The Origin of the Haitian Cholera Outbreak Strain

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Citation Report

| # | Article | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Bacterial epidemiology and biology - lessons from genome sequencing. Genome Biology, 2011, 12, 230. | 9.6 | 72 |
| 2 | The properties and applications of single-molecule DNA sequencing. Genome Biology, 2011, 12, 217. | 8.8 | 107 |
| 3 | Highlights & Happenings. Biosecurity and Bioterrorism, 2011, 9, 1-7. | 1.2 | 2 |
| 4 | Case 19-2011. New England Journal of Medicine, 2011, 364, 2452-2461. | 27.0 | 4 |
| 5 | Poverty, Global Health, and Infectious Disease: Lessons from Haiti and Rwanda. Infectious Disease Clinics of North America, 2011, 25, 611-622. | 5.1 | 68 |
| 6 | Prediction of the spatial evolution and effects of control measures for the unfolding Haiti cholera outbreak. Geophysical Research Letters, 2011, 38, n/a-n/a. | 4.0 | 82 |
| 7 | Electrons, Photons, and Force: Quantitative Single-Molecule Measurements from Physics to Biology. ACS Nano, 2011, 5, 693-729. | 14.6 | 95 |
| 8 | Genomic Analysis at the Single-Cell Level. Annual Review of Genetics, 2011, 45, 431-445. | 7.6 | 187 |
| 9 | Understanding the Cholera Epidemic, Haiti. Emerging Infectious Diseases, 2011, 17, 1161-1168. | 4.3 | 252 |
| 10 | Overview of DNA Sequencing Strategies. Current Protocols in Molecular Biology, 2011, 96, Unit7.1. | 2.9 | 71 |
| 11 | New-generation vaccines against cholera. Nature Reviews Gastroenterology and Hepatology, 2011, 8, 701-710. | 17.8 | 59 |
| 12 | Origins of the <i>E. coli</i> Strain Causing an Outbreak of Hemolytic–Uremic Syndrome in Germany. New England Journal of Medicine, 2011, 365, 709-717. | 27.0 | 778 |
| 13 | Genetic Screens and Biochemical Assays to Characterize <i>Vibrio cholerae</i> O1 Biotypes: Classical and El Tor. Current Protocols in Microbiology, 2011, 22, 6A.2.1-6A.2.17. | 6.5 | 5 |
| 14 | Hybrid selection for sequencing pathogen genomes from clinical samples. Genome Biology, 2011, 12, R73. | 9.6 | 97 |
| 16 | RNA-Seq-Based Monitoring of Infection-Linked Changes in Vibrio cholerae Gene Expression. Cell Host and Microbe, 2011, 10, 165-174. | 11.0 | 191 |
| 17 | Safety and immunogenicity study of a killed bivalent (O1 and O139) whole-cell oral cholera vaccine Shanchol, in Bangladeshi adults and children as young as 1 year of age. Vaccine, 2011, 29, 8285-8292. | 3.8 | 98 |
| 18 | Introduction and Historical Overview of DNA Sequencing. Current Protocols in Molecular Biology, 2011, 96, 7.0.1. | 2.9 | 1 |
| 19 | Understanding the Cholera Epidemic, Haiti. Emerging Infectious Diseases, 2011, 17, 2178-9; author reply 2179-80. | 4.3 | 6 |

TATION REPO

ARTICLE IF CITATIONS # Forensic Public Health., 2011, , 239-256. 20 1 Choleraâ€"Modern Pandemic Disease of Ancient Lineage. Emerging Infectious Diseases, 2011, 17, 2099-104. 4.3 Preparing Health Care Workers for a Cholera Epidemic, Dominican Republic, 2010. Emerging Infectious 22 4.3 2 Diseases, 2011, 17, 2177-8. Comparative Genomics of Vibrio cholerae from Haiti, Asia, and Africa. Emerging Infectious Diseases, 136 2011, 17, 2113-21. The Time of Cholera. Canadian Journal of Infectious Diseases and Medical Microbiology, 2011, 22, 7-9. 24 1.9 0 Cholera in the 21st century. Current Opinion in Infectious Diseases, 2011, 24, 472-477. 3.1 27 The Source of the Haitian Cholera Epidemic. AAP Grand Rounds, 2011, 25, 31-31. 0.0 0 Cholera Epidemic in Haiti, 2010: Using a Transmission Model to Explain Spatial Spread of Disease and 28 3.9 214 Identify Optimal Control Interventions. Annals of Internal Medicine, 2011, 154, 593. Cholera, canals, and contagion: Rediscovering Dr Beck's report. Journal of Public Health Policy, 2011, 29 2.0 6 32, 320-333. A decade's perspective on DNA sequencing technology. Nature, 2011, 470, 198-203. 27.8 WHO needs change. Nature, 2011, 473, 143-145. 31 27.8 28 Vibrio cholerae O1 lineages driving cholera outbreaks during seventh cholera pandemic in Ghana. 2.3 Infection, Genetics and Evolution, 2011, 11, 1951-1956. Identification of Salmonella enterica species- and subgroup-specific genomic regions using Panseq 2.0. 33 2.3 10 Infection, Genetics and Evolution, 2011, 11, 2151-2161. Everything at once: Comparative analysis of the genomes of bacterial pathogens. Veterinary Microbiology, 2011, 153, 13-26. 34 Next-generation sequencing technologies and applications for human genetic history and forensics. 35 3.3 101 Investigative Genetics, 2011, 2, 23. Landscape of Next-Generation Sequencing Technologies. Analytical Chemistry, 2011, 83, 4327-4341. 314 Comprehensive next-generation cancer genome sequencing in the era of targeted therapy and 37 1.4 83 personalized oncology. Biomarkers in Medicine, 2011, 5, 293-305. Principles and Practice of Disaster Relief: Lessons From Haiti. Mount Sinai Journal of Medicine, 2011, 38 78, 306-318.

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 39 | Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. MBio, 2011, 2, e00157-11. | 4.1 | 268 |
| 40 | Real-time sequencing. Nature Reviews Microbiology, 2011, 9, 633-633. | 28.6 | 11 |
| 41 | Prospects for the Future Using Genomics and Proteomics in Clinical Microbiology. Annual Review of Microbiology, 2011, 65, 169-188. | 7.3 | 53 |
| 42 | Microbial Genomics and Infectious Diseases. New England Journal of Medicine, 2011, 365, 347-357. | 27.0 | 156 |
| 43 | Genome variability in the altered variants of Vibrio cholerae biovar El Tor isolated in Russia. Molecular Genetics, Microbiology and Virology, 2011, 26, 102. | 0.3 | 11 |
| 44 | Evidence for several waves of global transmission in the seventh cholera pandemic. Nature, 2011, 477, 462-465. | 27.8 | 649 |
| 45 | Transcriptomes of Frankia sp. strain Ccl3 in growth transitions. BMC Microbiology, 2011, 11, 192. | 3.3 | 26 |
| 46 | Genomsequenzierer. Die dritte Generation. Chemie in Unserer Zeit, 2011, 45, 184-187. | 0.1 | 0 |
| 47 | Application of nanomaterials to arrays for infectious disease diagnosis. Nanomedicine, 2011, 6, 271-280. | 3.3 | 14 |
| 48 | South Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strains. MBio, 2011, 2, . | 4.1 | 9 |
| 49 | Rapidly Progressive, Fatal, Inhalation Anthrax-like Infection in a Human: Case Report, Pathogen Genome Sequencing, Pathology, and Coordinated Response. Archives of Pathology and Laboratory Medicine, 2011, 135, 1447-1459. | 2.5 | 64 |
| 50 | Pulse Oximetry. New England Journal of Medicine, 2011, 365, 184-185. | 27.0 | 3 |
| 51 | Responding to Cholera in Post-Earthquake Haiti. New England Journal of Medicine, 2011, 364, 3-5. | 27.0 | 105 |
| 52 | Recent Clonal Origin of Cholera in Haiti. Emerging Infectious Diseases, 2011, 17, 699-701. | 4.3 | 57 |
| 53 | Vibrio choleraein Traveler from Haiti to Canada. Emerging Infectious Diseases, 2011, 17, 1124-1125. | 4.3 | 10 |
| 54 | Identification of a Salmonellosis Outbreak by Means of Molecular Sequencing. New England Journal of Medicine, 2011, 364, 981-982. | 27.0 | 155 |
| 55 | Ecology and Genetic Structure of a Northern Temperate Vibrio cholerae Population Related to Toxigenic Isolates. Applied and Environmental Microbiology, 2011, 77, 7568-7575. | 3.1 | 32 |
| 56 | Vaccination strategies for epidemic cholera in Haiti with implications for the developing world. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7081-7085. | 7.1 | 143 |

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 57 | Integration and visualization of host–pathogen data related to infectious diseases. Bioinformatics, 2011, 27, 2279-2287. | 4.1 | 17 |
| 58 | Metagenomics and beyond: new toolboxes for microbial systematics. Microbiology Australia, 2011, 32, 86. | 0.4 | 1 |
| 59 | Meeting Cholera's Challenge to Haiti and the World: A Joint Statement on Cholera Prevention and Care. PLoS Neglected Tropical Diseases, 2011, 5, e1145. | 3.0 | 105 |
| 60 | Characterization of Vibrio cholerae O1 El Tor Biotype Variant Clinical Isolates from Bangladesh and Haiti, Including a Molecular Genetic Analysis of Virulence Genes. Journal of Clinical Microbiology, 2011, 49, 3739-3749. | 3.9 | 112 |
| 61 | Insights from Genomics into Bacterial Pathogen Populations. PLoS Pathogens, 2012, 8, e1002874. | 4.7 | 87 |
| 62 | Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. PLoS Pathogens, 2012, 8, e1002824. | 4.7 | 450 |
| 63 | The Regulatory Network of Natural Competence and Transformation of Vibrio cholerae. PLoS Genetics, 2012, 8, e1002778. | 3.5 | 156 |
| 64 | Comparison of Next-Generation Sequencing Systems. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-11. | 3.0 | 1,049 |
| 65 | Development and Evaluation of a PCR Assay for Tracking the Emergence and Dissemination of Haitian Variant <i>ctxB</i> in Vibrio cholerae O1 Strains Isolated from Kolkata, India. Journal of Clinical Microbiology, 2012, 50, 1733-1736. | 3.9 | 85 |
| 66 | NEW: Network-Enabled Wisdom in Biology, Medicine, and Health Care. Science Translational Medicine, 2012, 4, 115rv1. | 12.4 | 115 |
| 67 | National and international policies to mitigate disease threats. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 2893-2900. | 4.0 | 3 |
| 68 | An overview of cholera vaccines and their public health implications. Current Opinion in Pediatrics, 2012, 24, 85-91. | 2.0 | 18 |
| 69 | Possible Laboratory Contamination Leads to Incorrect Reporting of Vibrio cholerae O1 and Initiates an Outbreak Response. Journal of Clinical Microbiology, 2012, 50, 480-482. | 3.9 | 4 |
| 70 | Reassessment of the 2010–2011 Haiti cholera outbreak and rainfall-driven multiseason projections. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6602-6607. | 7.1 | 153 |
| 71 | A Framework for Scalable Genome Assembly on Clusters, Clouds, and Grids. IEEE Transactions on Parallel and Distributed Systems, 2012, 23, 2189-2197. | 5.6 | 14 |
| 72 | Characterization of DNA methyltransferase specificities using single-molecule, real-time DNA sequencing. Nucleic Acids Research, 2012, 40, e29-e29. | 14.5 | 306 |
| 73 | Social and News Media Enable Estimation of Epidemiological Patterns Early in the 2010 Haitian Cholera Outbreak. American Journal of Tropical Medicine and Hygiene, 2012, 86, 39-45. | 1.4 | 364 |
| 74 | Not All Sequence Tags Are Created Equal: Designing and Validating Sequence Identification Tags Robust to Indels. PLoS ONE, 2012, 7, e42543. | 2.5 | 267 |

| | Сітаті | CITATION REPORT | |
|----|---|-----------------|-----------|
| # | Article | IF | CITATIONS |
| 75 | Current Genomics in Cardiovascular Medicine. Current Genomics, 2012, 13, 446-462. | 1.6 | 5 |
| 76 | <i>In Silico</i> Analyses of Primers Used to Detect the Pathogenicity Genes of <i>Vibrio cholerae</i> . Microbes and Environments, 2012, 27, 250-256. | 1.6 | 5 |
| 77 | Cholera. Lancet, The, 2012, 379, 2466-2476. | 13.7 | 527 |
| 78 | Non-O1 Vibrio cholerae unlinked to cholera in Haiti. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3206-E3206. | 7.1 | 10 |
| 79 | Emerging real-time technologies in molecular medicine and the evolution of integrated †pharmacomics' approaches to personalized medicine and drug discovery. , 2012, 136, 295-304. | | 14 |
| 80 | Genome-wide mapping of methylated adenine residues in pathogenic Escherichia coli using single-molecule real-time sequencing. Nature Biotechnology, 2012, 30, 1232-1239. | 17.5 | 365 |
| 81 | Translational research in infectious disease: current paradigms and challenges ahead. Translational Research, 2012, 159, 430-453. | 5.0 | 39 |
| 82 | Tracking a Hospital Outbreak of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> with Whole-Genome Sequencing. Science Translational Medicine, 2012, 4, 148ra116. | 12.4 | 781 |
| 83 | Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612. | 16.3 | 684 |
| 84 | Genetic characteristics of drug-resistant Vibrio cholerae O1 causing endemic cholera in Dhaka, 2006–2011. Journal of Medical Microbiology, 2012, 61, 1736-1745. | 1.8 | 39 |
| 85 | Cholera epidemics in 2010: respective roles of environment, strain changes, and human-driven dissemination. Clinical Microbiology and Infection, 2012, 18, 231-238. | 6.0 | 37 |
| 86 | Rapid detection by multiplex PCR of Genomic Islands, prophages and Integrative Conjugative Elements in V. cholerae 7th pandemic variants. Journal of Microbiological Methods, 2012, 88, 98-102. | 1.6 | 14 |
| 87 | Short-read reading-frame predictors are not created equal: sequence error causes loss of signal. BMC Bioinformatics, 2012, 13, 183. | 2.6 | 39 |
| 88 | High resolution clustering of Salmonella enterica serovar Montevideo strains using a next-generation sequencing approach. BMC Genomics, 2012, 13, 32. | 2.8 | 140 |
| 89 | High depth, whole-genome sequencing of cholera isolates from Haiti and the Dominican Republic. BMC Genomics, 2012, 13, 468. | 2.8 | 16 |
| 90 | Genomic variation in Salmonella enterica core genes for epidemiological typing. BMC Genomics, 2012, 13, 88. | 2.8 | 76 |
| 91 | Bacterial frequent flyers. Nature Reviews Microbiology, 2012, 10, 734-734. | 28.6 | 2 |
| 92 | Molecular-genetic analysis of Vibrio cholerae El Tor strains of epidemic risk isolated in Siberian and Far East regions of Russia. Molecular Genetics, Microbiology and Virology, 2012, 27, 61-68. | 0.3 | 4 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 94 | Fighting Outbreaks with Bacterial Genomics: Case Review and Workflow Proposal. Public Health Genomics, 2012, 15, 341-351. | 1.0 | 10 |
| 95 | The continually evolving <i>Clostridium difficile</i> species. Future Microbiology, 2012, 7, 945-957. | 2.0 | 30 |
| 96 | Next-generation and whole-genome sequencing in the diagnostic clinical microbiology laboratory. European Journal of Clinical Microbiology and Infectious Diseases, 2012, 31, 1719-1726. | 2.9 | 133 |
| 97 | Cell Polarity: ParA-logs Gather around the Hub. Current Biology, 2012, 22, R1055-R1057. | 3.9 | 5 |
| 98 | Visual Neuroscience: A Moving Story of Neuromodulation. Current Biology, 2012, 22, R1057-R1059. | 3.9 | 1 |
| 99 | Tetracycline resistant V. cholerae O1 biotype El Tor serotype Ogawa with classical ctxB from a recent cholera outbreak in Orissa, Eastern India. Journal of Infection and Public Health, 2012, 5, 217-219. | 4.1 | 11 |
| 100 | Genome sequencing in clinical microbiology. Nature Biotechnology, 2012, 30, 1068-1071. | 17.5 | 37 |
| 102 | A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. BMJ Open, 2012, 2, e001124. | 1.9 | 228 |
| 103 | Detection of Non-Amplified Genomic DNA. Soft and Biological Matter, 2012, , . | 0.3 | 11 |
| 105 | Cholera: Something Old, Something New. Surgical Infections, 2012, 13, 216-222. | 1.4 | 10 |
| 107 | Whole Genome Sequencing and Evolutionary Analysis of Human Papillomavirus Type 16 in Central China. PLoS ONE, 2012, 7, e36577. | 2.5 | 27 |
| 108 | Genome-Wide Study of the Defective Sucrose Fermenter Strain of Vibrio cholerae from the Latin American Cholera Epidemic. PLoS ONE, 2012, 7, e37283. | 2.5 | 13 |
| 109 | Microbial Diversity and Potential Pathogens in Ornamental Fish Aquarium Water. PLoS ONE, 2012, 7, e39971. | 2.5 | 52 |
| 110 | Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. PLoS ONE, 2012, 7, e49602. | 2.5 | 78 |
| 111 | A Framework for Assessing the Concordance of Molecular Typing Methods and the True Strain Phylogeny of Campylobacter jejuni and C. coli Using Draft Genome Sequence Data. Frontiers in Cellular and Infection Microbiology, 2012, 2, 57. | 3.9 | 31 |
| 112 | Genetic Analysis of CTX Prophage and Antibiotic Resistance Determinants in Vibrio cholerae O1 Belonging to the Atypical El Tor Biotype from Kelantan, Malaysia. , 0, , . | | 0 |
| 113 | Chloroquine-Resistant Malaria in Travelers Returning from Haiti after 2010 Earthquake. Emerging Infectious Diseases, 2012, 18, 1346-1349. | 4.3 | 26 |
| 114 | The "First―Case of Cholera in Haiti: Lessons for Global Health. American Journal of Tropical Medicine and Hygiene, 2012, 86, 36-38. | 1.4 | 29 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 115 | Bugs, drugs and chemical genomics. Nature Chemical Biology, 2012, 8, 46-56. | 8.0 | 130 |
| 116 | Third-generation sequencing techniques and applications to drug discovery. Expert Opinion on Drug Discovery, 2012, 7, 231-243. | 5.0 | 54 |
| 117 | Nepalese origin of cholera epidemic in Haiti. Clinical Microbiology and Infection, 2012, 18, E158-E163. | 6.0 | 107 |
| 118 | Evolutionary perspective on the origin of Haitian cholera outbreak strain. Journal of Biomolecular Structure and Dynamics, 2012, 30, 338-346. | 3.5 | 8 |
| 119 | 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 |
| 120 | Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. New England Journal of Medicine, 2012, 366, 2267-2275. | 27.0 | 609 |
| 121 | Multi-locus variable number tandem repeat analysis of 7th pandemic Vibrio cholerae. BMC Microbiology, 2012, 12, 82. | 3.3 | 36 |
| 122 | A hybrid approach for the automated finishing of bacterial genomes. Nature Biotechnology, 2012, 30, 701-707. | 17.5 | 178 |
| 123 | Hybrid error correction and de novo assembly of single-molecule sequencing reads. Nature Biotechnology, 2012, 30, 693-700. | 17.5 | 946 |
| 124 | Toward the Single-Hour High-Quality Genome. Annual Review of Biochemistry, 2012, 81, 359-378. | 11.1 | 29 |
| 125 | Phenotypic and genetic characterization of Vibrio cholerae O1 clinical isolates collected through national antimicrobial resistance surveillance network in Nepal. World Journal of Microbiology and Biotechnology, 2012, 28, 2671-2678. | 3.6 | 9 |
| 126 | Real-time PCR and NASBA for rapid and sensitive detection of Vibrio cholerae in ballast water. Marine Pollution Bulletin, 2012, 64, 200-206. | 5.0 | 47 |
| 127 | Cholera: Lessons from Haiti and Beyond. Current Infectious Disease Reports, 2012, 14, 1-8. | 3.0 | 16 |
| 128 | Gastrointestinal Infections in the Setting of Natural Disasters. Current Infectious Disease Reports, 2012, 14, 47-52. | 3.0 | 16 |
| 130 | Modern clinical microbiology: new challenges and solutions. Nature Reviews Microbiology, 2013, 11, 574-585. | 28.6 | 264 |
| 131 | New concepts in diagnostics for infectious diarrhea. Mucosal Immunology, 2013, 6, 876-885. | 6.0 | 54 |
| 132 | Vibrios. , 2013, , 113-128. | | 1 |
| 133 | John Snow's legacy: epidemiology without borders. Lancet, The, 2013, 381, 1302-1311. | 13.7 | 34 |

8

| CITATION R | REPORT | |
|------------|--------|---------|
| | | |
| | IF | CITATIO |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 134 | Genomics and metagenomics in medical microbiology. Journal of Microbiological Methods, 2013, 95, 415-424. | 1.6 | 69 |
| 135 | Genomic Medicine: A Decade of Successes, Challenges, and Opportunities. Science Translational Medicine, 2013, 5, 189sr4. | 12.4 | 197 |
| 136 | The Role of Vibrio cholerae Genotyping in Africa. Journal of Infectious Diseases, 2013, 208, S32-S38. | 4.0 | 15 |
| 137 | An evaluation of the PacBio RS platform for sequencing and de novo assembly of a chloroplast genome. BMC Genomics, 2013, 14, 670. | 2.8 | 146 |
| 138 | Comparative molecular-genetic analysis of mobile elements in natural strains of cholera agent. Russian Journal of Genetics, 2013, 49, 898-908. | 0.6 | 7 |
| 139 | Genomic analysis to improve the management of outbreaks of bacterial infection. Expert Review of Anti-Infective Therapy, 2013, 11, 335-337. | 4.4 | 5 |
| 140 | Role of 6-Gingerol in Reduction of Cholera Toxin Activity <i>In Vitro</i> and <i>In Vivo</i> . Antimicrobial Agents and Chemotherapy, 2013, 57, 4373-4380. | 3.2 | 30 |
| 141 | Better Tests, Better Care: Improved Diagnostics for Infectious Diseases. Clinical Infectious Diseases, 2013, 57, S139-S170. | 5.8 | 496 |
| 142 | Next-generation sequencing: The future of molecular genetics in poultry production and food safety. Poultry Science, 2013, 92, 562-572. | 3.4 | 71 |
| 143 | Next-Generation Sequencing For Gene and Pathway Discovery and Analysis in Autism Spectrum Disorders. , 2013, , 169-177. | | 1 |
| 144 | Cues and regulatory pathways involved in natural competence and transformation in pathogenic and environmental Gram-negative bacteria. FEMS Microbiology Reviews, 2013, 37, 336-363. | 8.6 | 191 |
| 145 | Real-Time Sequencing To Decipher the Molecular Mechanism of Resistance of a Clinical Pan-Drug-Resistant Acinetobacter baumannii Isolate from Marseille, France. Antimicrobial Agents and Chemotherapy, 2013, 57, 592-596. | 3.2 | 70 |
| 146 | Advanced Methods for Detection of Foodborne Pathogens. , 2013, , 605-618. | | 0 |
| 147 | Diagnostic Applications of High-Throughput DNA Sequencing. Annual Review of Pathology: Mechanisms of Disease, 2013, 8, 381-410. | 22.4 | 58 |
| 148 | Tn-Seq Analysis of Vibrio cholerae Intestinal Colonization Reveals a Role for T6SS-Mediated Antibacterial Activity in the Host. Cell Host and Microbe, 2013, 14, 652-663. | 11.0 | 226 |
| 149 | Going Forward with Genetics. American Journal of Pathology, 2013, 182, 1462-1473. | 3.8 | 57 |
| 150 | Drug response and genetic properties of Vibrio cholerae associated with endemic cholera in north-eastern Thailand, 2003â ϵ "2011. Journal of Medical Microbiology, 2013, 62, 599-609. | 1.8 | 15 |
| 151 | Cholera Surveillance during the Haiti Epidemic — The First 2 Years. New England Journal of Medicine, 2013, 368, 599-609. | 27.0 | 225 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 152 | A predictive model of <i>Vibrio cholerae</i> for combined temperature and organic nutrient in aquatic environments. Journal of Applied Microbiology, 2013, 114, 574-585. | 3.1 | 10 |
| 153 | Large outbreak of cholera caused by El Tor variant Vibrio cholerae O1 in the eastern coast of Odisha, India during 2009. Epidemiology and Infection, 2013, 141, 2560-2567. | 2.1 | 12 |
| 154 | Prevalence and Molecular Characterization of <i>Vibrio cholerae</i> O1, Non-O1 and Non-O139 in Tropical Seafood in Cochin, India. Foodborne Pathogens and Disease, 2013, 10, 278-283. | 1.8 | 28 |
| 155 | Indigenous <i>Vibrio cholerae</i> strains from a non-endemic region are pathogenic. Open Biology, 2013, 3, 120181. | 3.6 | 35 |
| 156 | Rapid bacterial genome sequencing: methods and applications in clinical microbiology. Clinical Microbiology and Infection, 2013, 19, 803-813. | 6.0 | 186 |
| 157 | Human Genome Variation Discovery via Exome and Whole-Genome Sequencing. , 2013, , 94-101. | | 0 |
| 158 | Molecular Characterization of Vibrio cholerae O1 Reveals Continuous Evolution of Its New Variants in India. Indian Journal of Microbiology, 2013, 53, 137-141. | 2.7 | 9 |
| 160 | Whole genome sequencing in the prevention and control of Staphylococcus aureus infection. Journal of Hospital Infection, 2013, 83, 14-21. | 2.9 | 59 |
| 161 | The Need for High-Quality Whole-Genome Sequence Databases in Microbial Forensics. Biosecurity and Bioterrorism, 2013, 11, S78-S86. | 1.2 | 17 |
| 162 | Examining rainfall and cholera dynamics in Haiti using statistical and dynamic modeling approaches. Epidemics, 2013, 5, 197-207. | 3.0 | 96 |
| 163 | Bacterial genomes in epidemiology—present and future. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120202. | 4.0 | 51 |
| 164 | Modeling kinetic rate variation in third generation DNA sequencing data to detect putative modifications to DNA bases. Genome Research, 2013, 23, 129-141. | 5.5 | 99 |
| 165 | Analysis of Vibrio cholerae Genome Sequences Reveals Unique <i>rtxA</i> Variants in Environmental Strains and an <i>rtxA</i> -Null Mutation in Recent Altered El Tor Isolates. MBio, 2013, 4, e00624. | 4.1 | 43 |
| 166 | Pan-Genome and Comparative Genome Analyses of Propionibacterium acnes Reveal Its Genomic Diversity in the Healthy and Diseased Human Skin Microbiome. MBio, 2013, 4, e00003-13. | 4.1 | 159 |
| 167 | Deciphering the Origins and Tracking the Evolution of Cholera Epidemics with Whole-Genome-Based Molecular Epidemiology. MBio, 2013, 4, e00670-13. | 4.1 | 12 |
| 168 | Where are we heading with <i>Salmonella</i> molecular subtyping?. Future Microbiology, 2013, 8, 1231-1233. | 2.0 | 1 |
| 169 | Predictors of Disease Severity in Patients Admitted to a Cholera Treatment Center in Urban Haiti. American Journal of Tropical Medicine and Hygiene, 2013, 89, 625-632. | 1.4 | 18 |
| 170 | In Response. American Journal of Tropical Medicine and Hygiene, 2013, 89, 1231-1232. | 1.4 | 1 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 171 | Evolutionary Dynamics of Vibrio cholerae O1 following a Single-Source Introduction to Haiti. MBio, 2013, 4, . | 4.1 | 118 |
| 172 | Environmental Factors Influencing Epidemic Cholera. American Journal of Tropical Medicine and Hygiene, 2013, 89, 597-607. | 1.4 | 130 |
| 173 | Detection of Mixed Infection from Bacterial Whole Genome Sequence Data Allows Assessment of Its Role in Clostridium difficile Transmission. PLoS Computational Biology, 2013, 9, e1003059. | 3.2 | 75 |
| 174 | Aftermath of Typhoon Haiyan: The Imminent Epidemic of Waterborne Illnesses in Leyte, Philippines. Disaster Medicine and Public Health Preparedness, 2013, 7, 547-548. | 1.3 | 6 |
| 175 | Coalescent inference for infectious disease: meta-analysis of hepatitis C. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120314. | 4.0 | 43 |
| 176 | Selected insights from application of whole-genome sequencing for outbreak investigations. Current Opinion in Critical Care, 2013, 19, 432-439. | 3.2 | 45 |
| 177 | Rise of the microbes. Virulence, 2013, 4, 213-222. | 4.4 | 13 |
| 178 | Molecular Characterization of High-Level-Cholera-Toxin-Producing El Tor Variant Vibrio cholerae Strains in the Zanzibar Archipelago of Tanzania. Journal of Clinical Microbiology, 2013, 51, 1040-1045. | 3.9 | 40 |
| 179 | PBSIM: PacBio reads simulator—toward accurate genome assembly. Bioinformatics, 2013, 29, 119-121. | 4.1 | 279 |
| 180 | Next-Generation Anchor Based Phylogeny (NexABP): Constructing phylogeny from Next-generation sequencing data. Scientific Reports, 2013, 3, 2634. | 3.3 | 10 |
| 181 | Reducing assembly complexity of microbial genomes with single-molecule sequencing. Genome Biology, 2013, 14, R101. | 9.6 | 378 |
| 182 | Integrated whole-genome sequencing and temporospatial analysis of a continuing Group A <i>Streptococcus</i> epidemic. Emerging Microbes and Infections, 2013, 2, 1-8. | 6.5 | 16 |
| 183 | Efficient Depletion of Host DNA Contamination in Malaria Clinical Sequencing. Journal of Clinical Microbiology, 2013, 51, 745-751. | 3.9 | 63 |
| 184 | Reexamining El Niño and Cholera in Peru: A Climate Affairs Approach. Weather, Climate, and Society, 2013, 5, 148-161. | 1.1 | 14 |
| 185 | Recurrent epidemic cholera with high mortality in Cameroon: persistent challenges 40 years into the seventh pandemic. Epidemiology and Infection, 2013, 141, 2083-2093. | 2.1 | 23 |
| 186 | Cholera Vaccination in Urban Haiti. American Journal of Tropical Medicine and Hygiene, 2013, 89, 671-681. | 1.4 | 66 |
| 187 | On the Evolutionary History, Population Genetics and Diversity among Isolates of Salmonella Enteritidis PFGE Pattern JEGX01.0004. PLoS ONE, 2013, 8, e55254. | 2.5 | 146 |
| 188 | Phylogeny of Bacterial and Archaeal Genomes Using Conserved Genes: Supertrees and Supermatrices. PLoS ONE, 2013, 8, e62510. | 2.5 | 138 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 189 | A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. PLoS ONE, 2013, 8, e66129. | 2.5 | 62 |
| 191 | Genetic Characteristics and Relatedness of Imported <i>Vibrio cholerae</i> O1 Biotype El Tor in Korea. Annals of Clinical Microbiology, 2013, 16, 25. | 0.1 | 1 |
| 192 | A Conversion Formula for Comparing Pulse Oximeter Desaturation Rates Obtained with Different Averaging Times. PLoS ONE, 2014, 9, e87280. | 2.5 | 11 |
| 193 | Development of pVCR94ΔX from Vibrio cholerae, a prototype for studying multidrug resistant IncA/C conjugative plasmids. Frontiers in Microbiology, 2014, 5, 44. | 3.5 | 51 |
| 194 | Cholera Outbreaks in South and Southeast Asia: Descriptive Analysis, 2003–2012. Japanese Journal of Infectious Diseases, 2014, 67, 145-156. | 1.2 | 27 |
| 195 | Phenotypic and genetic characterization of vibrio cholera o1 isolated from various regions of Kenya between 2007 and 2010. Pan African Medical Journal, 2014, 19, 8. | 0.8 | 19 |
| 196 | Emerging and Reemerging Infectious Diseases. , 2014, , . | | 3 |
| 197 | Special Community Health Needs. , 2014, , 381-418. | | 1 |
| 199 | Transcriptional analysis of endocrine disruption using zebrafish and massively parallel sequencing. Journal of Molecular Endocrinology, 2014, 52, R241-R256. | 2.5 | 38 |
| 200 | Single molecule sequencing and genome assembly of a clinical specimen of Loa loa, the causative agent of loiasis. BMC Genomics, 2014, 15, 788. | 2.8 | 32 |
| 201 | Household Transmission of Vibrio cholerae in Bangladesh. PLoS Neglected Tropical Diseases, 2014, 8, e3314. | 3.0 | 45 |
| 202 | From Haiti to the Amazon: Public Health Issues Related to the Recent Immigration of Haitians to Brazil. PLoS Neglected Tropical Diseases, 2014, 8, e2685. | 3.0 | 13 |
| 203 | Molecular Insights Into the Evolutionary Pathway of Vibrio cholerae O1 Atypical El Tor Variants. PLoS Pathogens, 2014, 10, e1004384. | 4.7 | 45 |
| 204 | Whole-Genome Single-Nucleotide-Polymorphism Analysis for Discrimination of Clostridium botulinum Group I Strains. Applied and Environmental Microbiology, 2014, 80, 2125-2132. | 3.1 | 36 |
| 205 | Immunogenicity of a Killed Bivalent (O1 and O139) Whole Cell Oral Cholera Vaccine, Shanchol, in Haiti. PLoS Neglected Tropical Diseases, 2014, 8, e2828. | 3.0 | 45 |
| 206 | The 2010 Cholera Outbreak in Haiti: How Science Solved a Controversy. PLoS Pathogens, 2014, 10, e1003967. | 4.7 | 99 |
| 207 | Oligotyping reveals community level habitat selection within the genus Vibrio. Frontiers in Microbiology, 2014, 5, 563. | 3.5 | 56 |
| 208 | The Population Structure of Vibrio cholerae from the Chandigarh Region of Northern India. PLoS Neglected Tropical Diseases, 2014, 8, e2981. | 3.0 | 21 |

| # | Article | IF | CITATIONS |
|-----|---|-----|-----------|
| 209 | Draft Whole-Genome Sequence of a New Variant of Vibrio cholerae O1 El Tor Strain Isolated from a Cholera Patient in Russia. Genome Announcements, 2014, 2, . | 0.8 | 0 |
| 210 | Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721. | 4.1 | 112 |
| 211 | Phylodynamic Analysis of Clinical and Environmental Vibrio cholerae Isolates from Haiti Reveals Diversification Driven by Positive Selection. MBio, 2014, 5, . | 4.1 | 45 |
| 212 | The Haiti cholera epidemic: from surveillance to action. Pathogens and Global Health, 2014, 108, 3-3. | 2.3 | 0 |
| 213 | CE. American Journal of Nursing, 2014, 114, 38. | 0.4 | 3 |
| 214 | Monitoring Water Sources for Environmental Reservoirs of Toxigenic <i>Vibrio cholerae</i> O1, Haiti. Emerging Infectious Diseases, 2014, 20, 356-63. | 4.3 | 47 |
| 215 | Genomic Epidemiology ofSalmonella entericaSerotype Enteritidis based on Population Structure of Prevalent Lineages. Emerging Infectious Diseases, 2014, 20, 1481-1489. | 4.3 | 87 |
| 216 | Cholera Disease. , 2014, , . | | 0 |
| 217 | Epidemiologic data and pathogen genome sequences: a powerful synergy for public health. Genome Biology, 2014, 15, 538. | 8.8 | 97 |
| 218 | Clinical detection and characterization of bacterial pathogens in the genomics era. Genome Medicine, 2014, 6, 114. | 8.2 | 111 |
| 221 | Pre-earthquake non-epidemic Vibrio cholerae in Haiti. Journal of Infection in Developing Countries, 2014, 8, 120-122. | 1.2 | 4 |
| 222 | Application of deep sequence technology in hepatology. Hepatology Research, 2014, 44, 141-148. | 3.4 | 2 |
| 223 | Widespread epidemic cholera caused by a restricted subset of Vibrio cholerae clones. Clinical Microbiology and Infection, 2014, 20, 373-379. | 6.0 | 33 |
| 224 | Evaluation of enrichment method for the detection of <i><scp>V</scp>ibrio cholerae </i> <scp>O</scp> 1 using a rapid dipstick test in <scp>B</scp> angladesh. Tropical Medicine and International Health, 2014, 19, 301-307. | 2.3 | 39 |
| 225 | Genome sequence and comparative analysis of a Vibrio cholerae O139 strain E306 isolated from a cholera case in China. Gut Pathogens, 2014, 6, 3. | 3.4 | 8 |
| 226 | Investigation of an Influenza A (H3N2) outbreak in evacuation centres following the Great East Japan earthquake, 2011. BMC Public Health, 2014, 14, 34. | 2.9 | 13 |
| 227 | Revolution of nephrology research by deep sequencing: ChIP-seq and RNA-seq. Kidney International, 2014, 85, 31-38. | 5.2 | 38 |
| 228 | Haitian Variant <i>tcpA</i> in Vibrio cholerae O1 El Tor Strains in Kolkata, India. Journal of Clinical Microbiology, 2014, 52, 1020-1021. | 3.9 | 24 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 229 | Genomic Science in Understanding Cholera Outbreaks and Evolution of Vibrio cholerae as a Human Pathogen. Current Topics in Microbiology and Immunology, 2014, 379, 211-229. | 1.1 | 21 |
| 230 | Meta'omic Analytic Techniques for Studying the Intestinal Microbiome. Gastroenterology, 2014, 146, 1437-1448.e1. | 1.3 | 137 |
| 232 | Dynamics in genome evolution of Vibrio cholerae. Infection, Genetics and Evolution, 2014, 23, 32-41. | 2.3 | 44 |
| 233 | Genomics, Personalized Medicine, and Pediatrics. Academic Pediatrics, 2014, 14, 14-22. | 2.0 | 29 |
| 234 | Nucleic acid sequencing for characterizing infectious and/or novel agents in complex samples. , 2014, , 3-53. | | 1 |
| 235 | The Clostridium difficile PCR ribotype 027 lineage: a pathogen on the move. Clinical Microbiology and Infection, 2014, 20, 396-404. | 6.0 | 95 |
| 236 | Importance of Cholera and Other Etiologies of Acute Diarrhea in Post-Earthquake Port-au-Prince, Haiti. American Journal of Tropical Medicine and Hygiene, 2014, 90, 511-517. | 1.4 | 15 |
| 237 | Second-Pandemic Strain of <i>Vibrio cholerae</i> from the Philadelphia Cholera Outbreak of 1849. New England Journal of Medicine, 2014, 370, 334-340. | 27.0 | 134 |
| 238 | Research on Neonatal Microbiomes: What Neonatologists Need to Know. Neonatology, 2014, 105, 14-24. | 2.0 | 12 |
| 239 | 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 |
| 241 | The Genomics of Xanthomonas oryzae. , 2014, , 127-150. | | 7 |
| 242 | Implementation of a Symptomatic Approach Leads to Increased Efficiency of a Cholera Treatment Unit. American Journal of Tropical Medicine and Hygiene, 2014, 91, 570-573. | 1.4 | 0 |
| 243 | Sensitive Deep-Sequencing-Based HIV-1 Genotyping Assay To Simultaneously Determine Susceptibility to Protease, Reverse Transcriptase, Integrase, and Maturation Inhibitors, as Well as HIV-1 Coreceptor Tropism. Antimicrobial Agents and Chemotherapy, 2014, 58, 2167-2185. | 3.2 | 61 |
| 244 | Haitian variant ctxB producing Vibrio cholerae OI with reduced susceptibility to ciprofloxacin is persistent in Yavatmal, Maharashtra, India, after causing a cholera outbreak. Clinical Microbiology and Infection, 2014, 20, O292-O293. | 6.0 | 26 |
| 245 | Recombination drives genome evolution in outbreak-related Legionella pneumophila isolates. Nature Genetics, 2014, 46, 1205-1211. | 21.4 | 76 |
| 246 | Genome analysis of NDM-1 producing <i>Morganella morganii</i> clinical isolate. Expert Review of Anti-Infective Therapy, 2014, 12, 1297-1305. | 4.4 | 34 |
| 247 | Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. BMC Bioinformatics, 2014, 15, 262. | 2.6 | 55 |
| 248 | Cholera outbreaks (2012) in three districts of Nepal reveal clonal transmission of multi-drug resistant Vibrio choleraeO1. BMC Infectious Diseases, 2014, 14, 392. | 2.9 | 36 |

| # | ARTICLE | IF | Citations |
|-----|---|-----|-----------|
| 249 | Validation of high throughput sequencing and microbial forensics applications. Investigative Genetics, 2014, 5, 9. | 3.3 | 59 |
| 250 | A retrospective macrorestrictive analysis of Vibrio cholerae eltor strains isolated under epidemic complications in the Russian Far East. Molecular Genetics, Microbiology and Virology, 2014, 29, 77-85. | 0.3 | 0 |
| 251 | Omics approaches in food safety: fulfilling the promise?. Trends in Microbiology, 2014, 22, 275-281. | 7.7 | 103 |
| 252 | Cholera Outbreaks in the El Tor Biotype Era and the Impact of the New El Tor Variants. Current Topics in Microbiology and Immunology, 2014, 379, 17-47. | 1.1 | 37 |
| 253 | Proteomic analysis of <i>Vibrio cholerae</i> outer membrane vesicles. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1548-56. | 7.1 | 141 |
| 255 | Biology of Three ICE Families: SXT/R391, ICE <i>Bs1</i> , and ICE <i>St1</i> /ICE <i>St3</i> . Microbiology Spectrum, 2014, 2, . | 3.0 | 62 |
| 256 | Evolutionary consequences of intra-patient phage predation on microbial populations. ELife, 2014, 3, e03497. | 6.0 | 114 |
| 258 | Surveying Recent Themes in Translational Bioinformatics: Big Data in EHRs, Omics for Drugs, and Personal Genomics. Yearbook of Medical Informatics, 2014, 23, 199-205. | 1.0 | 18 |
| 259 | â€~Jistis ak Reparasyon pou Tout Viktim Kolera MINUSTAH': The United Nations and the Right to Health in Haiti. Leiden Journal of International Law, 2015, 28, 507-527. | 0.2 | 10 |
| 260 | Technical and Software Advances in Bacterial Pathogen Typing. Methods in Microbiology, 2015, , 289-327. | 0.8 | 2 |
| 261 | Genetics of Natural Competence in <i>Vibrio cholerae</i> and other Vibrios. Microbiology Spectrum, 2015, 3, . | 3.0 | 35 |
| 262 | Ebola in the context of conflict affected states and health systems: case studies of Northern Uganda and Sierra Leone. Conflict and Health, 2015, 9, 23. | 2.7 | 39 |
| 263 | Microbial Forensicsâ~†. , 2015, , . | | 3 |
| 264 | Outbreak Breakthrough: Using Whole-Genome Sequencing to Control Hospital Infection. Environmental Health Perspectives, 2015, 123, A281-6. | 6.0 | 3 |
| 265 | The Application of Metagenomic Approaches in the Management of Infectious Diseases. Tropical Medicine & Surgery, 2015, 03, . | 0.1 | 2 |
| 266 | Biology of Three ICE Families: SXT/R391, ICEBs1, and ICESt1/ICESt3. , 2015, , 289-309. | | 1 |
| 267 | Emerging and Reemerging Infectious Disease Threats. , 2015, , 158-177.e6. | | 17 |
| 268 | Molecular tools in understanding the evolution of Vibrio cholerae. Frontiers in Microbiology, 2015, 6, 1040. | 3.5 | 25 |

| # | Article | IF | Citations |
|---------|--|------|-----------|
| 269 | Minimizing the Risk of Disease Transmission in Emergency Settings: Novel In Situ Physico-Chemical Disinfection of Pathogen-Laden Hospital Wastewaters. PLoS Neglected Tropical Diseases, 2015, 9, e0003776. | 3.0 | 18 |
| 270 | Rare Strain of <i>Vibrio cholerae</i> Septicemia in a Patient with Multiple Myeloma. Case Reports in Critical Care, 2015, 2015, 1-4. | 0.4 | 2 |
| 271 | Protest in the time of cholera: disease and the metaphors of health and politics. Canadian Journal of Latin American and Caribbean Studies, 2015, 40, 63-80. | 0.1 | 3 |
| 272 | Low detection ofVibrio choleraecarriage in healthcare workers returning to 12 Latin American countries from Haiti. Epidemiology and Infection, 2015, 143, 1016-1019. | 2.1 | 5 |
| 273 | Vibriosis. Clinics in Laboratory Medicine, 2015, 35, 273-288. | 1.4 | 77 |
| 274 | The Cpx System Regulates Virulence Gene Expression in Vibrio cholerae. Infection and Immunity, 2015, 83, 2396-2408. | 2.2 | 32 |
| 275 | Hybrid Vibrio cholerae El Tor Lacking SXT Identified as the Cause of a Cholera Outbreak in the Philippines. MBio, 2015, 6, . | 4.1 | 11 |
| 276 | Widening participation would be key in enhancing bioinformatics and genomics research in Africa. Applied & Translational Genomics, 2015, 6, 35-41. | 2.1 | 4 |
| 277 | Making the Leap from Research Laboratory to Clinic: Challenges and Opportunities for Next-Generation Sequencing in Infectious Disease Diagnostics. MBio, 2015, 6, e01888-15. | 4.1 | 270 |
| 278 | Vibrio cholerae. , 2015, , 1079-1098. | | 1 |
| 279 | A Case of Cholera Imported From Haiti. Clinical Microbiology Newsletter, 2015, 37, 22-23. | 0.7 | 2 |
| 280 | Ancient pathogen genomics: insights into timing and adaptation. Journal of Human Evolution, 2015, 79, 137-149. | 2.6 | 60 |
| 281 | On the predictive ability of mechanistic models for the Haitian cholera epidemic. Journal of the Royal Society Interface, 2015, 12, 20140840. | 3.4 | 25 |
| 282 | One chromosome, one contig: complete microbial genomes from long-read sequencing and assembly. Current Opinion in Microbiology, 2015, 23, 110-120. | 5.1 | 413 |
| 283 | Characterization of Vibrio parahaemolyticus clinical strains from Maryland (2012ââ,¬â€œ2013) and comparisons to a locally and globally diverse V. parahaemolyticus strains by whole-genome sequence analysis. Frontiers in Microbiology, 2015, 6, 125. | 3.5 | 40 |
| 284 | Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. Nature Communications, 2015, 6, 7438. | 12.8 | 82 |
| 285 | Transfer activation of SXT/R391 integrative and conjugative elements: unraveling the SetCD regulon. Nucleic Acids Research, 2015, 43, 2045-2056. | 14.5 | 48 |
| 286 | The Role of China in the Global Spread of the Current Cholera Pandemic. PLoS Genetics, 2015, 11, e1005072. | 3.5 | 73 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 287 | Geographical Perspectives on Epidemic Transmission of Cholera in Haiti, October 2010 Through March 2013. Annals of the American Association of Geographers, 2015, 105, 665-683. | 3.0 | 4 |
| 288 | Chloroplast genome of Aconitum barbatum var. puberulum (Ranunculaceae) derived from CCS reads using the PacBio RS platform. Frontiers in Plant Science, 2015, 6, 42. | 3.6 | 59 |
| 289 | Cancer modelling in the NGS era – Part I: Emerging technology and initial modelling. Critical Reviews in Oncology/Hematology, 2015, 96, 274-307. | 4.4 | 9 |
| 290 | Tracking a hospital outbreak of KPC-producing ST11 Klebsiella pneumoniae with whole genome sequencing. Clinical Microbiology and Infection, 2015, 21, 1001-1007. | 6.0 | 48 |
| 291 | Genomic Applications in the Clinical Management of Infectious Diseases. , 2015, , 581-604. | | 0 |
| 292 | Whole-genome sequence comparisons reveal the evolution of Vibrio cholerae O1. Trends in Microbiology, 2015, 23, 479-489. | 7.7 | 75 |
| 293 | Whole-Genome Sequencing in Outbreak Analysis. Clinical Microbiology Reviews, 2015, 28, 541-563. | 13.6 | 200 |
| 294 | The role of pathogen genomics in assessing disease transmission. BMJ, The, 2015, 350, h1314-h1314. | 6.0 | 59 |
| 295 | Whole genome sequencing in clinical and public health microbiology. Pathology, 2015, 47, 199-210. | 0.6 | 226 |
| 296 | Rapid identification of pathogens using molecular techniques. Pathology, 2015, 47, 191-198. | 0.6 | 16 |
| 297 | A globally distributed mobile genetic element inhibits natural transformation of <i>Vibrio cholerae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10485-10490. | 7.1 | 58 |
| 298 | How Next-Generation Sequencing and Multiscale Data Analysis Will Transform Infectious Disease Management. Clinical Infectious Diseases, 2015, 61, civ670. | 5.8 | 32 |
| 299 | Whole-genome sequencing targets drug-resistant bacterial infections. Human Genomics, 2015, 9, 19. | 2.9 | 86 |
| 300 | Evaluation of a field appropriate membrane filtration method for the detection of Vibrio cholerae for the measurement of biosand filter performance in the Artibonite Valley, Haiti. Environmental Monitoring and Assessment, 2015, 187, 484. | 2.7 | 4 |
| 301 | Characterization of Foodborne Outbreaks of Salmonella enterica Serovar Enteritidis with Whole-Genome Sequencing Single Nucleotide Polymorphism-Based Analysis for Surveillance and Outbreak Detection. Journal of Clinical Microbiology, 2015, 53, 3334-3340. | 3.9 | 123 |
| 302 | First, Don't Be a Tourist. Annals of Emergency Medicine, 2015, 66, A17-A21. | 0.6 | 2 |
| 303 | The application of pulsed field gel electrophoresis for molecular typing of causative agents of especially dangerous infections. Molecular Genetics, Microbiology and Virology, 2015, 30, 141-147. | 0.3 | 0 |
| 304 | Twenty years of bacterial genome sequencing. Nature Reviews Microbiology, 2015, 13, 787-794. | 28.6 | 246 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 305 | Comparative Analysis of Subtyping Methods against a Whole-Genome-Sequencing Standard for Salmonella enterica Serotype Enteritidis. Journal of Clinical Microbiology, 2015, 53, 212-218. | 3.9 | 112 |
| 306 | A Phylogenetic Perspective on Molecular Epidemiology. , 2015, , 517-536. | | 11 |
| 307 | The application of genomics to tracing bacterial pathogen transmission. Current Opinion in Microbiology, 2015, 23, 62-67. | 5.1 | 84 |
| 308 | Large-scale genomic sequencing of extraintestinal pathogenic <i>Escherichia coli</i> strains. Genome Research, 2015, 25, 119-128. | 5.5 | 158 |
| 309 | Genomic Applications in Pathology. , 2015, , . | | 1 |
| 310 | On the probability of extinction of the Haiti cholera epidemic. Stochastic Environmental Research and Risk Assessment, 2016, 30, 2043-2055. | 4.0 | 41 |
| 311 | Staying Alive: Vibrio cholerae's Cycle of Environmental Survival, Transmission, and Dissemination. , 2016, , 593-633. | | 5 |
| 312 | Molecular Epidemiology and Antibiotic Susceptibility of Vibrio cholerae Associated with a Large Cholera Outbreak in Ghana in 2014. PLoS Neglected Tropical Diseases, 2016, 10, e0004751. | 3.0 | 41 |
| 313 | Emergence of Tetracycline Resistant <i>Vibrio cholerae</i> O1 Biotype El Tor Serotype Ogawa with Classical <i>ctxB</i> Gene from a Cholera Outbreak in Odisha, Eastern India. Journal of Pathogens, 2016, 2016, 1-6. | 1.4 | 23 |
| 314 | MICADo – Looking for Mutations in Targeted PacBio Cancer Data: An Alignment-Free Method. Frontiers in Genetics, 2016, 7, 214. | 2.3 | 4 |
| 315 | Metataxonomic and Metagenomic Approaches vs. Culture-Based Techniques for Clinical Pathology. Frontiers in Microbiology, 2016, 7, 484. | 3.5 | 78 |
| 316 | Mapping to Support Fine Scale Epidemiological Cholera Investigations: A Case Study of Spatial Video in Haiti. International Journal of Environmental Research and Public Health, 2016, 13, 187. | 2.6 | 13 |
| 317 | The Lake Chad Basin, an Isolated and Persistent Reservoir of Vibrio cholerae O1: A Genomic Insight into the Outbreak in Cameroon, 2010. PLoS ONE, 2016, 11, e0155691. | 2.5 | 25 |
| 318 | Practical Approaches for Detecting Selection in Microbial Genomes. PLoS Computational Biology, 2016, 12, e1004739. | 3.2 | 21 |
| 319 | Major Shift of Toxigenic V. cholerae O1 from Ogawa to Inaba Serotype Isolated from Clinical and Environmental Samples in Haiti. PLoS Neglected Tropical Diseases, 2016, 10, e0005045. | 3.0 | 25 |
| 320 | The Transmission and Antibiotic Resistance Variation in a Multiple Drug Resistance Clade of Vibrio cholerae Circulating in Multiple Countries in Asia. PLoS ONE, 2016, 11, e0149742. | 2.5 | 18 |
| 321 | Whole-Genome Sequencing for the Investigation of a Hospital Outbreak of MRSA in China. PLoS ONE, 2016, 11, e0149844. | 2.5 | 46 |
| 324 | Targeted Metabolomics: The Next Generation of Clinical Chemistry!. Translational Bioinformatics, 2016, , 175-211. | 0.0 | 2 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 325 | A Nonautochthonous U.S. Strain of Vibrio parahaemolyticus Isolated from Chesapeake Bay Oysters Caused the Outbreak in Maryland in 2010. Applied and Environmental Microbiology, 2016, 82, 3208-3216. | 3.1 | 28 |
| 326 | Catalytic Transformations of Biomass-Derived Acids into Advanced Biofuels. , 2016, , 241-260. | | 6 |
| 327 | Genomic Analysis of Bacterial Outbreaks. , 2016, , 203-232. | | 0 |
| 328 | Genomic analysis of the multi-host pathogen Erysipelothrix rhusiopathiae reveals extensive recombination as well as the existence of three generalist clades with wide geographic distribution. BMC Genomics, 2016, 17, 461. | 2.8 | 49 |
| 330 | Navigating Microbiological Food Safety in the Era of Whole-Genome Sequencing. Clinical Microbiology Reviews, 2016, 29, 837-857. | 13.6 | 130 |
| 331 | Considerations in centralizing whole genome sequencing for microbiology in a public health setting. Expert Review of Molecular Diagnostics, 2016, 16, 619-621. | 3.1 | 9 |
| 332 | Commentary: Next-Generation Epidemiology: Using Real-Time Core Genome Multilocus Sequence Typing To Support Infection Control Policy. Journal of Clinical Microbiology, 2016, 54, 2850-2853. | 3.9 | 34 |
| 333 | Construction of a draft reference transcripts of onion (Allium cepa) using long-read sequencing. Plant Biotechnology Reports, 2016, 10, 383-390. | 1.5 | 18 |
| 334 | Rethinking cholera pathogenesis- No longer all in the same "camp― Virulence, 2016, 7, 751-753. | 4.4 | 3 |
| 335 | Quantum changes in <i>Helicobacter pylori</i> gene expression accompany host-adaptation. DNA Research, 2017, 24, dsw046. | 3.4 | 8 |
| 337 | Staying Alive: <i>Vibrio cholerae</i> 's Cycle of Environmental Survival, Transmission, and Dissemination. Microbiology Spectrum, 2016, 4, . | 3.0 | 107 |
| 338 | Comparison of inferred relatedness based on multilocus variable-number tandem-repeat analysis and whole genome sequencing ofVibrio choleraeO1. FEMS Microbiology Letters, 2016, 363, fnw116. | 1.8 | 19 |
| 339 | Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. ISME Journal, 2016, 10, 2817-2830. | 9.8 | 47 |
| 340 | Phenotypic Analysis Reveals that the 2010 Haiti Cholera Epidemic Is Linked to a Hypervirulent Strain. Infection and Immunity, 2016, 84, 2473-2481. | 2.2 | 48 |
| 341 | Analysis of single nucleic acid molecules in micro- and nano-fluidics. Lab on A Chip, 2016, 16, 790-811. | 6.0 | 29 |
| 342 | Molecular epidemiology of Vibrio cholerae associated with flood in Brahamputra River valley, Assam, India. Infection, Genetics and Evolution, 2016, 40, 352-356. | 2.3 | 29 |
| 343 | Phylogenetic Diversity of Vibrio cholerae Associated with Endemic Cholera in Mexico from 1991 to 2008. MBio, 2016, 7, e02160. | 4.1 | 24 |
| 344 | Genome mining of astaxanthin biosynthetic genes from <i>Sphingomonas </i> sp. ATCC 55669 for heterologous overproduction in <i>Escherichia coli</i> . Biotechnology Journal, 2016, 11, 228-237. | 3.5 | 56 |

ARTICLE IF CITATIONS Expansion of Microbial Forensics. Journal of Clinical Microbiology, 2016, 54, 1964-1974. 3.9 72 345 Systems Immunology., 2016, , 3-44. 346 Functional Analysis of Bacteriophage Immunity through a Type I-E CRISPR-Cas System in Vibrio cholerae 347 2.2 83 and Its Application in Bacteriophage Genome Engineering. Journal of Bacteriology, 2016, 198, 578-590. Comparison of Whole-Genome Sequencing and Molecular-Epidemiological Techniques for <i>Clostridium difficile </i>Strain Typing. Journal of the Pediatric Infectious Diseases Society, 2016, 348 5, 329-332. Tracing Origins of the<i>Salmonella</i>Bareilly Strain Causing a Food-borne Outbreak in the United 349 4.0 145 States. Journal of Infectious Diseases, 2016, 213, 502-508. Transcriptomics and Gene Regulation. Translational Bioinformatics, 2016, , . Application of a paper based device containing a new culture medium to detect Vibrio cholerae in 351 1.6 10 water samples collected in Haiti. Journal of Microbiological Methods, 2017, 133, 23-31. Characterization of Vibrio cholerae isolates from 1976 to 2013 in Shandong Province, China. Brazilian 2.0 10 Journal of Microbiology, 2017, 48, 173-179. Challenges and opportunities for wholeâ€genome sequencing–based surveillance of antibiotic 353 3.8 87 resistance. Annals of the New York Academy of Sciences, 2017, 1388, 108-120. Single-Molecule Sequencing of the <i>Drosophila serrata</i> Genome. G3: Genes, Genomes, Genetics, 1.8 24 2017, 7, 781-788. Pandemics, pathogenicity and changing molecular epidemiology of cholera in the era of global 356 3.8 86 warming. Annals of Clinical Microbiology and Antimicrobials, 2017, 16, 10. Toward biotechnology in space: High-throughput instruments for in situ biological research beyond 357 11.7 Earth. Biotechnology Advances, 2017, 35, 905-932. Forensic Approaches to Detect Possible Agents of Bioterror. Microbiology Spectrum, 2017, 5, . 358 3.0 5 Evolution of Drug-resistant Acinetobacter baumannii After DCD Renal Transplantation. Scientific 3.3 Reports, 2017, 7, 1968. Defining a Core Genome Multilocus Sequence Typing Scheme for the Global Epidemiology of Vibrio 360 49 3.9 parahaemolyticus. Journal of Clinical Microbiology, 2017, 55, 1682-1697. Cholera. Lancet, The, 2017, 390, 1539-1549. 314 Emerging Concepts and Technologies for the Discovery of Microorganisms Involved in Human Disease. 362 22.4 13 Annual Review of Pathology: Mechanisms of Disease, 2017, 12, 217-244. Comparative genome analyses of Mycobacterium avium reveal genomic features of its subspecies and 3.3 strains that cause progression of pulmonary disease. Scientific Reports, 2017, 7, 39750.

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 364 | New Laboratory Tools for Emerging Bacterial Challenges. Clinical Infectious Diseases, 2017, 65, S39-S49. | 5.8 | 3 |
| 365 | Spatial disease dynamics of free-living pathogens under pathogen predation. Scientific Reports, 2017, 7, 7729. | 3.3 | 4 |
| 366 | Molecular-genetic properties of Vibrio cholerae El Tor strains circulating in Africa. Molecular Genetics, Microbiology and Virology, 2017, 32, 12-20. | 0.3 | 1 |
| 367 | Insights into the Draft Genome Sequence of a Haitian Variant Vibrio cholerae Strain Isolated from a Clinical Setting in Kerala, South India. Genome Announcements, 2017, 5, . | 0.8 | 2 |
| 368 | Great cormorants (Phalacrocorax carbo) as potential vectors for the dispersal of Vibrio cholerae. Scientific Reports, 2017, 7, 7973. | 3.3 | 38 |
| 369 | Post-earthquake Zika virus surge: Disaster and public health threat amid climatic conduciveness. Scientific Reports, 2017, 7, 15408. | 3.3 | 18 |
| 370 | Integrated view of <i>Vibrio cholerae</i> in the Americas. Science, 2017, 358, 789-793. | 12.6 | 128 |
| 371 | Characterization of Vibrio cholerae O1 strains that trace the origin of Haitian-like genetic traits. Infection, Genetics and Evolution, 2017, 54, 47-53. | 2.3 | 8 |
| 372 | Increasing the reach of forensic genetics with massively parallel sequencing. Forensic Science, Medicine, and Pathology, 2017, 13, 342-349. | 1.4 | 25 |
| 373 | Survey of (Meta)genomic Approaches for Understanding Microbial Community Dynamics. Indian Journal of Microbiology, 2017, 57, 23-38. | 2.7 | 21 |
| 374 | Rapid dipstick detection of <i>Vibrio cholerae</i> in household stored and municipal water in Dhaka, Bangladesh: CHoBI7 trial. Tropical Medicine and International Health, 2017, 22, 205-209. | 2.3 | 6 |
| 375 | Advances in Diagnostic Microbiology. , 2017, , 1386-1389.e1. | | 0 |
| 376 | Curved and Spiral Bacilli. , 2017, , 1600-1610.e2. | | 2 |
| 377 | Haitian cholera outbreak—United Nations admits involvement. Journal of Infection and Public Health, 2017, 10, 483-484. | 4.1 | 2 |
| 378 | Geography of Infectious Diseases. , 2017, , 938-947.e1. | | 3 |
| 379 | Analyzing the response to epidemics: concept of evidence-based Haddon matrix. Journal of Humanitarian Logistics and Supply Chain Management, 2017, 7, 266-283. | 2.8 | 20 |
| 380 | Public Goods and Donor Priorities: The Political Economy of Development Aid for Infectious Disease Control. Foreign Policy Analysis, 2017, 13, 986-1002. | 1.0 | 5 |
| 381 | Guinea pig complement potently measures vibriocidal activity of human antibodies in response to cholera vaccines. Journal of Microbiology, 2017, 55, 973-978. | 2.8 | 3 |

| # | Article | IF | Citations |
|-----|--|------|-----------|
| 382 | Computational Methods in Microbial Population Genomics. Population Genomics, 2017, , 3-29. | 0.5 | 2 |
| 383 | International Standards for Genomes, Transcriptomes, and Metagenomes. Journal of Biomolecular Techniques, 2017, 28, 8-18. | 1.5 | 33 |
| 384 | 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 |
| 385 | Fish as Hosts of Vibrio cholerae. Frontiers in Microbiology, 2017, 8, 282. | 3.5 | 108 |
| 386 | The Importance of Bacterial Culture to Food Microbiology in the Age of Genomics. Frontiers in Microbiology, 2017, 8, 777. | 3.5 | 38 |
| 387 | The Public Health Impact of a Publically Available, Environmental Database of Microbial Genomes. Frontiers in Microbiology, 2017, 8, 808. | 3.5 | 48 |
| 388 | Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. Frontiers in Microbiology, 2017, 8, 909. | 3.5 | 87 |
| 389 | 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 |
| 390 | Characterization and Genetic Variation of Vibrio cholerae Isolated from Clinical and Environmental Sources in Thailand. PLoS ONE, 2017, 12, e0169324. | 2.5 | 88 |
| 391 | Forensic genetics and genomics: Much more than just a human affair. PLoS Genetics, 2017, 13, e1006960. | 3.5 | 71 |
| 392 | Environmental Suitability of <i>Vibrio</i> Infections in a Warming Climate: An Early Warning System. Environmental Health Perspectives, 2017, 125, 107004. | 6.0 | 87 |
| 393 | Considering the Potential Application of Whole Genome Sequencing to Gonorrhea Prevention and Control. Sexually Transmitted Diseases, 2018, 45, e29-e32. | 1.7 | 0 |
| 394 | Phylogeny of dermatophytes with genomic character evaluation of clinically distinct <i>Trichophyton rubrum</i> and <i>T.Âviolaceum</i> . Studies in Mycology, 2018, 89, 153-175. | 7.2 | 50 |
| 395 | Comparative genomics of Vibrio cholerae El Tor strains isolated at epidemic complications in Siberia and at the Far East. Infection, Genetics and Evolution, 2018, 60, 80-88. | 2.3 | 11 |
| 396 | Tracking Vibrio cholerae Cell-Cell Interactions during Infection Reveals Bacterial Population Dynamics within Intestinal Microenvironments. Cell Host and Microbe, 2018, 23, 274-281.e2. | 11.0 | 40 |
| 397 | Pseudomonas aeruginosa intensive care unit outbreak: winnowing of transmissions with molecular and genomic typing. Journal of Hospital Infection, 2018, 98, 282-288. | 2.9 | 41 |
| 398 | Antagonism toward the intestinal microbiota and its effect on <i>Vibrio cholerae</i> virulence. Science, 2018, 359, 210-213. | 12.6 | 153 |
| 399 | Transforming bacterial disease surveillance and investigation using whole-genome sequence to probe the trace. Frontiers of Medicine, 2018, 12, 23-33. | 3.4 | 13 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 400 | Microbial sequence typing in the genomic era. Infection, Genetics and Evolution, 2018, 63, 346-359. | 2.3 | 50 |
| 401 | Whole Genome Sequencing for Outbreak Investigation. , 2018, , 187-196. | | Ο |
| 402 | Activation of Vibrio cholerae quorum sensing promotes survival of an arthropod host. Nature Microbiology, 2018, 3, 243-252. | 13.3 | 46 |
| 403 | Persistent diarrhoea in a 5-month-old baby carrying Vibrio cholerae nonO1/nonO139 producing Haitian cholera toxin. New Microbes and New Infections, 2018, 21, 72-74. | 1.6 | 7 |
| 404 | Bacteriophages in the control of pathogenic vibrios. Electronic Journal of Biotechnology, 2018, 31, 24-33. | 2.2 | 39 |
| 405 | Tracking a serial killer: Integrating phylogenetic relationships, epidemiology, and geography for two invasive meningococcal disease outbreaks. PLoS ONE, 2018, 13, e0202615. | 2.5 | 8 |
| 406 | The Impact of National Militaries on Global Health. , 2018, , . | | 0 |
| 407 | Near-Real-Time Detection of Pulse Oximeter PPG Peaks Using Wavelet Decomposition. IFAC-PapersOnLine, 2018, 51, 146-151. | 0.9 | 7 |
| 408 | Quantitative Approach in Clinical Microbiology: A Paradigm Shift Toward Culture-Free Methods. , 2018, , 599-615. | | 1 |
| 409 | Routine detection of carbapenem-resistant gram-negative bacilli in clinical laboratories. Journal of King Abdulaziz University, Islamic Economics, 2018, 39, 861-872. | 1.1 | 19 |
| 410 | Enterohemorrhagic E. coli (EHEC)—Secreted Serine Protease EspP Stimulates Electrogenic Ion Transport in Human Colonoid Monolayers. Toxins, 2018, 10, 351. | 3.4 | 16 |
| 411 | Methicillin-Resistant Staphylococcus aureus: Molecular Characterization, Evolution, and Epidemiology. Clinical Microbiology Reviews, 2018, 31, . | 13.6 | 872 |
| 412 | A Robust Method of Peak Detection in Noisy PPG Signals Using a Structure of IIR Filters. , 2018, , . | | 2 |
| 413 | John Snow, Cholera, the Broad Street Pump; Waterborne Diseases Then and Now. , 2018, , 77-99. | | 63 |
| 414 | Mutation Landscape of Base Substitutions, Duplications, and Deletions in the Representative Current Cholera Pandemic Strain. Genome Biology and Evolution, 2018, 10, 2072-2085. | 2.5 | 7 |
| 415 | Human Mobility and the Global Spread of Infectious Diseases: A Focus on Air Travel. Trends in Parasitology, 2018, 34, 772-783. | 3.3 | 176 |
| 416 | Graphene-based nanopore approaches for DNA sequencing: A literature review. Biosensors and Bioelectronics, 2018, 119, 191-203. | 10.1 | 63 |
| 417 | Environmental Surveillance of Vibrio cholerae O1/O139 in the Five African Great Lakes and Other Major Surface Water Sources in Uganda. Frontiers in Microbiology, 2018, 9, 1560. | 3.5 | 30 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 418 | HIV-1 subtype diversity, transmitted drug resistance and phylogenetics in Australia. Future Virology, 2018, 13, 575-584. | 1.8 | 4 |
| 419 | Vibrio spp. infections. Nature Reviews Disease Primers, 2018, 4, 1-19. | 30.5 | 572 |
| 420 | Planning for globally coordinated cessation of bivalent oral poliovirus vaccine: risks of non-synchronous cessation and unauthorized oral poliovirus vaccine use. BMC Infectious Diseases, 2018, 18, 165. | 2.9 | 8 |
| 421 | A live vaccine rapidly protects against cholera in an infant rabbit model. Science Translational Medicine, 2018, 10, . | 12.4 | 55 |
| 422 | GM1 ganglioside-independent intoxication by Cholera toxin. PLoS Pathogens, 2018, 14, e1006862. | 4.7 | 57 |
| 423 | Vibrio cholerae accessory colonisation factor AcfC: a chemotactic protein with a role in hyperinfectivity. Scientific Reports, 2018, 8, 8390. | 3.3 | 13 |
| 424 | Accumulating evidence suggests that some waterbird species are potential vectors of Vibrio cholerae. PLoS Pathogens, 2019, 15, e1007814. | 4.7 | 22 |
| 425 | Whole-Genome Sequencing Reveals a Prolonged and Persistent Intrahospital Transmission of Corynebacterium striatum, an Emerging Multidrug-Resistant Pathogen. Journal of Clinical Microbiology, 2019, 57, . | 3.9 | 23 |
| 426 | Rapid metagenomics analysis of EMS vehicles for monitoring pathogen load using nanopore DNA sequencing. PLoS ONE, 2019, 14, e0219961. | 2.5 | 9 |
| 427 | Revisiting the Global Epidemiology of Cholera in Conjunction With the Genomics of Vibrio cholerae. Frontiers in Public Health, 2019, 7, 203. | 2.7 | 56 |
| 428 | Forensic, investigative and diagnostic microbiology: similar technologies but different priorities. Future Microbiology, 2019, 14, 553-558. | 2.0 | 5 |
| 429 | Next Generation Sequencing and Bioinformatics Methodologies for Infectious Disease Research and Public Health: Approaches, Applications, and Considerations for Development of Laboratory Capacity. Journal of Infectious Diseases, 2020, 221, S292-S307. | 4.0 | 64 |
| 430 | Between a Rock and a Hard Place – Immunities of the United Nations and Human Rights. , 2019, , 579-594. | | 1 |
| 431 | Comparative Genomic Analysis of the 2016 Vibrio cholerae Outbreak in South Korea. Frontiers in Public Health, 2019, 7, 228. | 2.7 | 10 |
| 432 | Novel Insights Into the Spread of Enteric Pathogens Using Genomics. Journal of Infectious Diseases, 2019, 221, S319-S330. | 4.0 | 2 |
| 433 | DNA Sequencing Technologies. ACM Computing Surveys, 2020, 52, 1-30. | 23.0 | 8 |
| 434 | Complete Genome Sequence and Comparative Analysis of Synechococcus sp. CS-601 (SynAce01), a Cold-Adapted Cyanobacterium from an Oligotrophic Antarctic Habitat. International Journal of Molecular Sciences, 2019, 20, 152. | 4.1 | 27 |
| 435 | Recent mixing of <i>Vibrio parahaemolyticus</i> populations. ISME Journal, 2019, 13, 2578-2588. | 9.8 | 41 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 436 | Whole genome sequencing to characterize shiga toxin-producing Escherichia coli O26 in a public health setting. Journal of Infection and Public Health, 2019, 12, 884-889. | 4.1 | 14 |
| 437 | Oral immunization with a probiotic cholera vaccine induces broad protective immunity against Vibrio cholerae colonization and disease in mice. PLoS Neglected Tropical Diseases, 2019, 13, e0007417. | 3.0 | 23 |
| 438 | Application of digital PCR and next generation sequencing in the etiology investigation of a foodborne disease outbreak caused by Vibrio parahaemolyticus. Food Microbiology, 2019, 84, 103233. | 4.2 | 12 |
| 439 | Functional characterization of a subtilisin-like serine protease from Vibrio cholerae. Journal of Biological Chemistry, 2019, 294, 9888-9900. | 3.4 | 14 |
| 440 | Expanding dynamics of the virulence-related gene variations in the toxigenic Vibrio cholerae serogroup O1. BMC Genomics, 2019, 20, 360. | 2.8 | 9 |
| 441 | Integrated Detection of Copy Number Variation Based on the Assembly of NGS and 3GS Data. Lecture Notes in Computer Science, 2019, , 251-260. | 1.3 | 0 |
| 442 | Molecular Adaptations and Antibiotic Resistance in <i>Vibrio cholerae</i> : A Communal Challenge. Microbial Drug Resistance, 2019, 25, 1012-1022. | 2.0 | 17 |
| 443 | Emerging Challenges and Opportunities in Infectious Disease Epidemiology. American Journal of Epidemiology, 2019, 188, 873-882. | 3.4 | 14 |
| 444 | Emerging infectious diseases and biological invasions: a call for a One Health collaboration in science and management. Royal Society Open Science, 2019, 6, 181577. | 2.4 | 82 |
| 445 | High quality reference genomes for toxigenic and non-toxigenic Vibrio cholerae serogroup O139. Scientific Reports, 2019, 9, 5865. | 3.3 | 13 |
| 446 | Unsupervised Learning Approach for Comparing Multiple Transposon Insertion Sequencing Studies. MSphere, 2019, 4, . | 2.9 | 12 |
| 447 | Haitian Variant Vibrio cholerae O1 Strains Manifest Higher Virulence in Animal Models. Frontiers in Microbiology, 2019, 10, 111. | 3.5 | 25 |
| 448 | Seasonal dynamics of <i>Chironomus transvaalensis</i> populations and the microbial community composition of their egg masses. FEMS Microbiology Letters, 2019, 366, . | 1.8 | 12 |
| 449 | The DAGs of war. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23880-23882. | 7.1 | 1 |
| 450 | Conversion of a recA-Mediated Non-toxigenic Vibrio cholerae O1 Strain to a Toxigenic Strain Using Chitin-Induced Transformation. Frontiers in Microbiology, 2019, 10, 2562. | 3.5 | 11 |
| 451 | Cholera in travellers: a systematic review. Journal of Travel Medicine, 2019, 26, . | 3.0 | 26 |
| 452 | <i>Vibrio Species</i> ., 0, , 347-388. | | 19 |
| 453 | Genomic insights into the 2016–2017 cholera epidemic in Yemen. Nature, 2019, 565, 230-233. | 27.8 | 129 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 454 | Vibrio cholerae LMWPTP-2 display unique surface charge and grooves around the active site: Indicative of distinctive substrate specificity and scope to design specific inhibitor. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 114-124. | 2.3 | 1 |
| 455 | Clonality and non-linearity drive facultative-cooperation allele diversity. ISME Journal, 2019, 13, 824-835. | 9.8 | 7 |
| 456 | Bacillus species at the Canberra Airport: A comparison of real-time polymerase chain reaction and massively parallel sequencing for identification. Forensic Science International, 2019, 295, 169-178. | 2.2 | 2 |
| 457 | Next-Generation Sequencing for Biodefense: Biothreat Detection, Forensics, and the Clinic. Clinical Chemistry, 2019, 65, 383-392. | 3.2 | 23 |
| 458 | Genomic epidemiology of multidrugâ€resistant Gramâ€negative organisms. Annals of the New York Academy of Sciences, 2019, 1435, 39-56. | 3.8 | 16 |
| 459 | The global dissemination of bacterial infections necessitates the study of reverse genomic epidemiology. Briefings in Bioinformatics, 2020, 21, 741-750. | 6.5 | 56 |
| 460 | Cholera and Other Vibrios. , 2020, , 486-491. | | 3 |
| 461 | Molecular epidemiology and intercontinental spread of cholera. Vaccine, 2020, 38, A46-A51. | 3.8 | 14 |
| 462 | Tabu Variable Neighborhood Search for Designing DNA Barcodes. IEEE Transactions on Nanobioscience, 2020, 19, 127-131. | 3.3 | 21 |
| 463 | Forensic public health. , 2020, , 105-122. | | 2 |
| 464 | Forensic human identification using skin microbiome genetic signatures. , 2020, , 155-169. | | 1 |
| 465 | Scientific testimonial standards for microbial forensic evidence. , 2020, , 339-360. | | 0 |
| 468 | Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic Vibrio cholerae. Nature Communications, 2020, 11, 4918. | 12.8 | 12 |
| 469 | Microbe hunting in the modern era: reflecting on a decade of microbial genomic epidemiology. Current Biology, 2020, 30, R1124-R1130. | 3.9 | 7 |
| 470 | Species. , 2020, , 47-113. | | 0 |
| 471 | Populations. , 2020, , 114-224. | | 0 |
| 472 | Waterborne Disease. , 2020, , 225-339. | | 0 |
| 473 | Afterthoughts and Outlook. , 2020, , 340-361. | | 0 |

| # | Article | IF | Citations |
|-----|---|-----|-----------|
| 476 | Transcriptional Silencing by TsrA in the Evolution of Pathogenic Vibrio cholerae Biotypes. MBio, 2020, 11, . | 4.1 | 8 |
| 477 | Changes in Microbiota Composition Along the Metamorphosis Developmental Stages of Chironomus transvaalensis. Frontiers in Microbiology, 2020, 11, 586678. | 3.5 | 12 |
| 478 | Emerging nanobiomaterials against bacterial infections in postantibiotic era. View, 2020, 1, 20200014. | 5.3 | 37 |
| 479 | Zebrafish Models for Pathogenic Vibrios. Journal of Bacteriology, 2020, 202, . | 2.2 | 17 |
| 481 | Virulence Pattern and Genomic Diversity of Vibrio cholerae O1 and O139 Strains Isolated From Clinical and Environmental Sources in India. Frontiers in Microbiology, 2020, 11, 1838. | 3.5 | 2 |
| 482 | Comparative genomics in infectious disease. Current Opinion in Microbiology, 2020, 53, 61-70. | 5.1 | 11 |
| 483 | Cholera Toxin Production in Vibrio cholerae O1 El Tor Biotype Strains in Single-Phase Culture. Frontiers in Microbiology, 2020, 11, 825. | 3.5 | 7 |
| 484 | Transient Intestinal Colonization by a Live-Attenuated Oral Cholera Vaccine Induces Protective Immune Responses in Streptomycin-Treated Mice. Journal of Bacteriology, 2020, 202, . | 2.2 | 7 |
| 485 | The Impact of Climate Change on Cholera: A Review on the Global Status and Future Challenges. Atmosphere, 2020, 11, 449. | 2.3 | 19 |
| 486 | Closing Clostridium botulinum Group I Genomes Using a Combination of Short- and Long-Reads. Frontiers in Microbiology, 2020, 11, 239. | 3.5 | 10 |
| 487 | Genomic epidemiology of Vibrio cholerae reveals the regional and global spread of two epidemic non-toxigenic lineages. PLoS Neglected Tropical Diseases, 2020, 14, e0008046. | 3.0 | 16 |
| 488 | Alterations in glucose metabolism in Vibrio cholerae serogroup O1 El Tor biotype strains. Scientific Reports, 2020, 10, 308. | 3.3 | 16 |
| 489 | The Pangenome. , 2020, , . | | 32 |
| 490 | Comparative core/pan genome analysis of Vibrio cholerae isolates from Pakistan. Infection, Genetics and Evolution, 2020, 82, 104316. | 2.3 | 6 |
| 491 | Whole genome sequencing of Nontuberculous Mycobacterium (NTM) isolates from sputum specimens of co-habiting patients with NTM pulmonary disease and NTM isolates from their environment. BMC Genomics, 2020, 21, 322. | 2.8 | 27 |
| 492 | A Point Mutation in <i>carR</i> Is Involved in the Emergence of Polymyxin B-Sensitive Vibrio cholerae O1 El Tor Biotype by Influencing Gene Transcription. Infection and Immunity, 2020, 88, . | 2.2 | 11 |
| 493 | Deciphering the possible role of ctxB7 allele on higher production of cholera toxin by Haitian variant Vibrio cholerae O1. PLoS Neglected Tropical Diseases, 2020, 14, e0008128. | 3.0 | 19 |
| 494 | Quorumâ€sensing signaling by chironomid egg masses' microbiota, affects haemagglutinin/protease (HAP) production by <i>Vibrio cholerae</i> . Molecular Ecology, 2021, 30, 1736-1746. | 3.9 | 17 |

| # | Article | IF | CITATIONS |
|-----|---|-----|-----------|
| 495 | Dysbiosis of the endometrial microbiota and its association with inflammatory cytokines in endometrial cancer. International Journal of Cancer, 2021, 148, 1708-1716. | 5.1 | 54 |
| 496 | Framework for PESTEL dimensions of sustainable healthcare waste management: Learnings from COVID-19 outbreak. Journal of Cleaner Production, 2021, 287, 125562. | 9.3 | 75 |
| 497 | Decades of cholera in Odisha, India (1993–2015): lessons learned and the ways forward. Epidemiology and Infection, 2021, 149, e148. | 2.1 | 3 |
| 499 | Rethinking disease preparedness: incertitude and the politics of knowledge. Critical Public Health, 2022, 32, 82-96. | 2.4 | 25 |
| 500 | Dissecting serotype-specific contributions to live oral cholera vaccine efficacy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 7.1 | 6 |
| 501 | Dissemination of Vibrio cholerae O1 isolated from Odisha, India. Environmental Microbiology Reports, 2021, 13, 355-363. | 2.4 | 3 |
| 502 | Class A Penicillin-Binding Protein-Mediated Cell Wall Synthesis Promotes Structural Integrity during Peptidoglycan Endopeptidase Insufficiency in Vibrio cholerae. MBio, 2021, 12, . | 4.1 | 11 |
| 503 | Evolution, distribution and genetics of atypical Vibrio cholerae – A review. Infection, Genetics and Evolution, 2021, 89, 104726. | 2.3 | 20 |
| 505 | The Cholera Epidemic. , 2021, , 66-88. | | 0 |
| 506 | Metagenomic Next-generation Sequencing: Application in Infectious Diseases. Exploratory Research and Hypothesis in Medicine, 2021, 000, 000-000. | 0.4 | 0 |
| 507 | Virulence of Cholera Toxin Gene-Positive Vibrio cholerae Non-O1/non-O139 Strains Isolated From Environmental Water in Kolkata, India. Frontiers in Microbiology, 2021, 12, 726273. | 3.5 | 9 |
| 508 | MLST/MVLST Analysis and Antibiotic Resistance of Vibrio cholerae in Shandong Province of China. Iranian Journal of Public Health, 2021, 50, 1805-1815. | 0.5 | 1 |
| 509 | PHIAF: prediction of phage-host interactions with GAN-based data augmentation and sequence-based feature fusion. Briefings in Bioinformatics, 2022, 23, . | 6.5 | 18 |
| 510 | Flooding and abandonment have shaped rat demography across post-Katrina New Orleans. Landscape and Urban Planning, 2021, 215, 104218. | 7.5 | 2 |
| 511 | Pathogen-Omics: Challenges and Prospects in Research and Clinical Settings. , 2021, , 521-542. | | 0 |
| 512 | Vibrios. , 2021, , 105-124. | | 0 |
| 513 | Food Security: Microbiological and Chemical Risks. Advanced Sciences and Technologies for Security Applications, 2020, , 231-274. | 0.5 | 8 |
| 514 | The Bacterial Guide to Designing a Diversified Gene Portfolio. , 2020, , 51-87. | | 15 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 515 | Introduction to Isoform Sequencing Using Pacific Biosciences Technology (Iso-Seq). Translational Bioinformatics, 2016, , 141-160. | 0.0 | 55 |
| 516 | Multi-Hazard Risk Management During Pandemic. Disaster Resilience and Green Growth, 2020, , 445-461. | 0.2 | 3 |
| 517 | Vibrio cholerae O1 transmission in Bangladesh: insights from a nationally representative serosurvey. Lancet Microbe, The, 2020, 1, e336-e343. | 7.3 | 27 |
| 519 | Cholera Outbreak in Haiti. Infectious Diseases in Clinical Practice, 2019, 27, 3-11. | 0.3 | 4 |
| 520 | Modelling the aqueous transport of an infectious pathogen in regional communities: application to the cholera outbreak in Haiti. Journal of the Royal Society Interface, 2020, 17, 20200429. | 3.4 | 3 |
| 521 | Phenotypic and genetic characteristics of Vibrio cholerae O1 carrying Haitian ctxB and attributes of classical and El Tor biotypes isolated from Silvassa, India. Journal of Medical Microbiology, 2016, 65, 720-728. | 1.8 | 13 |
| 522 | Dissemination of newly emerged polymyxin B sensitive Vibrio cholerae O1 containing Haitian-like genetic traits in different parts of India. Journal of Medical Microbiology, 2018, 67, 1326-1333. | 1.8 | 14 |
| 523 | Vibrio cholerae genomic diversity within and between patients. Microbial Genomics, 2017, 3, . | 2.0 | 37 |
| 524 | Wave 2 strains of atypical Vibrio cholerae El Tor caused the 2009–2011 cholera outbreak in Papua New Guinea. Microbial Genomics, 2019, 5, . | 2.0 | 4 |
| 528 | Microbiological safety of readyâ€ŧoâ€eat foods in Iow―and middleâ€income countries: A comprehensive 10â€year (2009 to 2018) review. Comprehensive Reviews in Food Science and Food Safety, 2020, 19, 703-732. | 11.7 | 47 |
| 529 | <i>Vibrio</i> Species. , 0, , 401-439. | | 17 |
| 530 | The Dry Season in Haiti: a Window of Opportunity to Eliminate Cholera. PLOS Currents, 2013, 5, . | 1.4 | 23 |
| 531 | Strategies to Prevent Cholera Introduction during International Personnel Deployments: A Computational Modeling Analysis Based on the 2010 Haiti Outbreak. PLoS Medicine, 2016, 13, e1001947. | 8.4 | 21 |
| 532 | A Large-Scale Community-Based Outbreak of Paratyphoid Fever Caused by Hospital-Derived Transmission in Southern China. PLoS Neglected Tropical Diseases, 2015, 9, e0003859. | 3.0 | 17 |
| 533 | Resources and Costs for Microbial Sequence Analysis Evaluated Using Virtual Machines and Cloud Computing. PLoS ONE, 2011, 6, e26624. | 2.5 | 75 |
| 534 | Phylogenetics and Differentiation of Salmonella Newport Lineages by Whole Genome Sequencing. PLoS ONE, 2013, 8, e55687. | 2.5 | 63 |
| 535 | Clinical Isolates of Vibrio cholerae O1 El Tor Ogawa of 2009 from Kolkata, India: Preponderance of SXT Element and Presence of Haitian ctxB Variant. PLoS ONE, 2013, 8, e56477. | 2.5 | 26 |
| 536 | Population Structure and Evolution of Non-O1/Non-O139 Vibrio cholerae by Multilocus Sequence Typing. PLoS ONE, 2013, 8, e65342. | 2.5 | 77 |

| # | Article | IF | CITATIONS |
|-----|---|-----|-----------|
| 537 | Whole Genome Complete Resequencing of Bacillus subtilis Natto by Combining Long Reads with High-Quality Short Reads. PLoS ONE, 2014, 9, e109999. | 2.5 | 41 |
| 538 | Improved Lower Bounds of DNA Tags Based on a Modified Genetic Algorithm. PLoS ONE, 2015, 10, e0110640. | 2.5 | 9 |
| 539 | Genetic Traits of Vibrio cholerae O1 Haitian Isolates That Are Absent in Contemporary Strains from Kolkata, India. PLoS ONE, 2014, 9, e112973. | 2.5 | 27 |
| 541 | Infectious Disease Risk After the Great East Japan Earthquake. Journal of Disaster Research, 2012, 7, 741-745. | 0.7 | 3 |
| 542 | Communicable Diseases After the Disasters: with the Special Reference to the Great East Japan Earthquake. Journal of Disaster Research, 2012, 7, 746-753. | 0.7 | 3 |
| 543 | Cholera Specific Prophylaxis in Modern Conditions. Problemy Osobo Opasnykh Infektsii, 2011, , 5-12. | 0.6 | 7 |
| 544 | Cholera in the Early XXI Century: Global Prognosis. Problemy Osobo Opasnykh Infektsii, 2012, , 11-16. | 0.6 | 6 |
| 545 | The use and reporting of airline passenger data for infectious disease modelling: a systematic review. Eurosurveillance, 2019, 24, . | 7.0 | 12 |
| 546 | Overview of molecular typing methods for outbreak detection and epidemiological surveillance. Eurosurveillance, 2013, 18, 20380. | 7.0 | 435 |
| 547 | Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1. | 4.3 | 64 |
| 548 | Drug-Resistance Mechanisms in Vibrio cholerae O1 Outbreak Strain, Haiti, 2010. Emerging Infectious Diseases, 2011, 17, 2151-4. | 4.3 | 76 |
| 549 | Characterization of Toxigenic Vibrio cholerae from Haiti, 2010–2011. Emerging Infectious Diseases, 2011, 17, 2122-9. | 4.3 | 85 |
| 550 | Integrating Genome-based Informatics to Modernize Global Disease Monitoring, Information Sharing, and Response. Emerging Infectious Diseases, 2012, 18, e1-e1. | 4.3 | 61 |
| 551 | ACTUAL PROBLEMS OF EPIDEMIOLOGIC CONTROL, LABORATORY DIAGNOSTICS AND PROPHYLAXIS OF CHOLERA IN RUSSIAN FEDERATION. Zhurnal Mikrobiologii Epidemiologii I Immunobiologii, 2016, , 89-101. | 1.0 | 15 |
| 552 | Review of molecular subtyping methodologies used to investigate outbreaks due to multidrug-resistant enteric bacterial pathogens in sub-Saharan Africa. African Journal of Laboratory Medicine, 2019, 8, 760. | 0.6 | 6 |
| 553 | Haitian variant tcpA in Vibrio cholerae O1 El Tor strains in National Capital Region (India). Indian Journal of Medical Research, 2016, 144, 293. | 1.0 | 2 |
| 554 | Changing facades of Vibrio cholerae: An enigma in the epidemiology of cholera. Indian Journal of Medical Research, 2018, 147, 133. | 1.0 | 24 |
| 555 | Past, Present and Future of Molecular Technology Applications for the Epidemiology of Bacterial Diseases. Journal of Analytical & Bioanalytical Techniques, 0, s10, . | 0.6 | 5 |

| # | Article | IF | CITATIONS |
|-----|---|-----|-----------|
| 556 | Utilization of Small RNA Genes to Distinguish Vibrio cholerae Biotypes via Multiplex Polymerase Chain Reaction. American Journal of Tropical Medicine and Hygiene, 2019, 100, 1328-1334. | 1.4 | 2 |
| 557 | Rapidly Progressive, Fatal, Inhalation Anthrax-like Infection in a Human: Case Report, Pathogen Genome Sequencing, Pathology, and Coordinated Response. Archives of Pathology and Laboratory Medicine, 2011, , . | 2.5 | 1 |
| 558 | Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. ELife, 2015, 4, . | 6.0 | 111 |
| 559 | An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with <i>Salmonella</i> . PeerJ, 2014, 2, e620. | 2.0 | 45 |
| 561 | Proteomic analysis of the host–pathogen interface in experimental cholera. Nature Chemical Biology, 2021, 17, 1199-1208. | 8.0 | 11 |
| 562 | Spatiotemporal patterns and influencing factors of human migration networks in China during COVID-19. Geography and Sustainability, 2021, 2, 264-274. | 4.3 | 7 |
| 564 | Construction of the PCR Test-System for the Detection of <i>Vibrio cholerae</i> O1 Toxigenic Strains, for Indication of Their Biovar and for Differentiation between Typical and Altered El Tor-Vibrio Strains. Problemy Osobo Opasnykh Infektsii, 2011, , 49-52. | 0.6 | 3 |
| 565 | Cholera and Other Vibrio Infections. , 2012, , 1865-1868. | | 0 |
| 566 | The Genomics of Cholera. Advances in Microbial Ecology, 2012, , 21-38. | 0.1 | 0 |
| 567 | Recent Advances in Sequencing Technology. Soft and Biological Matter, 2012, , 281-308. | 0.3 | 0 |
| 568 | Challenges in Enteric Epidemics: Barometers of Inadequate Water and Sanitation. , 2013, , 147-202. | | 0 |
| 571 | - Sample-to-Result STR Genotyping Systems: Potential and Status. , 2013, , 366-397. | | 2 |
| 572 | Acquisition and dissemination mechanisms of CTXΦ inVibrio cholerae: New paradigm fordifresidents. World Journal of Medical Genetics, 2014, 4, 27. | 1.0 | 0 |
| 573 | Comparison of Next-Generation Sequencing Systems. , 2014, , 1-25. | | 0 |
| 575 | Activity of Collaborative Research Center of Okayama University for Infectious Disease in India. Journal of Disaster Research, 2014, 9, 774-783. | 0.7 | 0 |
| 577 | Vibrio cholerae. , 2015, , 2471-2479.e2. | | 0 |
| 579 | Regulating the Transition of <i>Vibrio cholerae</i> Out of the Host. , 0, , 566-585. | | 0 |
| 582 | Molecular-genetic properties of Vibrio Cholerae el tor strains circulat-ing in Africa. Molekuliarnaia Genetika, Mikrobiologiia I Virusologiia, 2017, 35, 12. | 0.4 | Ο |

| # | Article | IF | CITATIONS |
|-----|--|-------------------|-----------|
| 583 | Antimicrobial Resistance in Vibrio. , 2017, , 969-990. | | 0 |
| 584 | Existing and Emerging Molecular Technologies in Myeloid Neoplasms. Molecular Pathology Library, 2018, , 369-412. | 0.1 | 0 |
| 585 | Natural Disasters and Health Risks of First Responders. Advanced Sciences and Technologies for Security Applications, 2018, , 85-122. | 0.5 | 0 |
| 586 | Humanitarian aid policy changes following the 2010 cholera outbreak in Haiti. Journal of Anthropology at McMaster, 0, 25, . | 0.1 | 0 |
| 587 | Forensic Approaches to Detect Possible Agents of Bioterror. , 0, , 191-214. | | 0 |
| 590 | Vibrio cholerae: doença, manifestações clÃnicas e microbiologia. Revista De Epidemiologia E Controle De Infecção, 2018, 8, 483-488. | 0.0 | 0 |
| 591 | Climate Crisis Impact on AIDS, IRIS and Neuro-AIDS. , 2019, , 575-603. | | 0 |
| 592 | Detection of Haitian ctxB7 & tcpA alleles in Vibrio cholerae O1 El Tor biotype in Puri, Odisha, India. Indian Journal of Medical Research, 2019, 149, 558. | 1.0 | 1 |
| 594 | Whole Genome Sequencing. , 2020, , 1-10. | | 0 |
| 597 | Ecological features of the persistence of Vibrio cholerae: retrospective analysis and actual state of the problem. Zhurnal Mikrobiologii Epidemiologii I Immunobiologii, 2020, 97, 165-173. | 1.0 | 3 |
| 601 | A Strategy for the Rapid Development of a Safe Vibrio cholerae Candidate Vaccine Strain. International Journal of Molecular Sciences, 2021, 22, 11657. | 4.1 | 2 |
| 605 | The potential for liquid biopsies in the precision medical treatment of breast cancer. Cancer Biology and Medicine, 2016, 13, 19-40. | 3.0 | 12 |
| 607 | Whole Genome Sequencing. , 2021, , 5424-5433. | | 0 |
| 608 | Extração de dna genômico bacteriano: uma comparação de métodos comerciais e in house. Saúde, 202 46, . | 0, _{0.1} | 0 |
| 610 | New Insights into Molecular Diagnostics for Common Gastrointestinal Infections. Journal of Gastrointestinal Infections, 2022, 11, 15-23. | 0.2 | 0 |
| 612 | A Potent Inhibitor of the Cystic Fibrosis Transmembrane Conductance Regulator Blocks Disease and Morbidity Due to Toxigenic Vibrio cholerae. Toxins, 2022, 14, 225. | 3.4 | 8 |
| 613 | Genetic relatedness, virulence factors and antibiotics susceptibility pattern of Vibrio cholerae isolates from various regions during cholera outbreak in Tanzania. PLoS ONE, 2022, 17, e0265868. | 2.5 | 0 |
| 614 | Nontoxigenic Vibrio cholerae Challenge Strains for Evaluating Vaccine Efficacy and Inferring Mechanisms of Protection. MBio, 2022, 13, e0053922. | 4.1 | 4 |

| # | Article | IF | CITATIONS |
|-----|--|------|-----------|
| 615 | Cholera. Lancet, The, 2022, 399, 1429-1440. | 13.7 | 69 |
| 617 | Pacific bioscience sequence technology: Review. International Journal of Veterinary Science and Research, 2022, 8, 027-033. | 0.2 | 1 |
| 632 | Insight into impact of sewage discharge on microbial dynamics and pathogenicity in river ecosystem. Scientific Reports, 2022, 12, 6894. | 3.3 | 15 |
| 633 | Contribution of microbial genomics to cholera epidemiology. Comptes Rendus - Biologies, 2022, 345, 37-56. | 0.2 | 0 |
| 634 | The Notable Achievements and the Prospects of Bacterial Pathogen Genomics. Microorganisms, 2022, 10, 1040. | 3.6 | 11 |
| 635 | A Review of Next Generation Sequencing Methods and its Applications in Laboratory Diagnosis. Journal of Pure and Applied Microbiology, 0, , . | 0.9 | 2 |
| 636 | United Nations Missions in Haiti. , 2022, , 1606-1629. | | 0 |
| 637 | Detection of Salmonella enterica serovar Montevideo in food products using specific PCR primers developed by comparative genomics. LWT - Food Science and Technology, 2022, 165, 113677. | 5.2 | 5 |
| 638 | Cholera in Haiti. Presse Medicale, 2022, 51, 104136. | 1.9 | 6 |
| 641 | Altered molecular attributes and antimicrobial resistance patterns of Vibrio cholerae O1 El Tor strains isolated from the cholera endemic regions of India. Journal of Applied Microbiology, 2022, 133, 3605-3616. | 3.1 | 2 |
| 642 | Microbiome analysis: An emerging forensic investigative tool. Forensic Science International, 2022, 340, 111462. | 2.2 | 7 |
| 643 | Vibrio cholerae O1 El Tor strains linked to global cholera show region-specific patterns by pulsed-field gel electrophoresis. Infection, Genetics and Evolution, 2022, 105, 105363. | 2.3 | 1 |
| 645 | Skin-Attachable Sensors for Biomedical Applications. , 2023, 1, 256-268. | | 1 |
| 646 | Structural basis for the toxin-coregulated pilus–dependent secretion of <i>Vibrio cholerae</i> colonization factor. Science Advances, 2022, 8, . | 10.3 | 1 |
| 647 | A propeptide-based biosensor for the selective detection of Vibrio cholerae using an environment-sensitive fluorophore. Cell Chemical Biology, 2022, 29, 1505-1516.e7. | 5.2 | 0 |
| 648 | Inactivated <i>Vibrio cholerae</i> Strains That Express TcpA via the <i>toxT</i> -139F Allele Induce Antibody Responses against TcpA. Journal of Microbiology and Biotechnology, 2022, 32, 1396-1405. | 2.1 | 2 |
| 649 | Genomes of Vibrio cholerae O1 Serotype Ogawa Associated with Current Cholera Activity in Pakistan. Microbiology Resource Announcements, 2023, 12, . | 0.6 | 3 |
| 650 | Undecaprenyl phosphate translocases confer conditional microbial fitness. Nature, 2023, 613, 721-728. | 27.8 | 23 |

| # | Article | IF | CITATIONS |
|-----|---|------|-----------|
| 651 | Comparative analysis of the structure and expression of the <i>vasH</i> regulatory gene of type VI secretion system in toxigenic and non-toxigenic <i>Vibrio cholerae</i> strains. Zhurnal Mikrobiologii Epidemiologii I Immunobiologii, 2023, 99, 682-691. | 1.0 | 0 |
| 652 | Diseases spectrum in the field of spatiotemporal patterns mining of infectious diseases epidemics: A bibliometric and content analysis. Frontiers in Public Health, 0, 10, . | 2.7 | 2 |
| 653 | The Impact of Earthquakes on Public Health: A Narrative Review of Infectious Diseases in the Post-Disaster Period Aiming to Disaster Risk Reduction. Microorganisms, 2023, 11, 419. | 3.6 | 17 |
| 654 | Infection Diseases Following Natural Disaster in Children: Health Prevention and Assessment. Journal of Pediatric Infectious Diseases, 0, , . | 0.2 | 1 |
| 655 | Whole-genome analysis of a Vibrio cholerae O1 biotype classical strain isolated in 1946 in Sasebo city, Nagasaki prefecture, from a returnee from the northeast part of China. Tropical Medicine and Health, 2023, 51, . | 2.8 | 0 |
| 657 | Special community health needs. , 2023, , 551-602. | | 1 |
| 658 | What Whole Genome Sequencing Has Told Us About Pathogenic Vibrios. Advances in Experimental Medicine and Biology, 2023, , 337-352. | 1.6 | 1 |
| 659 | Environmental Reservoirs of Pathogenic Vibrio spp. and Their Role in Disease: The List Keeps Expanding. Advances in Experimental Medicine and Biology, 2023, , 99-126. | 1.6 | 2 |
| 660 | Cholera Dynamics and the Emergence of Pandemic Vibrio cholerae. Advances in Experimental Medicine and Biology, 2023, , 127-147. | 1.6 | 1 |
| 661 | Genomic attributes of Vibrio cholerae O1 responsible for 2022 massive cholera outbreak in Bangladesh. Nature Communications, 2023, 14, . | 12.8 | 3 |
| 662 | Dps-dependent in vivo mutation enhances long-term host adaptation in Vibrio cholerae. PLoS Pathogens, 2023, 19, e1011250. | 4.7 | 1 |
| 663 | Intracellular Expression of CTB in <i>Vibrio cholerae</i> Strains in Laboratory Culture Conditions. Journal of Microbiology and Biotechnology, 2023, 33, 736-744. | 2.1 | 0 |
| 664 | Population genomics implies potential public health risk of two non-toxigenic Vibrio cholerae lineages. Infection, Genetics and Evolution, 2023, 112, 105441. | 2.3 | 0 |
| 665 | A Cholera Case Imported from Bangladesh to Italy: Clinico-Epidemiological Management and Molecular Characterization in a Non-Endemic Country. Tropical Medicine and Infectious Disease, 2023, 8, 266. | 2.3 | 1 |
| 666 | Global Development, Humanitarian Aid, and the Toolbox Dialogue Method. , 2023, 5, . | | 0 |
| 667 | Advances in cholera research: from molecular biology to public health initiatives. Frontiers in Microbiology, 0, 14, . | 3.5 | 2 |
| 669 | Challenges and opportunities of molecular epidemiology: using omics to address complex One Health issues in tropical settings. Frontiers in Tropical Diseases, 0, 4, . | 1.4 | 1 |
| 670 | Expression of Cholera Toxin (CT) and the Toxin Co-Regulated Pilus (TCP) by Variants of ToxT in Vibrio cholerae Strains. Toxins, 2023, 15, 507. | 3.4 | 0 |

| # | Article | IF | CITATIONS |
|-----|--|-----|-----------|
| 671 | Seroprevalence of <i>Vibrio cholerae</i> in Adults, Haiti, 2017. Emerging Infectious Diseases, 2023, 29, . | 4.3 | 0 |
| 672 | Population-Based Serologic Survey of <i>Vibrio cholerae</i> Antibody Titers before Cholera Outbreak, Haiti, 2022. Emerging Infectious Diseases, 2023, 29, . | 4.3 | 0 |
| 673 | Impacts of Biotechnologically Developed Microorganisms on Ecosystems. The EuroBiotech Journal, 2023, 7, 196-205. | 1.0 | 0 |
| 674 | The clinical and epidemiological impacts of whole genomic sequencing on bacterial and virological agents. Infectious Diseases Now, 2024, 54, 104844. | 1.6 | 0 |
| 675 | Vibrio cholerae. , 2024, , 987-1007. | | 0 |