Rita R Colwell

List of Publications by Year
in descending order

235 papers	17,230 citations	19636 61 h-index	18115 120 g-index
246 all docs	246 docs citations	246 times ranked	14174 citing authors

#	Article	IF	Citations
1	DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae. Nature, 2000, 406, 477-483.	13.7	1,723
2	Longitudinal analysis of microbial interaction between humans and the indoor environment. Science, 2014, 345, 1048-1052.	6.0	751
3	Effects of Global Climate on Infectious Disease: the Cholera Model. Clinical Microbiology Reviews, 2002, 15, 757-770.	5.7	610
4	Global spread of microorganisms by ships. Nature, 2000, 408, 49-50.	13.7	509
5	Cholera Dynamics and El Nino-Southern Oscillation. Science, 2000, 289, 1766-1769.	6.0	446
6	Vibrio Parahaemolyticus and Related Halophilic Vibrios. CRC Critical Reviews in Microbiology, 1982, 10, 77-124.	4.8	441
7	Ecology of Vibrio parahaemolyticus in Chesapeake Bay. Journal of Bacteriology, 1973, 113, 24-32.	1.0	441
8	Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic Vibrio cholerae. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15442-15447.	3.3	351
9	Genotypes Associated with Virulence in Environmental Isolates of Vibrio cholerae. Applied and Environmental Microbiology, 2001, 67, 2421-2429.	1.4	317
10	Climate influence on Vibrio and associated human diseases during the past half-century in the coastal North Atlantic. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5062-71.	3.3	316
11	Reduction of cholera in Bangladeshi villages by simple filtration. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1051-1055.	3.3	308
12	Critical Factors Influencing the Occurrence of Vibrio cholerae in the Environment of Bangladesh. Applied and Environmental Microbiology, 2005, 71, 4645-4654.	1.4	281
13	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	3.8	260
14	Ocean Warming and Spread of Pathogenic Vibrios in the Aquatic Environment. Microbial Ecology, 2013, 65, 817-825.	1.4	256
15	Environmental signatures associated with cholera epidemics. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17676-17681.	3.3	255
16	Global impact of Vibrio cholerae interactions with chitin. Environmental Microbiology, 2008, 10, 1400-1410.	1.8	237
17	Analysis of 16S-23S rRNA Intergenic Spacer Regions of Vibrio cholerae and Vibrio mimicus. Applied and Environmental Microbiology, 1999, 65, 2202-2208.	1.4	231
18	Viable but nonculturable Vibrio cholerae O1 in biofilms in the aquatic environment and their role in cholera transmission. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17801-17806.	3.3	204

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19	Long-term effects of ocean warming on the prokaryotic community: evidence from the vibrios. ISME Journal, 2012, 6, 21-30.	4.4	193
20	Genomic Encyclopedia of Bacteria and Archaea: Sequencing a Myriad of Type Strains. PLoS Biology, 2014, 12, e1001920.	2.6	190
21	A 4â€Year Study of the Epidemiology ofVibrio choleraein Four Rural Areas of Bangladesh. Journal of Infectious Diseases, 2003, 187, 96-101.	1.9	189
22	Viable but nonculturable bacteria: a survival strategy. Journal of Infection and Chemotherapy, 2000, 6, 121-125.	0.8	182
23	Ecology of Vibrio parahaemolyticus and Vibrio vulnificus in the Coastal and Estuarine Waters of Louisiana, Maryland, Mississippi, and Washington (United States). Applied and Environmental Microbiology, 2012, 78, 7249-7257.	1.4	176
24	Microbial Community Profiling of Human Saliva Using Shotgun Metagenomic Sequencing. PLoS ONE, 2014, 9, e97699.	1.1	176
25	Vibrios in the Environment: Viable but Nonculturable Vibrio cholerae. , 0, , 117-133.		176
26	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.	3.3	173
27	Predictability of Vibrio cholerae in Chesapeake Bay. Applied and Environmental Microbiology, 2003, 69, 2773-2785.	1.4	171
28	Ecological Aspects of Microbial Degradation of Petroleum in the Marine Environment. CRC Critical Reviews in Microbiology, 1977, 5, 423-445.	4.8	167
29	Distribution and dynamics of epidemic and pandemic Vibrio parahaemolyticus virulence factors. Frontiers in Cellular and Infection Microbiology, 2013, 3, 97.	1.8	164
30	Virulence Genes in Environmental Strains of Vibrio cholerae. Applied and Environmental Microbiology, 2000, 66, 4022-4028.	1.4	146
31	Toxigenic Vibrio cholerae in the Aquatic Environment of Mathbaria, Bangladesh. Applied and Environmental Microbiology, 2006, 72, 2849-2855.	1.4	145
32	Enrichment dynamics of Listeria monocytogenes and the associated microbiome from naturally contaminated ice cream linked to a listeriosis outbreak. BMC Microbiology, 2016, 16, 275.	1.3	143
33	Emerging and Reemerging Infectious Diseases: Biocomplexity as an Interdisciplinary Paradigm. EcoHealth, 2005, 2, 244.	0.9	139
34	Environmental Factors Influencing Epidemic Cholera. American Journal of Tropical Medicine and Hygiene, 2013, 89, 597-607.	0.6	130
35	The Ecology of Vibrio cholerae. , 1992, , 107-127.		127
36	Environmental reservoirs of Vibrio cholerae and their role in cholera. Environmental Microbiology Reports, 2010, 2, 27-33.	1.0	125

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37	Occurrence and distribution of Vibrio cholerae in the coastal environment of Peru. Environmental Microbiology, 2004, 6, 699-706.	1.8	122
38	Seasonal Cholera Caused by Vibrio cholerae Serogroups O1 and O139 in the Coastal Aquatic Environment of Bangladesh. Applied and Environmental Microbiology, 2006, 72, 4096-4104.	1.4	121
39	Metagenomic Next-Generation Sequencing of Nasopharyngeal Specimens Collected from Confirmed and Suspect COVID-19 Patients. MBio, 2020, 11, .	1.8	117
40	Extractable Lipids of Gram-Negative Marine Bacteria: Phospholipid Composition. Journal of Bacteriology, 1973, 114, 897-908.	1.0	116
41	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. Scientific Reports, 2017, 7, 16324.	1.6	115
42	Cross-talk among flesh-eatingAeromonas hydrophilastrains in mixed infection leading to necrotizing fasciitis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 722-727.	3.3	113
43	Purification and properties of the extracellular lipase, LipA, of Acinetobacter sp. RAG-1. FEBS Journal, 2002, 269, 5771-5779.	0.2	111
44	REISOLATION AND EMENDATION OF DESCRIPTION OFVIBRIO MARINUS(RUSSELL) FORD. Journal of Bacteriology, 1964, 88, 831-837.	1.0	111
45	Microbial resolution of whole genome shotgun and 16S amplicon metagenomic sequencing using publicly available NEON data. PLoS ONE, 2020, 15, e0228899.	1.1	107
46	Characterization of a Marine Bacterium Associated with Crassostrea virginica (the Eastern) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.4	107
47	Viability of the Nonculturable Vibrio cholerae O1 and O139. Systematic and Applied Microbiology, 2001, 24, 331-341.	1.2	104
48	Association of Vibrio cholerae O1 El Tor and O139 Bengal with the Copepods Acartia tonsa and Eurytemora affinis. Applied and Environmental Microbiology, 2007, 73, 7926-7933.	1.4	100
49	Warming Oceans, Phytoplankton, and River Discharge: Implications for Cholera Outbreaks. American Journal of Tropical Medicine and Hygiene, 2011, 85, 303-308.	0.6	94
50	Barophilic Bacteria Associated with Digestive Tracts of Abyssal Holothurians. Applied and Environmental Microbiology, 1982, 44, 1222-1230.	1.4	93
51	Filterable marine bacteria found in the deep sea: Distribution, taxonomy, and response to starvation. Microbial Ecology, 1981, 7, 67-83.	1.4	92
52	Simple Procedure for Rapid Identification of Vibrio cholerae from the Aquatic Environment. Applied and Environmental Microbiology, 2002, 68, 995-998.	1.4	92
53	Non-O1/Non-O139 Vibrio cholerae Carrying Multiple Virulence Factors and V. cholerae O1 in the Chesapeake Bay, Maryland. Applied and Environmental Microbiology, 2015, 81, 1909-1918.	1.4	90
54	Viable but Nonculturable Vibrio cholerae O1 in the Aquatic Environment of Argentina. Applied and Environmental Microbiology, 2004, 70, 7481-7486.	1.4	82

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55	Ultrastructure of coccoid viable but non-culturable Vibrio cholerae. Environmental Microbiology, 2007, 9, 393-402.	1.8	81
56	Microbial oceanography in a sea of opportunity. Nature, 2009, 459, 180-184.	13.7	79
57	Detection, Isolation, and Identification of Vibrio cholerae from the Environment. Current Protocols in Microbiology, 2012, 26, Unit6A.5.	6.5	79
58	Acquisition and Evolution of SXT-R391 Integrative Conjugative Elements in the Seventh-Pandemic Vibrio cholerae Lineage. MBio, 2014, 5, .	1.8	78
59	Environmental Vibrio spp., isolated in Mozambique, contain a polymorphic group of integrative conjugative elements and class 1 integrons. FEMS Microbiology Ecology, 2008, 64, 45-54.	1.3	77
60	Infectious disease and environment: cholera as a paradigm for waterborne disease. International Microbiology, 2004, 7, 285-9.	1.1	76
61	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, .	3.3	70
62	Using Satellite Images of Environmental Changes to Predict Infectious Disease Outbreaks. Emerging Infectious Diseases, 2009, 15, 1341-1346.	2.0	70
63	Simple Sari Cloth Filtration of Water Is Sustainable and Continues To Protect Villagers from Cholera in Matlab, Bangladesh. MBio, 2010, 1, .	1.8	69
64	Multi-omics analysis reveals the influence of genetic and environmental risk factors on developing gut microbiota in infants at risk of celiac disease. Microbiome, 2020, 8, 130.	4.9	66
65	Genetic Diversity of Vibrio cholerae in Chesapeake Bay Determined by Amplified Fragment Length Polymorphism Fingerprinting. Applied and Environmental Microbiology, 2000, 66, 140-147.	1.4	65
66	Role of Zooplankton Diversity in Vibrio cholerae Population Dynamics and in the Incidence of Cholera in the Bangladesh Sundarbans. Applied and Environmental Microbiology, 2011, 77, 6125-6132.	1.4	64
67	Discovery of novel Vibrio choleraeâ€ƒVSP-II genomic islands using comparative genomic analysis. FEMS Microbiology Letters, 2010, 308, no-no.	0.7	63
68	Deep-sea hydrothermal vent bacteria related to human pathogenic Vibrio species. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2813-9.	3.3	63
69	Marine ecosystems and cholera. Hydrobiologia, 2001, 460, 141-145.	1.0	62
70	Validation of high throughput sequencing and microbial forensics applications. Investigative Genetics, 2014, 5, 9.	3.3	59
71	IncA/C Conjugative Plasmids Mobilize a New Family of Multidrug Resistance Islands in Clinical Vibrio cholerae Non-O1/Non-O139 Isolates from Haiti. MBio, 2016, 7, .	1.8	57
72	Diet, obesity, and the gut microbiome as determinants modulating metabolic outcomes in a non-human primate model. Microbiome, 2021, 9, 100.	4.9	56

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73	Observations of Barophilic Microbial Activity in Samples of Sediment and Intercepted Particulates from the Demerara Abyssal Plain. Applied and Environmental Microbiology, 1985, 50, 1002-1006.	1.4	55
74	Conversion of viable but nonculturable Vibrio cholerae to the culturable state by coâ€culture with eukaryotic cells. Microbiology and Immunology, 2010, 54, 502-507.	0.7	54
75	Enumeration, Isolation, and Characterization of N ₂ -Fixing Bacteria from Seawater. Applied and Environmental Microbiology, 1985, 50, 350-355.	1.4	54
76	Genomic and Phenotypic Characterization of Vibrio cholerae Non-O1 Isolates from a US Gulf Coast Cholera Outbreak. PLoS ONE, 2014, 9, e86264.	1.1	54
77	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). Journal of Biomolecular Techniques, 2017, 28, 31-39.	0.8	53
78	Dual role colonization factors connecting Vibrio cholerae's lifestyles in human and aquatic environments open new perspectives for combating infectious diseases. Current Opinion in Biotechnology, 2008, 19, 254-259.	3.3	51
79	Predicting the Distribution of Vibrio spp. in the Chesapeake Bay: A Vibrio cholerae Case Study. EcoHealth, 2009, 6, 378-389.	0.9	51
80	Acinetobacter lipases: molecular biology, biochemical properties and biotechnological potential. Journal of Industrial Microbiology and Biotechnology, 2004, 31, 391-400.	1.4	50
81	Comparative genomic analysis reveals evidence of two novel Vibrio species closely related to V. cholerae. BMC Microbiology, 2010, 10, 154.	1.3	50
82	Quantification of Vibrio parahaemolyticus, Vibrio vulnificus and Vibrio cholerae in French Mediterranean coastal lagoons. Research in Microbiology, 2013, 164, 867-874.	1.0	50
83	Drinking Water Microbiome Project: Is it Time?. Trends in Microbiology, 2019, 27, 670-677.	3.5	50
84	Environmental parameters associated with incidence and transmission of pathogenic Vibrio spp.. Environmental Microbiology, 2021, 23, 7314-7340.	1.8	50
85	Metagenomic Profiling of Microbial Pathogens in the Little Bighorn River, Montana. International Journal of Environmental Research and Public Health, 2019, 16, 1097.	1.2	49
86	Bacterial Death Revisited. , 2000, , 325-342.		49
87	Plant Growth Promoters Isolated from a Marine Bacterium Associated withPalythoasp. Natural Product Research, 1998, 11, 271-278.	0.4	48
88	Hydroclimatic influences on seasonal and spatial cholera transmission cycles: Implications for public health intervention in the Bengal Delta. Water Resources Research, 2011, 47, .	1.7	45
89	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	6.0	45
90	Cholera Outbreak in Senegal in 2005: Was Climate a Factor?. PLoS ONE, 2012, 7, e44577.	1.1	44

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91	A Microbiological Paradox: Viable but Nonculturable Bacteria with Special Reference to Vibrio cholerae. Journal of Food Protection, 1996, 59, 96-101.	0.8	43
92	Rapid Proliferation of Vibrio parahaemolyticus, Vibrio vulnificus, and Vibrio cholerae during Freshwater Flash Floods in French Mediterranean Coastal Lagoons. Applied and Environmental Microbiology, 2015, 81, 7600-7609.	1.4	43
93	Characterization of the Microbiome at the Worldâ€™s Largest Potable Water Reuse Facility. Frontiers in Microbiology, 2018, 9, 2435.	1.5	43
94	Metagenome sequencing-based strain-level and functional characterization of supragingival microbiome associated with dental caries in children. Journal of Oral Microbiology, 2019, 11, 1557986.	1.2	43
95	Molecular diversity and predictability of Vibrio parahaemolyticus along the Georgian coastal zone of the Black Sea. Frontiers in Microbiology, 2014, 5, 45.	1.5	40
96	Microbiome Analysis for Wastewater Surveillance during COVID-19. MBio, 2022, 13, .	1.8	40
97	Genetic characteristics of drug-resistant Vibrio cholerae O1 causing endemic cholera in Dhaka, 2006â€“2011. Journal of Medical Microbiology, 2012, 61, 1736-1745.	0.7	39
98	Vibrio metoecus sp. nov., a close relative of Vibrio cholerae isolated from coastal brackish ponds and clinical specimens. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 3208-3214.	0.8	39
99	Role of Shrimp Chitin in the Ecology of Toxigenic Vibrio cholerae and Cholera Transmission. Frontiers in Microbiology, 2012, 2, 260.	1.5	38
100	Epidemiological Significance of Viable but Nonculturable Microorganisms. , 2000, , 301-323.		38
101	Using Satellite Images of Environmental Changes to Predict Infectious Disease Outbreaks. Emerging Infectious Diseases, 2009, 15, 1341-1346.	2.0	37
102	Diversity and distribution of cholix toxin, a novel ADPâ€ribosylating factor from Vibrio cholerae. Environmental Microbiology Reports, 2010, 2, 198-207.	1.0	37
103	Distinct consequences of amoxicillin and ertapenem exposure in the porcine gut microbiome. Anaerobe, 2018, 53, 82-93.	1.0	37
104	Comparative Genomics of Escherichia coli Isolated from Skin and Soft Tissue and Other Extraintestinal Infections. MBio, 2017, 8, .	1.8	36
105	Occurrence and Diversity of Clinically Important Vibrio Species in the Aquatic Environment of Georgia. Frontiers in Public Health, 2015, 3, 232.	1.3	35
106	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.	1.2	35
107	Comparison of Infant Gut and Skin Microbiota, Resistome and Virulome Between Neonatal Intensive Care Unit (NICU) Environments. Frontiers in Microbiology, 2018, 9, 1361.	1.5	35
108	Cholera and climate: a demonstrated relationship. Transactions of the American Clinical and Climatological Association, 2009, 120, 119-28.	0.9	34

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109	Serogroup conversion of Vibrio cholerae non-O1 to Vibrio cholerae O1: effect of growth state of cells, temperature, and salinity. Canadian Journal of Microbiology, 1996, 42, 87-93.	0.8	33
110	Occurrence of theVibrio choleraeSeventh Pandemic VSP-I Island and a New Variant. OMICS A Journal of Integrative Biology, 2010, 14, 1-7.	1.0	33
111	Temporal and Spatial Variability in the Distribution of Vibrio vulnificus in the Chesapeake Bay: A Hindcast Study. EcoHealth, 2011, 8, 456-467.	0.9	32
112	Vibrio cholerae O1 detection in estuarine and coastal zooplankton. Journal of Plankton Research, 2011, 33, 51-62.	0.8	32
113	Vibrio cholerae Classical Biotype Strains Reveal Distinct Signatures in Mexico. Journal of Clinical Microbiology, 2012, 50, 2212-2216.	1.8	32
114	Distribution of Virulence Genes in Clinical and Environmental Vibrio cholerae Strains in Bangladesh. Applied and Environmental Microbiology, 2013, 79, 5782-5785.	1.4	32
115	Species Composition and Barotolerance of Gut Microflora of Deep-Sea Benthic Macrofauna Collected at Various Depths in the Atlantic Ocean. Applied and Environmental Microbiology, 1980, 40, 746-755.	1.4	32
116	Oral Metallo-Beta-Lactamase Protects the Gut Microbiome From Carbapenem-Mediated Damage and Reduces Propagation of Antibiotic Resistance in Pigs. Frontiers in Microbiology, 2019, 10, 101.	1.5	31
117	Oil Spills and Human Health: Contributions of the Gulf of Mexico Research Initiative. GeoHealth, 2019, 3, 391-406.	1.9	31
118	Response and tolerance of toxigenic Vibro cholerae O1 to cold temperatures. Antonie Van Leeuwenhoek, 2001, 79, 377-384.	0.7	30
119	Serogroup, Virulence, and Genetic Traits of Vibrio parahaemolyticus in the Estuarine Ecosystem of Bangladesh. Applied and Environmental Microbiology, 2009, 75, 6268-6274.	1.4	30
120	Vibrio ecology, pathogenesis, and evolution. Frontiers in Microbiology, 2014, 5, 256.	1.5	30
121	Natural Disasters and Cholera Outbreaks: Current Understanding and Future Outlook. Current Environmental Health Reports, 2017, 4, 99-107.	3.2	30
122	Climate Change and Human Health. Science, 1998, 279, 963g-963.	6.0	30
123	Effect of Transport at Ambient Temperature on Detection and Isolation of Vibrio cholerae from Environmental Samples. Applied and Environmental Microbiology, 2006, 72, 2185-2190.	1.4	29
124	A comparative analysis of drinking water employing metagenomics. PLoS ONE, 2020, 15, e0231210.	1.1	28
125	Satellite Based Assessment of Hydroclimatic Conditions Related to Cholera in Zimbabwe. PLoS ONE, 2015, 10, e0137828.	1.1	27
126	Membrane Bioreactor-Based Wastewater Treatment Plant in Saudi Arabia: Reduction of Viral Diversity, Load, and Infectious Capacity. Water (Switzerland), 2017, 9, 534.	1.2	27

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127	Viable but Not Cultivable Bacteria. Microbiology Monographs, 2009, , 121-129.	0.3	26
128	Vibrio cholerae in a historically choleraâ€free country. Environmental Microbiology Reports, 2012, 4, 381-389.	1.0	25
129	Molecular tools in understanding the evolution of Vibrio cholerae. Frontiers in Microbiology, 2015, 6, 1040.	1.5	25
130	Nontoxigenic Vibrio cholerae Non-O1/O139 Isolate from a Case of Human Gastroenteritis in the U.S. Gulf Coast. Journal of Clinical Microbiology, 2015, 53, 9-14.	1.8	25
131	Vibrio cholerae O1 with Reduced Susceptibility to Ciprofloxacin and Azithromycin Isolated from a Rural Coastal Area of Bangladesh. Frontiers in Microbiology, 2017, 8, 252.	1.5	25
132	A Metagenomic Approach to Evaluating Surface Water Quality in Haiti. International Journal of Environmental Research and Public Health, 2018, 15, 2211.	1.2	25
133	Phylogenetic Diversity of Vibrio cholerae Associated with Endemic Cholera in Mexico from 1991 to 2008. MBio, 2016, 7, e02160.	1.8	24
134	A voyage of discovery: cholera, climate and complexity. Environmental Microbiology, 2002, 4, 67-69.	1.8	23
135	Population Vulnerability to Biannual Cholera Outbreaks and Associated Macro-Scale Drivers in the Bengal Delta. American Journal of Tropical Medicine and Hygiene, 2013, 89, 950-959.	0.6	23
136	Characterization of Microbial Signatures From Advanced Treated Wastewater Biofilms. Journal - American Water Works Association, 2017, 109, E503.	0.2	23
137	Occurrence of Vibrio cholerae in water reservoirs of Burkina Faso. Research in Microbiology, 2018, 169, 1-10.	1.0	23
138	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. Nutrients, 2020, 12, 2764.	1.7	23
139	Antibiotic Resistance in Vibrio cholerae: Mechanistic Insights from IncC Plasmid-Mediated Dissemination of a Novel Family of Genomic Islands Inserted at trmE. MSphere, 2020, 5, .	1.3	23
140	Reduced Susceptibility to Extended-Spectrum Î²-Lactams in Vibrio cholerae Isolated in Bangladesh. Frontiers in Public Health, 2016, 4, 231.	1.3	22
141	Characterization of Pathogenic Vibrio parahaemolyticus from the Chesapeake Bay, Maryland. Frontiers in Microbiology, 2017, 8, 2460.	1.5	22
142	Viewing Marine Bacteria, Their Activity and Response to Environmental Drivers from Orbit. Microbial Ecology, 2014, 67, 489-500.	1.4	21
143	The influence of environmental conditions on the production of pigment bySerratia marcescens. Biotechnology and Bioprocess Engineering, 2002, 7, 100-104.	1.4	20
144	Occurrence in Mexico, 1998â€“2008, of Vibrio cholerae 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.	3.3	20

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145	Environmental Surveillance for Toxigenic Vibrio cholerae in Surface Waters of Haiti. American Journal of Tropical Medicine and Hygiene, 2015, 92, 118-125.	0.6	20
146	Biofilms Comprise a Component of the Annual Cycle of Vibrio cholerae in the Bay of Bengal Estuary. MBio, 2018, 9, .	1.8	20
147	Microbial Ecology of Petroleum Utilization in Chesapeake Bay. International Oil Spill Conference Proceedings, 1973, 1973, 685-690.	0.1	20
148	Assessment of Risk of Cholera in Haiti following Hurricane Matthew. American Journal of Tropical Medicine and Hygiene, 2017, 97, 896-903.	0.6	19
149	Gut-associated microflora of Limnoria tripunctata in marine creosote-treated wood pilings. Nature, 1979, 282, 716-717.	13.7	18
150	Genomic analysis of ICEVchBan8: An atypical genetic element in Vibrio cholerae. FEBS Letters, 2012, 586, 1617-1621.	1.3	18
151	Nanopore-based metagenomics analysis reveals prevalence of mobile antibiotic and heavy metal resistome in wastewater. Ecotoxicology, 2021, 30, 1572-1585.	1.1	18
152	CRISPR-Cas and Contact-Dependent Secretion Systems Present on Excisable Pathogenicity Islands with Conserved Recombination Modules. Journal of Bacteriology, 2017, 199, .	1.0	17
153	Hydrocarbon Mineralization in Sediments and Plasmid Incidence in Sediment Bacteria from the Campeche Bank. Applied and Environmental Microbiology, 1990, 56, 1565-1570.	1.4	17
154	Solar geoengineering could redistribute malaria risk in developing countries. Nature Communications, 2022, 13, 2150.	5.8	17
155	Vibrio choleraeO1 El Tor and O139 Bengal Strains CarryingctxB^{ET}, Bangladesh. Emerging Infectious Diseases, 2013, 19, 1713-1715.	2.0	16
156	Global diarrhoea action plan needs integrated climate-based surveillance. The Lancet Global Health, 2014, 2, e69-e70.	2.9	16
157	Temporal Resistome and Microbial Community Dynamics in an Intensive Aquaculture Facility with Prophylactic Antimicrobial Treatment. Microorganisms, 2020, 8, 1984.	1.6	16
158	Ecology and taxonomy of chitinoclasticCytophaga and related chitin-degrading bacteria isolated from an estuary. Microbial Ecology, 1983, 9, 273-294.	1.4	15
159	Evaluation of media for recovery of aerosolized bacteria. Aerobiologia, 1997, 13, 219-226.	0.7	15
160	Chitin promotesMycobacterium ulceransgrowth. FEMS Microbiology Ecology, 2016, 92, fiw067.	1.3	15
161	Metagenomic Sequencing and Quantitative Real-Time PCR for Fecal Pollution Assessment in an Urban Watershed. Frontiers in Water, 2021, 3, 626849.	1.0	15
162	Covariability of Vibrio cholerae Microdiversity and Environmental Parameters. Applied and Environmental Microbiology, 2008, 74, 2915-2920.	1.4	14

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163	Prosthetic joint infections present diverse and unique microbial communities using combined whole-genome shotgun sequencing and culturing methods. Journal of Medical Microbiology, 2019, 68, 1507-1516.	0.7	14
164	Detection of <scp>V</scp>ibrio cholerae in environmental waters including drinking water reservoirs of <scp>A</scp>zerbaijan. Environmental Microbiology Reports, 2013, 5, 30-38.	1.0	13
165	Beyond cost-effectiveness: Using systems analysis for infectious disease preparedness. Vaccine, 2017, 35, A46-A49.	1.7	13
166	A new integrative conjugative element detected in Haitian isolates of Vibrio cholerae non-O1/non-O139. Research in Microbiology, 2013, 164, 891-893.	1.0	12
167	Gut microbiota of frugo-folivorous sifakas across environments. Animal Microbiome, 2021, 3, 39.	1.5	12
168	A Review of the Environmental Trigger and Transmission Components for Prediction of Cholera. Tropical Medicine and Infectious Disease, 2021, 6, 147.	0.9	12
169	Transesterification activity of a novel lipase from AcinetobacterÂvenetianus RAG-1. Antonie Van Leeuwenhoek, 2008, 94, 621-625.	0.7	11
170	Occurrence of Vibrio cholerae in Municipal and Natural Waters and Incidence of Cholera in Azerbaijan. EcoHealth, 2011, 8, 468-477.	0.9	11
171	Hybrid Vibrio cholerae El Tor Lacking SXT Identified as the Cause of a Cholera Outbreak in the Philippines. MBio, 2015, 6, .	1.8	11
172	Characterization of Two Cryptic Plasmids Isolated in Haiti from Clinical Vibrio cholerae Non-O1/Non-O139. Frontiers in Microbiology, 2017, 8, 2283.	1.5	11
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