Jaime Martinez-Urtaza

List of Publications by Year
in descending order

88 papers	8,219 citations	101384 36 h-index	49773 87 g-index
94 all docs	94 docs citations	94 times ranked	7423 citing authors

#	Article	IF	Citations
1	The 2020 report of The Lancet Countdown on health and climate change: responding to converging crises. Lancet, The, 2021, 397, 129-170.	6.3	1,030
2	The 2019 report of The Lancet Countdown on health and climate change: ensuring that the health of a child born today is not defined by a changing climate. Lancet, The, 2019, 394, 1836-1878.	6.3	905
3	The 2021 report of the Lancet Countdown on health and climate change: code red for a healthy future. Lancet, The, 2021, 398, 1619-1662.	6.3	669
4	The 2018 report of the Lancet Countdown on health and climate change: shaping the health of nations for centuries to come. Lancet, The, 2018, 392, 2479-2514.	6.3	595
5	Vibrio spp. infections. Nature Reviews Disease Primers, 2018, 4, 1-19.	18.1	572
6	Emerging Vibrio risk at high latitudes in response to ocean warming. Nature Climate Change, 2013, 3, 73-77.	8.1	473
7	Non-Cholera Vibrios: The Microbial Barometer of Climate Change. Trends in Microbiology, 2017, 25, 76-84.	3.5	282
8	Environmental occurrence and clinical impact of Vibrio vulnificus and Vibrio parahaemolyticus: a European perspective. Environmental Microbiology Reports, 2010, 2, 7-18.	1.0	236
9	Climate anomalies and the increasing risk of Vibrio parahaemolyticus and Vibrio vulnificus illnesses. Food Research International, 2010, 43, 1780-1790.	2.9	196
10	Determination of Molecular Phylogenetics of Vibrio parahaemolyticus Strains by Multilocus Sequence Typing. Journal of Bacteriology, 2008, 190, 2831-2840.	1.0	191
11	PandemicVibrio parahaemolyticusO3:K6, Europe. Emerging Infectious Diseases, 2005, 11, 1319-1320.	2.0	146
12	Characterization of Pathogenic Vibrio parahaemolyticus Isolates from Clinical Sources in Spain and Comparison with Asian and North American Pandemic Isolates. Journal of Clinical Microbiology, 2004, 42, 4672-4678.	1.8	136
13	Environmental Determinants of the Occurrence and Distribution of Vibrio parahaemolyticus in the Rias of Galicia, Spain. Applied and Environmental Microbiology, 2008, 74, 265-274.	1.4	127
14	Influence of Environmental Factors and Human Activity on the Presence of Salmonella Serovars in a Marine Environment. Applied and Environmental Microbiology, 2004, 70, 2089-2097.	1.4	122
15	Identification oftdh-positiveVibrio parahaemolyticusfrom an outbreak associated with raw oyster consumption in Spain. FEMS Microbiology Letters, 2003, 226, 281-284.	0.7	117
16	Heat Waveâ€“Associated Vibriosis, Sweden and Finland, 2014. Emerging Infectious Diseases, 2016, 22, 1216-1220.	2.0	112
17	Spread of Pacific Northwest Vibrio parahaemolyticus Strain. New England Journal of Medicine, 2013, 369, 1573-1574.	13.9	97
18	Computational methods for 16S metabarcoding studies using Nanopore sequencing data. Computational and Structural Biotechnology Journal, 2020, 18, 296-305.	1.9	92

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19	Emergence of Asiatic Vibrio Diseases in South America in Phase With El NiÃ±o. Epidemiology, 2008, 19, 829-837.	1.2	91
20	Environmental Suitability of Vibrio Infections in a Warming Climate: An Early Warning System. Environmental Health Perspectives, 2017, 125, 107004.	2.8	87
21	Contamination of bivalve molluscs by Cryptosporidiumoocysts: the need for new quality control standards. International Journal of Food Microbiology, 2003, 87, 97-105.	2.1	84
22	Epidemiology ofVibrio parahaemolyticusOutbreaks, Southern Chile. Emerging Infectious Diseases, 2009, 15, 163-168.	2.0	80
23	Acquired Type III Secretion System Determines Environmental Fitness of Epidemic Vibrio parahaemolyticus in the Interaction with Bacterivorous Protists. PLoS ONE, 2011, 6, e20275.	1.1	68
24	Evaluation of different procedures for the optimized detection of Vibrio parahaemolyticus in mussels and environmental samples. International Journal of Food Microbiology, 2009, 129, 229-236.	2.1	65
25	Characteristics and Dynamics of Salmonella Contamination along the Coast of Agadir, Morocco. Applied and Environmental Microbiology, 2009, 75, 7700-7709.	1.4	62
26	mcr-Colistin Resistance Genes Mobilized by IncX4, IncHI2, and IncI2 Plasmids in Escherichia coli of Pigs and White Stork in Spain. Frontiers in Microbiology, 2019, 10, 3072.	1.5	57
27	Identification of Salmonella Serovars Isolated from Live Molluscan Shellfish and Their Significance in the Marine Environment. Journal of Food Protection, 2003, 66, 226-232.	0.8	56
28	Genomic Variation and Evolution of Vibrio parahaemolyticus ST36 over the Course of a Transcontinental Epidemic Expansion. MBio, 2017, 8, .	1.8	53
29	Characterization of Salmonella enterica Serovar Typhimurium from Marine Environments in Coastal Waters of Galicia (Spain). Applied and Environmental Microbiology, 2004, 70, 4030-4034.	1.4	50
30	Defining a Core Genome Multilocus Sequence Typing Scheme for the Global Epidemiology of Vibrio parahaemolyticus. Journal of Clinical Microbiology, 2017, 55, 1682-1697.	1.8	49
31	Climate Patterns Governing the Presence and Permanence of Salmonellae in Coastal Areas of Bahia de Todos Santos, Mexico. Applied and Environmental Microbiology, 2008, 74, 5918-5924.	1.4	48
32	Ecological determinants of the occurrence and dynamics of Vibrio parahaemolyticus in offshore areas. ISME Journal, 2012, 6, 994-1006.	4.4	48
33	Prevalence and genetic diversity of pathogenic populations of Vibrio parahaemolyticus in coastal waters of Galicia, Spain. Environmental Microbiology Reports, 2010, 2, 58-66.	1.0	47
34	Epidemiological investigation of a foodborne outbreak in Spain associated with U.S. West Coast genotypes of Vibrio parahaemolyticus. SpringerPlus, 2016, 5, 87.	1.2	47
35	Global emergence of environmental <scp>nonâ€O1</scp>/<scp>O139</scp>Vibrio cholerae infections linked with climate change: a neglected research field?. Environmental Microbiology, 2020, 22, 4342-4355.	1.8	47
36	Molecular Epidemiology and Genetic Variation of Pathogenic Vibrio parahaemolyticus in Peru. PLoS Neglected Tropical Diseases, 2013, 7, e2210.	1.3	45

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37	Recent mixing of Vibrio parahaemolyticus populations. ISME Journal, 2019, 13, 2578-2588.	4.4	41
38	Detection and quantification of pathogenic Vibrio parahaemolyticus in shellfish by using multiplex PCR and loop-mediated isothermal amplification assay. Food Control, 2015, 47, 664-671.	2.8	38
39	Future scenarios of risk of Vibrio infections in a warming planet: a global mapping study. Lancet Planetary Health, The, 2021, 5, e426-e435.	5.1	38
40	Diversity and distribution of cholix toxin, a novel ADPâ€ribosylating factor from Vibrio cholerae. Environmental Microbiology Reports, 2010, 2, 198-207.	1.0	37
41	New Invasive Nemertean Species (Cephalothrix Simula) in England with High Levels of Tetrodotoxin and a Microbiome Linked to Toxin Metabolism. Marine Drugs, 2018, 16, 452.	2.2	36
42	Epidemic Dynamics ofVibrio parahaemolyticusIllness in a Hotspot of Disease Emergence, Galicia, Spain. Emerging Infectious Diseases, 2018, 24, 852-859.	2.0	36
43	Molecular analysis and antimicrobial resistance of Salmonella isolates recovered from raw meat marketed in the area of â€œGrand Tunisâ€, Tunisia. Pathologie Et Biologie, 2012, 60, e49-e54.	2.2	35
44	Transoceanic Spreading of Pathogenic Strains of Vibrio parahaemolyticus with Distinctive Genetic Signatures in the recA Gene. PLoS ONE, 2015, 10, e0117485.	1.1	32
45	Differences in the API 20E biochemical patterns of clinical and environmentalVibrio parahaemolyticusisolates. FEMS Microbiology Letters, 2006, 255, 75-81.	0.7	28
46	Prevalence and genetic diversity of Salmonella spp. in a river in a tropical environment in Mexico. Journal of Water and Health, 2014, 12, 874-884.	1.1	28
47	Occurrence of Vibrio and Salmonella species in mussels (Mytilus galloprovincialis) collected along the Moroccan Atlantic coast. SpringerPlus, 2014, 3, 265.	1.2	28
48	Vibrios from the Norwegian marine environment: Characterization of associated antibiotic resistance and virulence genes. MicrobiologyOpen, 2020, 9, e1093.	1.2	28
49	Is El NiÃ±o a long-distance corridor for waterborne disease?. Nature Microbiology, 2016, 1, 16018.	5.9	27
50	Antarctic Streptomyces fildesensis So13.3 strain as a promising source for antimicrobials discovery. Scientific Reports, 2019, 9, 7488.	1.6	27
51	Detection of colistin resistance mcr-1 gene in Salmonella enterica serovar Rissen isolated from mussels, Spain, 2012Â to 2016. Eurosurveillance, 2019, 24, .	3.9	27
52	Use of pulsed-field gel electrophoresis to characterize the genetic diversity and clonal persistence of Salmonella senftenberg in mussel processing facilities. International Journal of Food Microbiology, 2005, 105, 153-163.	2.1	26
53	Outbreak ofVibrio parahaemolyticusSequence Type 120, Peru, 2009. Emerging Infectious Diseases, 2016, 22, 1235-1237.	2.0	26
54	Multidisciplinary investigation of a multicountry outbreak of Salmonella Stanley infections associated with turkey meat in the European Union, August 2011 to January 2013. Eurosurveillance, 2014, 19, .	3.9	25

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55	Complete Genome Sequence of Vibrio parahaemolyticus Environmental Strain UCM-V493. Genome Announcements, 2014, 2, .	0.8	24
56	Global Expansion of Pacific Northwest Vibrio parahaemolyticus Sequence Type 36. Emerging Infectious Diseases, 2020, 26, 323-326.	2.0	24
57	Detection of Salmonella Senftenberg Associated with High Saline Environments in Mussel Processing Facilities. Journal of Food Protection, 2004, 67, 256-263.	0.8	23
58	Geographical and Temporal Dissemination of Salmonellae Isolated from Domestic Animal Hosts in the Culiacan Valley, Mexico. Microbial Ecology, 2011, 61, 811-820.	1.4	23
59	The Application of Nanopore Sequencing Technology to the Study of Dinoflagellates: A Proof of Concept Study for Rapid Sequence-Based Discrimination of Potentially Harmful Algae. Frontiers in Microbiology, 2020, 11, 844.	1.5	23
60	Pediatric Infection Due to Multiresistant Salmonella enterica Serotype Infantis in Honduras. Journal of Clinical Microbiology, 2004, 42, 4885-4888.	1.8	21
61	Investigation of clonal distribution and persistence of Salmonella Senftenberg in the marine environment and identification of potential sources of contamination. FEMS Microbiology Ecology, 2005, 52, 255-263.	1.3	21
62	Viewing Marine Bacteria, Their Activity and Response to Environmental Drivers from Orbit. Microbial Ecology, 2014, 67, 489-500.	1.4	21
63	Origins and colonization history of pandemic Vibrio parahaemolyticus in South America. Molecular Ecology, 2010, 19, 3924-3937.	2.0	20
64	Tracking the impacts of climate change on human health via indicators: lessons from the Lancet Countdown. BMC Public Health, 2022, 22, 663.	1.2	20
65	Genome diversification within a clonal population of pandemic Vibrio parahaemolyticus seems to depend on the life circumstances of each individual bacteria. BMC Genomics, 2015, 16, 176.	1.2	18
66	Isolation and characterization of potentially pathogenic Vibrio species in a temperate, higher latitude hotspot. Environmental Microbiology Reports, 2020, 12, 424-434.	1.0	18
67	Vibrio parahaemolyticus. Trends in Microbiology, 2020, 28, 867-868.	3.5	18
68	Vibrio choleraeandVibrio parahaemolyticusDetected in Seafood Products from Senegal. Foodborne Pathogens and Disease, 2013, 10, 1050-1058.	0.8	16
69	Association between heavy precipitation events and waterborne outbreaks in four Nordic countries, 1992â€“2012. Journal of Water and Health, 2016, 14, 1019-1027.	1.1	16
70	Antimicrobial resistance and molecular analysis of non-typhoidal Salmonella isolates from human in Tunisia. Pathologie Et Biologie, 2011, 59, 207-212.	2.2	14
71	Whole Genome Sequencing of Hepatitis A Virus Using a PCR-Free Single-Molecule Nanopore Sequencing Approach. Frontiers in Microbiology, 2020, 11, 874.	1.5	14
72	Molecular characterizations of Vibrio parahaemolyticus in seafood from the Black Sea, Turkey. Letters in Applied Microbiology, 2016, 62, 494-500.	1.0	13

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73	Genomic epidemiology of domestic and travel-associated Vibrio parahaemolyticus infections in the UK, 2008â€“2018. Food Control, 2020, 115, 107244.	2.8	13
74	Microevolution of Pandemic Vibrio parahaemolyticus Assessed by the Number of Repeat Units in Short Sequence Tandem Repeat Regions. PLoS ONE, 2012, 7, e30823.	1.1	11
75	The new tools revolutionizing Vibrio science. Environmental Microbiology, 2020, 22, 4096-4100.	1.8	8
76	Comparative Genomics of Clinical and Environmental Isolates of Vibrio spp. of Colombia: Implications of Traits Associated with Virulence and Resistance. Pathogens, 2021, 10, 1605.	1.2	8
77	Phenotypic and Genotypic Characterization of Salmonella enterica Serotype Paratyphi B Isolates from Environmental and Human Sources in Galicia, Spain. Journal of Food Protection, 2006, 69, 1280-1285.	0.8	7
78	Differences in carbon source utilization of Salmonella Oranienburg and Saintpaul isolated from river water. International Journal of Environmental Health Research, 2017, 27, 252-263.	1.3	7
79	Continuous Plankton Recorder in the omics era: from marine microbiome to global ocean observations. Current Opinion in Biotechnology, 2022, 73, 61-66.	3.3	7
80	Microbial risk assessment of Vibrio parahaemolyticus in bloody clams in Malaysia: A preliminary model from retail to consumption. Microbial Risk Analysis, 2016, 4, 43-51.	1.3	6
81	Effect of river water exposition on adhesion and invasion abilities ofSalmonellaOranienburg and Saintpaul. International Journal of Environmental Health Research, 2018, 28, 43-54.	1.3	5
82	Two Archaeal Metagenome-Assembled Genomes from El Tatio Provide New Insights into the Crenarchaeota Phylum. Genes, 2021, 12, 391.	1.0	5
83	Metagenomic Characterization of Resistance Genes in Deception Island and Their Association with Mobile Genetic Elements. Microorganisms, 2022, 10, 1432.	1.6	5
84	Prevalence of Salmonella species among asymptomatic food handlers in Khartoum State, Sudan. British Journal of Biomedical Science, 2013, 70, 88-89.	1.2	4
85	Closed Genome Sequences of Three Salmonella enterica Strains Belonging to Serovars Saintpaul, Weltevreden, and Thompson, Isolated from Mexico. Microbiology Resource Announcements, 2019, 8, .	0.3	4
86	Aquatic reservoir of Vibrio cholerae in an African Great Lake assessed by large scale plankton sampling and ultrasensitive molecular methods. ISME Communications, 2021, 1, .	1.7	4
87	Prevalence and Genomic Diversity of Salmonella enterica Recovered from River Water in a Major Agricultural Region in Northwestern Mexico. Microorganisms, 2022, 10, 1214.	1.6	4
88	Bacterial Communities in Fecal Samples of Myotis chiloensis from Southern, Chile. International Journal of Morphology, 2021, 39, 57-63.	0.1	2