

Putative household outbreaks of campylobacteriosis ty genotypes

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Analysis of Multilocus Sequence Typing for Identification of <i>Leptospira</i> Isolates in Brazil. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3940-3942.	3.9	34
2	Campylobacter sequence typing databases: applications and future prospects. <i>Microbiology (United Kingdom)</i> , 2011, 155, 1843-1854.	1.8	64
3	Operationalising Factors That Explain the Emergence of Infectious Diseases: A Case Study of the Human Campylobacteriosis Epidemic. <i>PLoS ONE</i> , 2013, 8, e79331.	2.5	17
4	Genotypic Analysis of <i>Klebsiella pneumoniae</i> Isolates in a Beijing Hospital Reveals High Genetic Diversity and Clonal Population Structure of Drug-Resistant Isolates. <i>PLoS ONE</i> , 2013, 8, e57091.	2.5	41
6	Campylobacteriosis in returning travellers and potential secondary transmission of exotic strains. <i>Epidemiology and Infection</i> , 2014, 142, 1277-1288.	2.1	34
9	Multilocus sequence typing of <i>Blastocystis</i> isolates in Aydin, Turkey. <i>Parasitology International</i> , 2016, 65, 760-762.	1.3	2
10	Outbreak of Campylobacteriosis Following a Dairy Farm Visit: Confirmation by Genotyping. <i>Foodborne Pathogens and Disease</i> , 2017, 14, 326-332.	1.8	23
11	Knowledge gaps in control of <i>Campylobacter</i> for prevention of campylobacteriosis. <i>Transboundary and Emerging Diseases</i> , 2018, 65, 30-48.	3.0	111
12	Bacteriophage Therapy to Reduce Colonization of <i>Campylobacter jejuni</i> in Broiler Chickens before Slaughter. <i>Viruses</i> , 2021, 13, 1428.	3.3	20