

Rita R Colwell

List of Publications by Year in descending order

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Version: 2024-02-01

235
papers

17,230
citations

19657

61
h-index

18130

120
g-index

246
all docs

246
docs citations

246
times ranked

14174
citing authors

#	ARTICLE	IF	CITATIONS
1	Addressing our planetary crisis. Sustainability Science, 2022, 17, 5-7.	4.9	5
2	Loop-mediated isothermal amplification (LAMP) assay for rapid detection of viable but non-culturable <i>Vibrio cholerae</i> O1. Canadian Journal of Microbiology, 2022, 68, 103-110.	1.7	3
3	Asymmetric Relationship between Ambient Air Temperature and Incidence of COVID-19 in the Human Population. American Journal of Tropical Medicine and Hygiene, 2022, , .	1.4	4
4	Genomic Characteristics of Recently Recognized <i>Vibrio cholerae</i> El Tor Lineages Associated with Cholera in Bangladesh, 1991 to 2017. Microbiology Spectrum, 2022, 10, e0039122.	3.0	3
5	Solar geoengineering could redistribute malaria risk in developing countries. Nature Communications, 2022, 13, 2150.	12.8	17
6	Thank You to Our 2021 Peer Reviewers. GeoHealth, 2022, 6, e2022GH000639.	4.0	0
7	Microbiome Analysis for Wastewater Surveillance during COVID-19. MBio, 2022, 13, .	4.1	40
8	Prior exposure to microcystin alters host gut resistome and is associated with dysregulated immune homeostasis in translatable mouse models. Scientific Reports, 2022, 12, .	3.3	6
9	Beyond 2020: converging crises demand integrated responses. Sustainability Science, 2021, 16, 691-693.	4.9	2
10	Metagenomic Sequencing and Quantitative Real-Time PCR for Fecal Pollution Assessment in an Urban Watershed. Frontiers in Water, 2021, 3, 626849.	2.3	15
11	Thank You to Our 2020 Peer Reviewers. GeoHealth, 2021, 5, e2021GH000404.	4.0	0
12	Does improved risk information increase the value of cholera prevention? An analysis of stated vaccine demand in slum areas of urban Bangladesh. Social Science and Medicine, 2021, 272, 113716.	3.8	1
13	Gut microbiota of frugo-folivorous sifakas across environments. Animal Microbiome, 2021, 3, 39.	3.8	12
14	Diet, obesity, and the gut microbiome as determinants modulating metabolic outcomes in a non-human primate model. Microbiome, 2021, 9, 100.	11.1	56
15	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
16	Dynamics, Diversity, and Virulence of <i>Aeromonas</i> spp. in Homestead Pond Water in Coastal Bangladesh. Frontiers in Public Health, 2021, 9, 692166.	2.7	8
17	Microbiome signatures of progression toward celiac disease onset in at-risk children in a longitudinal prospective cohort study. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	70
18	A Review of the Environmental Trigger and Transmission Components for Prediction of Cholera. Tropical Medicine and Infectious Disease, 2021, 6, 147.	2.3	12

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19	Environmental parameters associated with incidence and transmission of pathogenic <i>Vibrio</i> spp. <i>Environmental Microbiology</i> , 2021, 23, 7314-7340.	3.8	50
20	The U.S. Needs a National Human Health Observing System. <i>Frontiers in Public Health</i> , 2021, 9, 705597.	2.7	3
21	Nanopore-based metagenomics analysis reveals prevalence of mobile antibiotic and heavy metal resistome in wastewater. <i>Ecotoxicology</i> , 2021, 30, 1572-1585.	2.4	18
22	Reply to Chen and Vitetta: Unraveling the complex interactions among organisms in the microbiome is necessary to identify unique signatures predicting CD onset. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2114053118.	7.1	0
23	Metagenomic Next-Generation Sequencing of Nasopharyngeal Specimens Collected from Confirmed and Suspect COVID-19 Patients. <i>MBio</i> , 2020, 11, .	4.1	117
24	Genotype-phenotype correlation of β -lactamase-producing uropathogenic <i>Escherichia coli</i> (UPEC) strains from Bangladesh. <i>Scientific Reports</i> , 2020, 10, 14549.	3.3	11
25	Obesity Worsens Gulf War Illness Symptom Persistence Pathology by Linking Altered Gut Microbiome Species to Long-Term Gastrointestinal, Hepatic, and Neuronal Inflammation in a Mouse Model. <i>Nutrients</i> , 2020, 12, 2764.	4.1	23
26	Multi-omics analysis reveals the influence of genetic and environmental risk factors on developing gut microbiota in infants at risk of celiac disease. <i>Microbiome</i> , 2020, 8, 130.	11.1	66
27	Antibiotic Resistance in <i>Vibrio cholerae</i> : Mechanistic Insights from IncC Plasmid-Mediated Dissemination of a Novel Family of Genomic Islands Inserted at <i>trmE</i> . <i>MSphere</i> , 2020, 5, .	2.9	23
28	Temporal Resistome and Microbial Community Dynamics in an Intensive Aquaculture Facility with Prophylactic Antimicrobial Treatment. <i>Microorganisms</i> , 2020, 8, 1984.	3.6	16
29	Thank You to Our 2019 Peer Reviewers. <i>GeoHealth</i> , 2020, 4, e2020GH000250.	4.0	0
30	Microbial resolution of whole genome shotgun and 16S amplicon metagenomic sequencing using publicly available NEON data. <i>PLoS ONE</i> , 2020, 15, e0228899.	2.5	107
31	SYN-007, an Orally Administered Beta-Lactamase Enzyme, Protects the Gut Microbiome from Oral Amoxicillin/Clavulanate without Adversely Affecting Antibiotic Systemic Absorption in Dogs. <i>Microorganisms</i> , 2020, 8, 152.	3.6	8
32	A comparative analysis of drinking water employing metagenomics. <i>PLoS ONE</i> , 2020, 15, e0231210.	2.5	28
33	<i>Vibrio cholerae</i> O139 Attached to Zooplankton: Reservoir Diversity and Distribution over an Estuarine-Coastal Gradient. <i>Journal of Coastal Research</i> , 2020, 95, 92.	0.3	1
34	The Role of GeoHealth in Science During Crisis. <i>GeoHealth</i> , 2019, 3, 176-177.	4.0	2
35	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
36	Metagenome sequencing-based strain-level and functional characterization of supragingival microbiome associated with dental caries in children. <i>Journal of Oral Microbiology</i> , 2019, 11, 1557986.	2.7	43

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37	Oral Beta-Lactamase Protects the Canine Gut Microbiome from Oral Amoxicillin-Mediated Damage. <i>Microorganisms</i> , 2019, 7, 150.	3.6	8
38	Thank You to Our 2018 Peer Reviewers. <i>GeoHealth</i> , 2019, 3, 82-83.	4.0	0
39	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	12.6	5
40	Long-Range River Discharge Forecasting Using the Gravity Recovery and Climate Experiment. <i>Journal of Water Resources Planning and Management - ASCE</i> , 2019, 145, .	2.6	8
41	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019, 27, 670-677.	7.7	50
42	Science during crisis. <i>Science</i> , 2019, 364, 5-5.	12.6	6
43	Estimating cholera risk from an exploratory analysis of its association with satellite-derived land surface temperatures. <i>International Journal of Remote Sensing</i> , 2019, 40, 4898-4909.	2.9	4
44	Metagenomic Profiling of Microbial Pathogens in the Little Bighorn River, Montana. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 1097.	2.6	49
45	Oral Metallo-Beta-Lactamase Protects the Gut Microbiome From Carbapenem-Mediated Damage and Reduces Propagation of Antibiotic Resistance in Pigs. <i>Frontiers in Microbiology</i> , 2019, 10, 101.	3.5	31
46	Oil Spills and Human Health: Contributions of the Gulf of Mexico Research Initiative. <i>GeoHealth</i> , 2019, 3, 391-406.	4.0	31
47	Prosthetic joint infections present diverse and unique microbial communities using combined whole-genome shotgun sequencing and culturing methods. <i>Journal of Medical Microbiology</i> , 2019, 68, 1507-1516.	1.8	14
48	Low dose oral beta-lactamase protects the gut microbiome from oral beta-lactam-mediated damage in dogs. <i>AIMS Public Health</i> , 2019, 6, 477-487.	2.6	7
49	Biofilms Comprise a Component of the Annual Cycle of <i>Vibrio cholerae</i> in the Bay of Bengal Estuary. <i>MBio</i> , 2018, 9, .	4.1	20
50	Distinct consequences of amoxicillin and ertapenem exposure in the porcine gut microbiome. <i>Anaerobe</i> , 2018, 53, 82-93.	2.1	37
51	Virulence-Related Genes Identified from the Genome Sequence of the Non-O1/Non-O139 <i>Vibrio cholerae</i> Strain VcN1, Isolated from Dhaka, Bangladesh. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
52	Occurrence of <i>Vibrio cholerae</i> in water reservoirs of Burkina Faso. <i>Research in Microbiology</i> , 2018, 169, 1-10.	2.1	23
53	620. Oral β -Lactamase Therapies Prevent Microbiome Damage and Attenuate Antibiotic Resistance From IV and Oral Antibiotics in Large Animal Models of Antibiotic-Mediated Gut Dysbiosis. <i>Open Forum Infectious Diseases</i> , 2018, 5, S226-S226.	0.9	1
54	Characterization of the Microbiome at the World's Largest Potable Water Reuse Facility. <i>Frontiers in Microbiology</i> , 2018, 9, 2435.	3.5	43

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55	A Metagenomic Approach to Evaluating Surface Water Quality in Haiti. International Journal of Environmental Research and Public Health, 2018, 15, 2211.	2.6	25
56	Environmental and hydroclimatic factors influencing Vibrio populations in the estuarine zone of the Bengal delta. Environmental Monitoring and Assessment, 2018, 190, 565.	2.7	11
57	Potential application of SMART II for Vibrio cholerae O1 and O139 detection in ship's ballast water. Marine Pollution Bulletin, 2018, 136, 79-83.	5.0	1
58	Comparison of Infant Gut and Skin Microbiota, Resistome and Virulome Between Neonatal Intensive Care Unit (NICU) Environments. Frontiers in Microbiology, 2018, 9, 1361.	3.5	35
59	Evaluation of Risk of Cholera after a Natural Disaster: Lessons Learned from the 2015 Nepal Earthquake. Journal of Water Resources Planning and Management - ASCE, 2018, 144, .	2.6	11
60	Satellites and Cell Phones Form a Cholera Early-Warning System. Eos, 2018, 99, .	0.1	7
61	Application of a paper based device containing a new culture medium to detect Vibrio cholerae in water samples collected in Haiti. Journal of Microbiological Methods, 2017, 133, 23-31.	1.6	10
62	Natural Disasters and Cholera Outbreaks: Current Understanding and Future Outlook. Current Environmental Health Reports, 2017, 4, 99-107.	6.7	30
63	CRISPR-Cas and Contact-Dependent Secretion Systems Present on Excisable Pathogenicity Islands with Conserved Recombination Modules. Journal of Bacteriology, 2017, 199, .	2.2	17
64	Beyond cost-effectiveness: Using systems analysis for infectious disease preparedness. Vaccine, 2017, 35, A46-A49.	3.8	13
65	Comparative Genomics of <i>Escherichia coli</i> Isolated from Skin and Soft Tissue and Other Extraintestinal Infections. MBio, 2017, 8, .	4.1	36
66	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. Scientific Reports, 2017, 7, 16324.	3.3	115
67	Characterization of Microbial Signatures From Advanced Treated Wastewater Biofilms. Journal - American Water Works Association, 2017, 109, E503.	0.3	23
68	Comparative genomic analysis and characterization of incompatibility group FIB plasmid encoded virulence factors of Salmonella enterica isolated from food sources. BMC Genomics, 2017, 18, 570.	2.8	35
69	Membrane Bioreactor-Based Wastewater Treatment Plant in Saudi Arabia: Reduction of Viral Diversity, Load, and Infectious Capacity. Water (Switzerland), 2017, 9, 534.	2.7	27
70	Vibrio cholerae O1 with Reduced Susceptibility to Ciprofloxacin and Azithromycin Isolated from a Rural Coastal Area of Bangladesh. Frontiers in Microbiology, 2017, 8, 252.	3.5	25
71	Characterization of Two Cryptic Plasmids Isolated in Haiti from Clinical Vibrio cholerae Non-O1/Non-O139. Frontiers in Microbiology, 2017, 8, 2283.	3.5	11
72	Characterization of Pathogenic Vibrio parahaemolyticus from the Chesapeake Bay, Maryland. Frontiers in Microbiology, 2017, 8, 2460.	3.5	22

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73	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. <i>Genome Biology</i> , 2017, 18, 182.	8.8	260
74	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). <i>Journal of Biomolecular Techniques</i> , 2017, 28, 31-39.	1.5	53
75	Assessment of Risk of Cholera in Haiti following Hurricane Matthew. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 97, 896-903.	1.4	19
76	Reduced Susceptibility to Extended-Spectrum β -Lactams in <i>Vibrio cholerae</i> Isolated in Bangladesh. <i>Frontiers in Public Health</i> , 2016, 4, 231.	2.7	22
77	Enrichment dynamics of <i>Listeria monocytogenes</i> and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. <i>BMC Microbiology</i> , 2016, 16, 275.	3.3	143
78	Chitin promotes <i>Mycobacterium ulcerans</i> growth. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw067.	2.7	15
79	Climate influence on <i>Vibrio</i> and associated human diseases during the past half-century in the coastal North Atlantic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5062-71.	7.1	316
80	IncA/C Conjugative Plasmids Mobilize a New Family of Multidrug Resistance Islands in Clinical <i>Vibrio cholerae</i> Non-O1/Non-O139 Isolates from Haiti. <i>MBio</i> , 2016, 7, .	4.1	57
81	Phylogenetic Diversity of <i>Vibrio cholerae</i> Associated with Endemic Cholera in Mexico from 1991 to 2008. <i>MBio</i> , 2016, 7, e02160.	4.1	24
82	Cross-talk among flesh-eating <i>Aeromonas hydrophila</i> strains in mixed infection leading to necrotizing fasciitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 722-727.	7.1	113
83	Molecular tools in understanding the evolution of <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1040.	3.5	25
84	Satellite Based Assessment of Hydroclimatic Conditions Related to Cholera in Zimbabwe. <i>PLoS ONE</i> , 2015, 10, e0137828.	2.5	27
85	Occurrence and Diversity of Clinically Important <i>Vibrio</i> Species in the Aquatic Environment of Georgia. <i>Frontiers in Public Health</i> , 2015, 3, 232.	2.7	35
86	Building Infectious Disease Research Programs to Promote Security and Enhance Collaborations with Countries of the Former Soviet Union. <i>Frontiers in Public Health</i> , 2015, 3, 271.	2.7	4
87	Predictive Time Series Analysis Linking Bengal Cholera with Terrestrial Water Storage Measured from Gravity Recovery and Climate Experiment Sensors. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 93, 1179-1186.	1.4	7
88	Hybrid <i>Vibrio cholerae</i> El Tor Lacking SXT Identified as the Cause of a Cholera Outbreak in the Philippines. <i>MBio</i> , 2015, 6, .	4.1	11
89	Non-O1/Non-O139 <i>Vibrio cholerae</i> Carrying Multiple Virulence Factors and <i>V. cholerae</i> O1 in the Chesapeake Bay, Maryland. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1909-1918.	3.1	90
90	Nontoxigenic <i>Vibrio cholerae</i> Non-O1/O139 Isolate from a Case of Human Gastroenteritis in the U.S. Gulf Coast. <i>Journal of Clinical Microbiology</i> , 2015, 53, 9-14.	3.9	25

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91	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
92	Diagnostic Approach for Monitoring Hydroclimatic Conditions Related to Emergence of West Nile Virus in West Virginia. Frontiers in Public Health, 2015, 3, 10.	2.7	2
93	Rapid Proliferation of <i>Vibrio parahaemolyticus</i> , <i>Vibrio vulnificus</i> , and <i>Vibrio cholerae</i> during Freshwater Flash Floods in French Mediterranean Coastal Lagoons. Applied and Environmental Microbiology, 2015, 81, 7600-7609.	3.1	43
94	Environmental Surveillance for Toxigenic <i>Vibrio cholerae</i> in Surface Waters of Haiti. American Journal of Tropical Medicine and Hygiene, 2015, 92, 118-125.	1.4	20
95	Concordance and discordance of sequence survey methods for molecular epidemiology. PeerJ, 2015, 3, e761.	2.0	5
96	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
97	<i>Vibrio metoecus</i> sp. nov., a close relative of <i>Vibrio cholerae</i> isolated from coastal brackish ponds and clinical specimens. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 3208-3214.	1.7	39
98	<i>Vibrio</i> ecology, pathogenesis, and evolution. Frontiers in Microbiology, 2014, 5, 256.	3.5	30
99	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	5.6	190
100	Acquisition and Evolution of SXT-R391 Integrative Conjugative Elements in the Seventh-Pandemic <i>Vibrio cholerae</i> Lineage. MBio, 2014, 5, .	4.1	78
101	Microbial Community Profiling of Human Saliva Using Shotgun Metagenomic Sequencing. PLoS ONE, 2014, 9, e97699.	2.5	176
102	Viewing Marine Bacteria, Their Activity and Response to Environmental Drivers from Orbit. Microbial Ecology, 2014, 67, 489-500.	2.8	21
103	Longitudinal analysis of microbial interaction between humans and the indoor environment. Science, 2014, 345, 1048-1052.	12.6	751
104	Occurrence in Mexico, 1998–2008, of <i>Vibrio cholerae</i> CTX ⁺ El Tor carrying an additional truncated CTX prophage. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9917-9922.	7.1	20
105	Validation of high throughput sequencing and microbial forensics applications. Investigative Genetics, 2014, 5, 9.	3.3	59
106	Global diarrhoea action plan needs integrated climate-based surveillance. The Lancet Global Health, 2014, 2, e69-e70.	6.3	16
107	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
108	Ocean Warming and Spread of Pathogenic Vibrios in the Aquatic Environment. Microbial Ecology, 2013, 65, 817-825.	2.8	256

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109	Quantification of <i>Vibrio parahaemolyticus</i> , <i>Vibrio vulnificus</i> and <i>Vibrio cholerae</i> in French Mediterranean coastal lagoons. <i>Research in Microbiology</i> , 2013, 164, 867-874.	2.1	50
110	A new integrative conjugative element detected in Haitian isolates of <i>Vibrio cholerae</i> non-O1/non-O139. <i>Research in Microbiology</i> , 2013, 164, 891-893.	2.1	12
111	Detection of <i>Vibrio cholerae</i> in environmental waters including drinking water reservoirs of Azerbaijan. <i>Environmental Microbiology Reports</i> , 2013, 5, 30-38.	2.4	13
112	Genome Sequences of Clinical <i>Vibrio cholerae</i> Isolates from an Oyster-Borne Cholera Outbreak in Florida. <i>Genome Announcements</i> , 2013, 1, .	0.8	5
113	<i>Vibrio cholerae</i> O1 El Tor and O139 Bengal Strains Carrying <i>ctxB</i> ^{ET} , Bangladesh. <i>Emerging Infectious Diseases</i> , 2013, 19, 1713-1715.	4.3	16
114	Environmental Factors Influencing Epidemic Cholera. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 597-607.	1.4	130
115	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
116	Population Vulnerability to Biannual Cholera Outbreaks and Associated Macro-Scale Drivers in the Bengal Delta. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013, 89, 950-959.	1.4	23
117	Distribution and dynamics of epidemic and pandemic <i>Vibrio parahaemolyticus</i> virulence factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2013, 3, 97.	3.9	164
118	Ecology of <i>Vibrio parahaemolyticus</i> and <i>Vibrio vulnificus</i> in the Coastal and Estuarine Waters of Louisiana, Maryland, Mississippi, and Washington (United States). <i>Applied and Environmental Microbiology</i> , 2012, 78, 7249-7257.	3.1	176
119	Long-term effects of ocean warming on the prokaryotic community: evidence from the vibrios. <i>ISME Journal</i> , 2012, 6, 21-30.	9.8	193
120	Genetic characteristics of drug-resistant <i>Vibrio cholerae</i> O1 causing endemic cholera in Dhaka, 2006–2011. <i>Journal of Medical Microbiology</i> , 2012, 61, 1736-1745.	1.8	39
121	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
122	Role of Shrimp Chitin in the Ecology of Toxigenic <i>Vibrio cholerae</i> and Cholera Transmission. <i>Frontiers in Microbiology</i> , 2012, 2, 260.	3.5	38
123	Cholera Outbreak in Senegal in 2005: Was Climate a Factor?. <i>PLoS ONE</i> , 2012, 7, e44577.	2.5	44
124	<i>Vibrio cholerae</i> Classical Biotype Strains Reveal Distinct Signatures in Mexico. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2212-2216.	3.9	32
125	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
126	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

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127	<i>Vibrio cholerae</i> in a historically cholera-free country. <i>Environmental Microbiology Reports</i> , 2012, 4, 381-389.	2.4	25
128	Hydroclimatic influences on seasonal and spatial cholera transmission cycles: Implications for public health intervention in the Bengal Delta. <i>Water Resources Research</i> , 2011, 47, .	4.2	45
129	Temporal and Spatial Variability in the Distribution of <i>Vibrio vulnificus</i> in the Chesapeake Bay: A Hindcast Study. <i>EcoHealth</i> , 2011, 8, 456-467.	2.0	32
130	Occurrence of <i>Vibrio cholerae</i> in Municipal and Natural Waters and Incidence of Cholera in Azerbaijan. <i>EcoHealth</i> , 2011, 8, 468-477.	2.0	11
131	<i>Vibrio cholerae</i> O1 detection in estuarine and coastal zooplankton. <i>Journal of Plankton Research</i> , 2011, 33, 51-62.	1.8	32
132	Role of Zooplankton Diversity in <i>Vibrio cholerae</i> Population Dynamics and in the Incidence of Cholera in the Bangladesh Sundarbans. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6125-6132.	3.1	64
133	Warming Oceans, Phytoplankton, and River Discharge: Implications for Cholera Outbreaks. <i>American Journal of Tropical Medicine and Hygiene</i> , 2011, 85, 303-308.	1.4	94
134	Aquatic Realm and Cholera. , 2011, , 311-339.		2
135	Detection of toxigenic <i>Vibrio cholerae</i> O1 in freshwater lakes of the former Soviet Republic of Georgia. <i>Environmental Microbiology Reports</i> , 2010, 2, 2-6.	2.4	7
136	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
137	Water, Ecology, and Health. <i>EcoHealth</i> , 2010, 7, 151-152.	2.0	6
138	Comparative genomic analysis reveals evidence of two novel <i>Vibrio</i> species closely related to <i>V. cholerae</i> . <i>BMC Microbiology</i> , 2010, 10, 154.	3.3	50
139	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
140	Conversion of viable but nonculturable <i>Vibrio cholerae</i> to the culturable state by co-culture with eukaryotic cells. <i>Microbiology and Immunology</i> , 2010, 54, 502-507.	1.4	54
141	Simple Sari Cloth Filtration of Water Is Sustainable and Continues To Protect Villagers from Cholera in Matlab, Bangladesh. <i>MBio</i> , 2010, 1, .	4.1	69
142	Environmental reservoirs of <i>Vibrio cholerae</i> and their role in cholera. <i>Environmental Microbiology Reports</i> , 2010, 2, 27-33.	2.4	125
143	Diversity and distribution of cholix toxin, a novel ADP-ribosylating factor from <i>Vibrio cholerae</i> . <i>Environmental Microbiology Reports</i> , 2010, 2, 198-207.	2.4	37
144	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

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145	Using Satellite Images of Environmental Changes to Predict Infectious Disease Outbreaks. <i>Emerging Infectious Diseases</i> , 2009, 15, 1341-1346.	4.3	37
146	RNA Colony Blot Hybridization Method for Enumeration of Culturable <i>Vibrio cholerae</i> and <i>Vibrio mimicus</i> Bacteria. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5439-5444.	3.1	8
147	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
148	Serogroup, Virulence, and Genetic Traits of <i>Vibrio parahaemolyticus</i> in the Estuarine Ecosystem of Bangladesh. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6268-6274.	3.1	30
149	Professional Science Master's Programs Merit Wider Support. <i>Science</i> , 2009, 323, 1676-1677.	12.6	10
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