elimination from wastewater of antibiotics reserved for hospital settings, with a Fenton process based on zero-valent iron. Chemosphere, 2021, 283, 131170.	4.2	19
6	Bioplastic accumulates antibiotic and metal resistance genes in coastal marine sediments. Environmental Pollution, 2021, 291, 118161.	3.7	20
7	Antibiotic Resistance Genes and Potentially Pathogenic Bacteria in the Central Adriatic Sea: Are They Connected to Urban Wastewater Inputs?. Water (Switzerland), 2021, 13, 3335.	1.2	12
8	Different substrates within a lake harbour connected but specialised microbial communities. Hydrobiologia, 2020, 847, 1689-1704.	1.0	17
9	The vertical distribution of tetA and intI1 in a deep lake is rather due to sedimentation than to resuspension. FEMS Microbiology Ecology, 2020, 96, .	1.3	8
10	Tossed â€˜good luckâ€™ coins as vectors for anthropogenic pollution into aquatic environment. Environmental Pollution, 2020, 259, 113800.	3.7	4
11	A global multinational survey of cefotaxime-resistant coliforms in urban wastewater treatment plants. Environment International, 2020, 144, 106035.	4.8	55
12	Impact of disinfection processes on bacterial community in urban wastewater: Should we rethink microbial assessment methods?. Journal of Environmental Chemical Engineering, 2020, 8, 104393.	3.3	24
13	Combination of flow cytometry and molecular analysis to monitor the effect of UVC/H2O2 vs UVC/H2O2/Cu-IDS processes on pathogens and antibiotic resistant genes in secondary wastewater effluents. Water Research, 2020, 184, 116194.	5.3	34
14	Spatial distribution of antibiotic and heavy metal resistance genes in the Black Sea. Marine Pollution Bulletin, 2020, 160, 111635.	2.3	19
15	An Environmental Escherichia coli Strain Is Naturally Competent to Acquire Exogenous DNA. Frontiers in Microbiology, 2020, 11, 574301.	1.5	11
16	The role of metal contamination in shaping microbial communities in heavily polluted marine sediments. Environmental Pollution, 2020, 265, 114823.	3.7	65
17	Every fifth published metagenome is not available to science. PLoS Biology, 2020, 18, e3000698.	2.6	18
18	Impact of industrial wastewater on the dynamics of antibiotic resistance genes in a full-scale urban wastewater treatment plant. Science of the Total Environment, 2019, 646, 1204-1210.	3.9	47

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19	Seasonality of the antibiotic resistance gene blaCTX-M in temperate Lake Maggiore. Hydrobiologia, 2019, 843, 143-153.	1.0	10
20	Dynamics of the Pacific oyster pathobiota during mortality episodes in Europe assessed by 16S rRNA gene profiling and a new target enrichment nextâ€generation sequencing strategy. Environmental Microbiology, 2019, 21, 4548-4562.	1.8	49
21	High-quality treated wastewater causes remarkable changes in natural microbial communities and intI1 gene abundance. Water Research, 2019, 167, 114895.	5.3	33
22	Evaluation and quantification of antimicrobial residues and antimicrobial resistance genes in two Italian swine farms. Environmental Pollution, 2019, 255, 113183.	3.7	17
23	Antibiotic disturbance affects aquatic microbial community composition and food web interactions but not community resilience. Molecular Ecology, 2019, 28, 1170-1182.	2.0	39
24	Insights Into the Evolution of Picocyanobacteria and Phycoerythrin Genes (mpeBA and cpeBA). Frontiers in Microbiology, 2019, 10, 45.	1.5	56
25	Effluents of wastewater treatment plants promote the rapid stabilization of the antibiotic resistome in receiving freshwater bodies. Water Research, 2019, 158, 72-81.	5.3	82
26	The mesopelagic anoxic Black Sea as an unexpected habitat for Synechococcus challenges our understanding of global â€œdeep red fluorescenceâ€. ISME Journal, 2019, 13, 1676-1687.	4.4	39
27	Persistence of antibiotic resistance genes in large subalpine lakes: the role of anthropogenic pollution and ecological interactions. Hydrobiologia, 2018, 824, 93-108.	1.0	52
28	Microplastics increase impact of treated wastewater on freshwater microbial community. Environmental Pollution, 2018, 234, 495-502.	3.7	195
29	Antibiotic and heavy metal resistance in enterococci from coastal marine sediment. Environmental Pollution, 2018, 237, 406-413.	3.7	43
30	Detection of viable but non-culturable Pseudomonas aeruginosa in cystic fibrosis by qPCR: a validation study. BMC Infectious Diseases, 2018, 18, 701.	1.3	20
31	ChAMBRe: a new atmospheric simulation chamber for aerosol modelling and bio-aerosol research. Atmospheric Measurement Techniques, 2018, 11, 5885-5900.	1.2	17
32	Assessing antimicrobial resistance gene load in vegan, vegetarian and omnivore human gut microbiota. International Journal of Antimicrobial Agents, 2018, 52, 702-705.	1.1	18
33	Assessing the Influence of Vegan, Vegetarian and Omnivore Oriented Westernized Dietary Styles on Human Gut Microbiota: A Cross Sectional Study. Frontiers in Microbiology, 2018, 9, 317.	1.5	78
34	ddPCR applied on archived Continuous Plankton Recorder samples reveals longâ€term occurrence of class 1 integrons and a sulphonamide resistance gene in marine plankton communities. Environmental Microbiology Reports, 2018, 10, 458-464.	1.0	16
35	Genome analysis of the freshwater planktonic Vulcanococcus limneticus sp. nov. reveals horizontal transfer of nitrogenase operon and alternative pathways of nitrogen utilization. BMC Genomics, 2018, 19, 259.	1.2	41
36	Disinfection of urban wastewater by a new photo-Fenton like process using Cu-iminodisuccinic acid complex as catalyst at neutral pH. Water Research, 2018, 146, 206-215.	5.3	46

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37	Rainfall increases the abundance of antibiotic resistance genes within a riverine microbial community. Environmental Pollution, 2017, 226, 473-478.	3.7	103
38	pHTÎ²-promoted mobilization of non-conjugative resistance plasmids from Enterococcus faecium to Enterococcus faecalis. Journal of Antimicrobial Chemotherapy, 2017, 72, 2447-2453.	1.3	27
39	The microbiome associated with two Synechococcus ribotypes at different levels of ecological interaction. Journal of Phycology, 2017, 53, 1151-1158.	1.0	10
40	Defence strategies and antibiotic resistance gene abundance in enterococci under stress by exposure to low doses of peracetic acid. Chemosphere, 2017, 185, 480-488.	4.2	34
41	Co-selection of antibiotic and heavy metal resistance in freshwater bacteria. Journal of Limnology, 2016, 75, .	0.3	98
42	Resistance to Biocides in Listeria monocytogenes Collected in Meat-Processing Environments. Frontiers in Microbiology, 2016, 7, 1627.	1.5	48
43	Diverse distribution of Toxin-Antitoxin II systems in Salmonella enterica serovars. Scientific Reports, 2016, 6, 28759.	1.6	44
44	Fitness and Recovery of Bacterial Communities and Antibiotic Resistance Genes in Urban Wastewaters Exposed to Classical Disinfection Treatments. Environmental Science & Technology, 2016, 50, 10153-10161.	4.6	110
45	Daphnia as a refuge for an antibiotic resistance gene in an experimental freshwater community. Science of the Total Environment, 2016, 571, 77-81.	3.9	43
46	Enterococcus faeciumST17 from Coastal Marine Sediment Carrying Transferable Multidrug Resistance Plasmids. Microbial Drug Resistance, 2016, 22, 523-530.	0.9	12
47	Co-occurrence of integrase 1, antibiotic and heavy metal resistance genes in municipal wastewater treatment plants. Water Research, 2016, 94, 208-214.	5.3	397
48	Constitutive presence of antibiotic resistance genes within the bacterial community of a large subalpine lake. Molecular Ecology, 2015, 24, 3888-3900.	2.0	108
49	Effect of starvation on survival and virulence expression of Aeromonas hydrophila from different sources. Archives of Microbiology, 2015, 197, 431-438.	1.0	25
50	Adhesion of marine cryptic Escherichia isolates to human intestinal epithelial cells. ISME Journal, 2015, 9, 508-515.	4.4	28
51	Adherence and intracellular survival within human macrophages of Enterococcus faecalis isolates from coastal marine sediment. Microbes and Infection, 2015, 17, 660-664.	1.0	13
52	Role of Daptomycin in the Induction and Persistence of the Viable but Non-Culturable State of Staphylococcus Aureus Biofilms. Pathogens, 2014, 3, 759-768.	1.2	30
53	Role of Biofilm in Protection of the Replicative Form of Legionella pneumophila. Current Microbiology, 2014, 69, 769-774.	1.0	8
54	The marine environment as a reservoir of enterococci carrying resistance and virulence genes strongly associated with clinical strains. Environmental Microbiology Reports, 2014, 6, 184-190.	1.0	33

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55	Erythromycin- and copper-resistant Enterococcus hirae from marine sediment and co-transfer of erm(B) and tcrB to human Enterococcus faecalis. Diagnostic Microbiology and Infectious Disease, 2014, 80, 26-28.	0.8	25
56	Aquaculture Can Promote the Presence and Spread of Antibiotic-Resistant Enterococci in Marine Sediments. PLoS ONE, 2013, 8, e62838.	1.1	126
57	Antibiotic-Resistant Enterococci in Seawater and Sediments from a Coastal Fish Farm. Microbial Drug Resistance, 2012, 18, 502-509.	0.9	69
58	Calves as Main Reservoir of Antibiotic Resistance Genes in Dairy Farms. Frontiers in Public Health, 0, 10, .	1.3	2