

Elisa Taviani

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,456
citations

430874

18
h-index

395702

33
g-index

35
all docs

35
docs citations

35
times ranked

1573
citing authors

#	ARTICLE	IF	CITATIONS
1	Impact of the aquatic pathobiome in low-income and middle-income countries (LMICs) quest for safe water and sanitation practices. <i>Current Opinion in Biotechnology</i> , 2022, 73, 220-224.	6.6	4
2	Polyclonal emergence of MDR <i>Enterobacter cloacae</i> complex isolates producing multiple extended spectrum beta-lactamases at Maputo Central Hospital, Mozambique. <i>Rendiconti Lincei</i> , 2022, 33, 39-45.	2.2	5
3	Molecular characterization of diarrheagenic <i>Escherichia coli</i> isolates from children with diarrhea: A cross-sectional study in four provinces of Mozambique. <i>International Journal of Infectious Diseases</i> , 2022, 121, 190-194.	3.3	10
4	Aquatic reservoir of <i>Vibrio cholerae</i> in an African Great Lake assessed by large scale plankton sampling and ultrasensitive molecular methods. <i>ISME Communications</i> , 2021, 1, .	4.2	4
5	Genomic Analysis of Antibiotic-Resistant and -Susceptible <i>Escherichia coli</i> Isolated from Bovine Sources in Maputo, Mozambique. <i>Foodborne Pathogens and Disease</i> , 2021, 18, 426-435.	1.8	2
6	A deep-sea bacterium related to coastal marine pathogens. <i>Environmental Microbiology</i> , 2021, 23, 5349-5363.	3.8	4
7	Emergence of unusual vanA/vanB genotype in a highly mutated vanB-vancomycin-resistant hospital-associated <i>E. faecium</i> background in Vietnam. <i>International Journal of Antimicrobial Agents</i> , 2018, 52, 586-592.	2.5	11
8	Promising primers for detection of phytoplasma causing coconut lethal yellowing disease in Mozambique. <i>Phytoparasitica</i> , 2018, 46, 301-308.	1.2	1
9	Characterization of Pathogenic <i>Vibrio parahaemolyticus</i> from the Chesapeake Bay, Maryland. <i>Frontiers in Microbiology</i> , 2017, 8, 2460.	3.5	22
10	Vancomycin-resistant <i>Enterococcus faecium</i> high-resolution typing by core genome multilocus sequence typing. <i>Journal of Infection in Developing Countries</i> , 2016, 10, 1159-1161.	1.2	1
11	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2813-9.	7.1	63
12	Genetic determinants of pathogenicity of <i>Escherichia coli</i> isolated from children with acute diarrhea in Maputo, Mozambique. <i>Journal of Infection in Developing Countries</i> , 2015, 9, 661-664.	1.2	11
13	Epidemic waves of cholera in the last two decades in Mozambique. <i>Journal of Infection in Developing Countries</i> , 2015, 9, 635-641.	1.2	19
14	Molecular diversity and predictability of <i>Vibrio parahaemolyticus</i> along the Georgian coastal zone of the Black Sea. <i>Frontiers in Microbiology</i> , 2014, 5, 45.	3.5	40
15	Acquisition and Evolution of SXT-R391 Integrative Conjugative Elements in the Seventh-Pandemic <i>Vibrio cholerae</i> Lineage. <i>MBio</i> , 2014, 5, .	4.1	78
16	Genomic and Phenotypic Characterization of <i>Vibrio cholerae</i> Non-O1 Isolates from a US Gulf Coast Cholera Outbreak. <i>PLoS ONE</i> , 2014, 9, e86264.	2.5	54
17	Distribution of Virulence Genes in Clinical and Environmental <i>Vibrio cholerae</i> Strains in Bangladesh. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5782-5785.	3.1	32
18	<i>Vibrio cholerae</i> O1 epidemic variants in Angola: a retrospective study between 1992 and 2006. <i>Frontiers in Microbiology</i> , 2013, 4, 354.	3.5	11

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19	Detection, Isolation, and Identification of <i>Vibrio cholerae</i> from the Environment. <i>Current Protocols in Microbiology</i> , 2012, 26, Unit6A.5.	6.5	79
20	Genomic diversity of 2010 Haitian cholera outbreak strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2010-7.	7.1	173
21	Genomic analysis of ICE _{Vch} Ban8: An atypical genetic element in <i>Vibrio cholerae</i> . <i>FEBS Letters</i> , 2012, 586, 1617-1621.	2.8	18
22	<i>Vibrio cholerae</i> in a historically cholera-free country. <i>Environmental Microbiology Reports</i> , 2012, 4, 381-389.	2.4	25
23	Environmental <i>Vibrio parahaemolyticus</i> DNA signatures validation. <i>Systematic and Applied Microbiology</i> , 2011, 34, 617-620.	2.8	2
24	Occurrence of the <i>Vibrio cholerae</i> Seventh Pandemic VSP-I Island and a New Variant. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 1-7.	2.0	33
25	Discovery of novel <i>Vibrio cholerae</i> VSP-II genomic islands using comparative genomic analysis. <i>FEMS Microbiology Letters</i> , 2010, 308, no-no.	1.8	63
26	Comparative genomics of clinical and environmental <i>Vibrio mimicus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21134-21139.	7.1	52
27	Genome Sequence of Hybrid <i>Vibrio cholerae</i> O1 MJ-1236, B-33, and CIRS101 and Comparative Genomics with <i>V. cholerae</i> . <i>Journal of Bacteriology</i> , 2010, 192, 3524-3533.	2.2	101
28	The pre-seventh pandemic <i>Vibrio cholerae</i> BX 330286 El Tor genome: evidence for the environment as a genome reservoir. <i>Environmental Microbiology Reports</i> , 2010, 2, 208-216.	2.4	4
29	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15442-15447.	7.1	351
30	Genomic analysis of a novel integrative conjugative element in <i>Vibrio cholerae</i> . <i>FEBS Letters</i> , 2009, 583, 3630-3636.	2.8	24
31	Environmental <i>Vibrio</i> spp., isolated in Mozambique, contain a polymorphic group of integrative conjugative elements and class I integrons. <i>FEMS Microbiology Ecology</i> , 2008, 64, 45-54.	2.7	77
32	Occurrence and Expression of Luminescence in <i>Vibrio cholerae</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 708-715.	3.1	14
33	Comprehensive DNA Signature Discovery and Validation. <i>PLoS Computational Biology</i> , 2007, 3, e98.	3.2	63
34	Use of Environmental Parameters to Model Pathogenic Vibrios in Chesapeake Bay. <i>Journal of Environmental Informatics</i> , 0, , .	6.0	4