

Elisa Taviani

List of Publications by Year in descending order

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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	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic <i>Vibrio cholerae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15442-15447.	7.1	351
2	Genomic diversity of 2010 Haitian cholera outbreak strains. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2010-7.	7.1	173
3	Genome Sequence of Hybrid <i>V. cholerae</i> O1 MJ-1236, B-33, and CIRS101 and Comparative Genomics with <i>V. cholerae</i> . Journal of Bacteriology, 2010, 192, 3524-3533.	2.2	101
4	Detection, Isolation, and Identification of <i>Vibrio cholerae</i> from the Environment. Current Protocols in Microbiology, 2012, 26, Unit6A.5.	6.5	79
5	Acquisition and Evolution of SXT-R391 Integrative Conjugative Elements in the Seventh-Pandemic <i>Vibrio cholerae</i> Lineage. MBio, 2014, 5, .	4.1	78
6	Environmental <i>Vibrio</i> spp., isolated in Mozambique, contain a polymorphic group of integrative conjugative elements and class 1 integrons. FEMS Microbiology Ecology, 2008, 64, 45-54.	2.7	77
7	Comprehensive DNA Signature Discovery and Validation. PLoS Computational Biology, 2007, 3, e98.	3.2	63
8	Discovery of novel <i>Vibrio cholerae</i> VSP-II genomic islands using comparative genomic analysis. FEMS Microbiology Letters, 2010, 308, no-no.	1.8	63
9	Deep-sea hydrothermal vent bacteria related to human pathogenic <i>Vibrio</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2813-9.	7.1	63
10	Genomic and Phenotypic Characterization of <i>Vibrio cholerae</i> Non-O1 Isolates from a US Gulf Coast Cholera Outbreak. PLoS ONE, 2014, 9, e86264.	2.5	54
11	Comparative genomics of clinical and environmental <i>Vibrio mimicus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21134-21139.	7.1	52
12	Molecular diversity and predictability of <i>Vibrio parahaemolyticus</i> along the Georgian coastal zone of the Black Sea. Frontiers in Microbiology, 2014, 5, 45.	3.5	40
13	Occurrence of the <i>Vibrio cholerae</i> Seventh Pandemic VSP-I Island and a New Variant. OMICS A Journal of Integrative Biology, 2010, 14, 1-7.	2.0	33
14	Distribution of Virulence Genes in Clinical and Environmental <i>Vibrio cholerae</i> Strains in Bangladesh. Applied and Environmental Microbiology, 2013, 79, 5782-5785.	3.1	32
15	<i>Vibrio cholerae</i> in a historically cholera-free country. Environmental Microbiology Reports, 2012, 4, 381-389.	2.4	25
16	Genomic analysis of a novel integrative conjugative element in <i>Vibrio cholerae</i> . FEBS Letters, 2009, 583, 3630-3636.	2.8	24
17	Characterization of Pathogenic <i>Vibrio parahaemolyticus</i> from the Chesapeake Bay, Maryland. Frontiers in Microbiology, 2017, 8, 2460.	3.5	22
18	Epidemic waves of cholera in the last two decades in Mozambique. Journal of Infection in Developing Countries, 2015, 9, 635-641.	1.2	19

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19	Genomic analysis of ICE<i>Vch</i>Ban8: An atypical genetic element in <i>Vibrio cholerae</i>. FEBS Letters, 2012, 586, 1617-1621.	2.8	18
20	Occurrence and Expression of Luminescence in <i>Vibrio cholerae</i>. Applied and Environmental Microbiology, 2008, 74, 708-715.	3.1	14
21	Vibrio cholerae O1 epidemic variants in Angola: a retrospective study between 1992 and 2006. Frontiers in Microbiology, 2013, 4, 354.	3.5	11
22	Emergence of unusual vanA/vanB genotype in a highly mutated vanB-vancomycin-resistant hospital-associated E. faecium background in Vietnam. International Journal of Antimicrobial Agents, 2018, 52, 586-592.	2.5	11
23	Genetic determinants of pathogenicity of Escherichia coli isolated from children with acute diarrhea in Maputo, Mozambique. Journal of Infection in Developing Countries, 2015, 9, 661-664.	1.2	11
24	Molecular characterization of diarrheagenic Escherichia coli isolates from children with diarrhea: A cross-sectional study in four provinces of Mozambique. International Journal of Infectious Diseases, 2022, 121, 190-194.	3.3	10
25	Polyclonal emergence of MDR Enterobacter cloacae complex isolates producing multiple extended spectrum beta-lactamases at Maputo Central Hospital, Mozambique. Rendiconti Lincei, 2022, 33, 39-45.	2.2	5
26	The pre-€seventh pandemic <i>Vibrio cholerae</i> BX 330286 El Tor genome: evidence for the environment as a genome reservoir. Environmental Microbiology Reports, 2010, 2, 208-216.	2.4	4
27	Aquatic reservoir of <i>Vibrio cholerae</i> in an African Great Lake assessed by large scale plankton sampling and ultrasensitive molecular methods. ISME Communications, 2021, 1, .	4.2	4
28	A deep-€sea bacterium related to coastal marine pathogens. Environmental Microbiology, 2021, 23, 5349-5363.	3.8	4
29	Impact of the aquatic pathobiome in low-income and middle-income countries (LMICs) quest for safe water and sanitation practices. Current Opinion in Biotechnology, 2022, 73, 220-224.	6.6	4
30	Use of Environmental Parameters to Model Pathogenic Vibrios in Chesapeake Bay. Journal of Environmental Informatics, 0, , .	6.0	4
31	Environmental Vibrio parahaemolyticus DNA signatures validation. Systematic and Applied Microbiology, 2011, 34, 617-620.	2.8	2
32	Genomic Analysis of Antibiotic-Resistant and -Susceptible <i>Escherichia coli</i> Isolated from Bovine Sources in Maputo, Mozambique. Foodborne Pathogens and Disease, 2021, 18, 426-435.	1.8	2
33	Promising primers for detection of phytoplasma causing coconut lethal yellowing disease in Mozambique. Phytoparasitica, 2018, 46, 301-308.	1.2	1
34	Vancomycin-resistant Enterococcus faecium high-resolution typing by core genome multilocus sequence typing. Journal of Infection in Developing Countries, 2016, 10, 1159-1161.	1.2	1