Eduardo N Taboada

List of Publications by Year
in descending order

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80 papers	3,742 citations	147726 31 h-index	138417 58 g-index
88 all docs	88 docs citations	88 times ranked	3796 citing authors

#	Article	IF	Citations
1	Clinical Metagenomics Is Increasingly Accurate and Affordable to Detect Enteric Bacterial Pathogens in Stool. Microorganisms, 2022, 10, 441.	1.6	4
2	Epidemiology of Campylobacter jejuni in raccoons (Procyon lotor) on swine farms and in conservation areas in southern Ontario. Zoonoses and Public Health, 2021, 68, 19-28.	0.9	1
3	Analysis of Campylobacter jejuni Subtype Distribution in the Chicken Broiler Production Continuum: a Longitudinal Examination To Identify Primary Contamination Points. Applied and Environmental Microbiology, 2021, 87, .	1.4	5
4	Rates of fluoroquinolone resistance in domestically acquiredCampylobacter jejuniare increasing in people living within a model study location in Canada. Canadian Journal of Microbiology, 2021, 67, 37-52.	0.8	13
5	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. Microbial Genomics, 2021, 7, .	1.0	4
6	Campylobacter coli isolated in Brazil typed by core genome Multilocus Sequence Typing shows high genomic diversity in a global context. Infection, Genetics and Evolution, 2021, 95, 105018.	1.0	3
7	Systematic Evaluation of Whole-Genome Sequencing Based Prediction of Antimicrobial Resistance in Campylobacter jejuni and C. coli. Frontiers in Microbiology, 2021, 12, 776967.	1.5	14
8	Clinically Relevant Campylobacter jejuni Subtypes Are Readily Found and Transmitted within the Cattle Production Continuum but Present a Limited Foodborne Risk. Applied and Environmental Microbiology, 2020, 86, .	1.4	10
9	Campylobacter jejuni Strain Dynamics in a Raccoon (Procyon lotor) Population in Southern Ontario, Canada: High Prevalence and Rapid Subtype Turnover. Frontiers in Veterinary Science, 2020, 7, 27.	0.9	6
10	Generalizability and comparability of prevalence estimates in the wild bird literature: methodological and epidemiological considerations. Animal Health Research Reviews, 2020, 21, 89-95.	1.4	12
11	Tetracycline Resistant Campylobacter jejuni Subtypes Emanating from Beef Cattle Administered Non-Therapeutic Chlortetracycline are Longitudinally Transmitted within the Production Continuum but are Not Detected in Ground Beef. Microorganisms, 2020, 8, 23.	1.6	9
12	â€œThese Arenâ€™t the Strains Youâ€™re Looking forâ€: Recovery Bias of Common Campylobacter jejuni Subtypes in Mixed Cultures. Frontiers in Microbiology, 2020, 11, 541.	1.5	9
13	A strain comparison of Campylobacter isolated from retail poultry and human clinical cases in Atlantic Canada. PLoS ONE, 2019, 14, e0215928.	1.1	10
14	Salmonella, Campylobacter, Clostridium difficile, and antiâ€microbial resistant Escherichia coli in the faeces of sympatric mesoâ€mammals in southern Ontario, Canada. Zoonoses and Public Health, 2019, 66, 406-416.	0.9	14
15	Enhanced microbiological surveillance reveals that temporal case clusters contribute to the high rates of campylobacteriosis in a model agroecosystem. International Journal of Medical Microbiology, 2019, 309, 232-244.	1.5	9
16	Carriage of Campylobacter, Salmonella, and Antimicrobial-Resistant, Nonspecific Escherichia coli by Waterfowl Species Collected from Three Sources in Southern Ontario, Canada. Journal of Wildlife Diseases, 2019, 55, 917.	0.3	4
17	Integrating Whole-Genome Sequencing Data Into Quantitative Risk Assessment of Foodborne Antimicrobial Resistance: A Review of Opportunities and Challenges. Frontiers in Microbiology, 2019, 10, 1107.	1.5	73
18	A repeated crossâ€sectional study of the epidemiology of Campylobacter and antimicrobial resistant Enterobacteriaceae in freeâ€living Canada geese in Guelph, Ontario, Canada. Zoonoses and Public Health, 2019, 66, 60-72.	0.9	5

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19	Carriage of , , and Antimicrobial-Resistant, Nonspecific by Waterfowl Species Collected from Three Sources in Southern Ontario, Canada. Journal of Wildlife Diseases, 2019, 55, 917-922.	0.3	1
20	Subtype-Specific Selection for Resistance to Fluoroquinolones but Not to Tetracyclines Is Evident in Campylobacter jejuni Isolates from Beef Cattle in Confined Feeding Operations in Southern Alberta, Canada. Applied and Environmental Microbiology, 2018, 84, .	1.4	24
21	Genome-wide identification of geographical segregated genetic markers in Salmonella enterica serovar Typhimurium variant 4,[5],12:i:-. Scientific Reports, 2018, 8, 15251.	1.6	30
22	Frequent Implication of Multistress-TolerantCampylobacter jejuniin Human Infections. Emerging Infectious Diseases, 2018, 24, 1037-1044.	2.0	32
23	Therapeutic administration of enrofloxacin in mice does not select for fluoroquinolone resistance inCampylobacter jejuni. Canadian Journal of Microbiology, 2018, 64, 681-694.	0.8	9
24	Epidemiology of Campylobacter, Salmonella and antimicrobial resistant Escherichia coli in freeâ€living Canada geese (Branta canadensis) from three sources in southern Ontario. Zoonoses and Public Health, 2018, 65, 873-886.	0.9	18
25	Comprehensive assessment of the quality of Salmonella whole genome sequence data available in public sequence databases using the Salmonella in silico Typing Resource (SISTR). Microbial Genomics, 2018, 4, .	1.0	46
26	The EpiQuant Framework for Computing Epidemiological Concordance of Microbial Subtyping Data. Journal of Clinical Microbiology, 2017, 55, 1334-1349.	1.8	2
27	Whole-Genome Sequencing in Epidemiology of Campylobacter jejuni Infections. Journal of Clinical Microbiology, 2017, 55, 1269-1275.	1.8	97
28	Prevalence and diversity of waterborneArcobacter butzleriin southwestern Alberta, Canada. Canadian Journal of Microbiology, 2017, 63, 330-340.	0.8	8
29	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic Campylobacter populations. Molecular Ecology, 2017, 26, 4497-4508.	2.0	36
30	Epidemiology of antimicrobial resistant Campylobacter spp. isolated from retail meats in Canada. International Journal of Food Microbiology, 2017, 253, 43-47.	2.1	49
31	Comparative genomic fingerprinting of Campylobacter: application in routine public health surveillance and epidemiological investigations. Epidemiology and Infection, 2017, 145, 299-309.	1.0	8
32	Molecular and Statistical Analysis of Campylobacter spp. and Antimicrobialâ€Resistant Campylobacter Carriage in Wildlife and Livestock from Ontario Farms. Zoonoses and Public Health, 2017, 64, 194-203.	0.9	10
33	Cluster Analysis of Campylobacter jejuni Genotypes Isolated from Small and Mediumâ€Sized Mammalian Wildlife and Bovine Livestock from Ontario Farms. Zoonoses and Public Health, 2017, 64, 185-193.	0.9	6
34	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. Frontiers in Microbiology, 2017, 8, 909.	1.5	87
35	The Validation and Implications of Using Whole Genome Sequencing as a Replacement for Traditional Serotyping for a National Salmonella Reference Laboratory. Frontiers in Microbiology, 2017, 8, 1044.	1.5	86
36	A Genome-Wide Association Study to Identify Diagnostic Markers for Human Pathogenic Campylobacter jejuni Strains. Frontiers in Microbiology, 2017, 8, 1224.	1.5	40

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37	Source attribution of human campylobacteriosis at the point of exposure by combining comparative exposure assessment and subtype comparison based on comparative genomic fingerprinting. PLoS ONE, 2017, 12, e0183790.	1.1	61
38	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. Microbial Genomics, 2017, 3, e000116.	1.0	119
39	Evaluation of real-time PCR assays and standard curve optimisation for enhanced accuracy in quantification of Campylobacter environmental water isolates. Journal of Microbiological Methods, 2016, 129, 70-77.	0.7	12
40	Efficacy of wastewater treatment on Arcobacter butzleri density and strain diversity. Water Research, 2016, 105, 291-296.	5.3	20
41	Genomic insights from whole genome sequencing of four clonal outbreak Campylobacter jejuni assessed within the global C. jejuni population. BMC Genomics, 2016, 17, 990.	1.2	28
42	SuperPhy: predictive genomics for the bacterial pathogen Escherichia coli. BMC Microbiology, 2016, 16, 65.	1.3	18
43	Comparative Detection and Quantification of Arcobacter butzleri in Stools from Diarrheic and Nondiarrheic People in Southwestern Alberta, Canada. Journal of Clinical Microbiology, 2016, 54, 1082-1088.	1.8	32
44	Monomorphic genotypes within a generalist lineage of Campylobacter jejuni show signs of global dispersion. Microbial Genomics, 2016, 2, e000088.	1.0	31
45	The Salmonella In Silico Typing Resource (SISTR): An Open Web-Accessible Tool for Rapidly Typing and Subtyping Draft Salmonella Genome Assemblies. PLoS ONE, 2016, 11, e0147101.	1.1	426
46	Development of a comparative genomic fingerprinting assay for rapid and high resolution genotyping of Arcobacter butzleri. BMC Microbiology, 2015, 15, 94.	1.3	48
47	Extensive characterization of Campylobacter jejuni chicken isolates to uncover genes involved in the ability to compete for gut colonization. BMC Microbiology, 2015, 15, 97.	1.3	21
48	Molecular Epidemiology ofCampylobacter jejuniHuman and Chicken Isolates from Two Health Units. Foodborne Pathogens and Disease, 2014, 11, 150-155.	0.8	13
49	A Systematic Review Characterizing On-Farm Sources of Campylobacter spp. for Broiler Chickens. PLoS ONE, 2014, 9, e104905.	1.1	96
50	Comparative Variation within the Genome of Campylobacter jejuni NCTC 11168 in Human and Murine Hosts. PLoS ONE, 2014, 9, e88229.	1.1	34
51	Current methods for molecular typing of Campylobacter species. Journal of Microbiological Methods, 2013, 95, 24-31.	0.7	57
52	Subtyping of a Large Collection of Historical Listeria monocytogenes Strains from Ontario, Canada, by an Improved Multilocus Variable-Number Tandem-Repeat Analysis (MLVA). Applied and Environmental Microbiology, 2013, 79, 6472-6480.	1.4	21
53	Evaluation of MALDI-TOF mass spectroscopy methods for determination of Escherichia coli pathotypes. Journal of Microbiological Methods, 2013, 94, 180-191.	0.7	66
54	Detection of Genetic Diversity in Campylobacter jejuni Isolated from a Commercial Turkey Flock Using flaA Typing, MLST Analysis and Microarray Assay. PLoS ONE, 2013, 8, e51582.	1.1	31

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55	Comparison of Molecular Typing Methods Useful for Detecting Clusters of Campylobacter jejuni and C. coli Isolates through Routine Surveillance. Journal of Clinical Microbiology, 2012, 50, 798-809.	1.8	52
56	Development and Validation of a Comparative Genomic Fingerprinting Method for High-Resolution Genotyping of Campylobacter jejuni. Journal of Clinical Microbiology, 2012, 50, 788-797.	1.8	63
57	An enhanced technique combining pre-enrichment and passive filtration increases the isolation efficiency of Campylobacter jejuni and Campylobacter coli from water and animal fecal samples. Journal of Microbiological Methods, 2012, 91, 506-513.	0.7	43
58	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.	1.8	31
59	Spatial and Temporal Drivers of Zoonotic Pathogen Contamination of an Agricultural Watershed. Journal of Environmental Quality, 2012, 41, 242-252.	1.0	59
60	Molecular subtypes of Campylobacter spp., Salmonella enterica, and Escherichia coli O157:H7 isolated from faecal and surface water samples in the Oldman River watershed, Alberta, Canada. Water Research, 2011, 45, 1247-1257.	5.3	88
61	Identification of Salmonella enterica species- and subgroup-specific genomic regions using Panseq 2.0. Infection, Genetics and Evolution, 2011, 11, 2151-2161.	1.0	10
62	Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. BMC Bioinformatics, 2010, 11, 461.	1.2	249
63	The occurrence and sources of Campylobacter spp., Salmonellaenterica and Escherichia coli O157:H7 in the Salmon River, British Columbia, Canada. Journal of Water and Health, 2010, 8, 374-386.	1.1	51
64	Genomic Regions Conserved in Lineage II Escherichia coli O157:H7 Strains. Applied and Environmental Microbiology, 2009, 75, 3271-3280.	1.4	13
65	Genomics-Based Molecular Epidemiology of Campylobacter jejuni Isolates from Feedlot Cattle and from People in Alberta, Canada. Journal of Clinical Microbiology, 2009, 47, 410-420.	1.8	19
66	In silico genomic analyses reveal three distinct lineages of Escherichia coli O157:H7, one of which is associated with hyper-virulence. BMC Genomics, 2009, 10, 287.	1.2	68
67	Comparative genomic assessment of Multi-Locus Sequence Typing: rapid accumulation of genomic heterogeneity among clonal isolates of Campylobacter jejuni. BMC Evolutionary Biology, 2008, 8, 229.	3.2	34
68	Genotypic Characterization and Prevalence of Virulence Factors among Canadian Escherichia coli O157:H7 Strains. Applied and Environmental Microbiology, 2008, 74, 4314-4323.	1.4	48
69	Rapid Determination ofEscherichia coliO157:H7 Lineage Types and Molecular Subtypes by Using Comparative Genomic Fingerprinting. Applied and Environmental Microbiology, 2008, 74, 6606-6615.	1.4	30
70	Epidemiology, Relative Invasive Ability, Molecular Characterization, and Competitive Performance of Campylobacter jejuni Strains in the Chicken Gut. Applied and Environmental Microbiology, 2007, 73, 7959-7966.	1.4	17
71	Methodologies towards the development of an oligonucleotide microarray for determination of Salmonella serotypes. Journal of Microbiological Methods, 2007, 70, 261-271.	0.7	49
72	Genome evolution in major Escherichia coli O157:H7 lineages. BMC Genomics, 2007, 8, 121.	1.2	138

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73	Comparative genomic analysis of Campylobacter jejuni associated with Guillain-BarrÃ© and Miller Fisher syndromes: neuropathogenic and enteritis-associated isolates can share high levels of genomic similarity. BMC Genomics, 2007, 8, 359.	1.2	36
74	Studying Bacterial Genome Dynamics Using Microarray-Based Comparative Genomic Hybridization. Methods in Molecular Biology, 2007, 396, 223-253.	0.4	7
75	Comparative genomics profiling of clinical isolates of Aeromonas salmonicida using DNA microarrays. BMC Genomics, 2006, 7, 43.	1.2	27
76	Transcriptional and translational expression patterns associated with immobilized growth of Campylobacter jejuni. Microbiology (United Kingdom), 2006, 152, 567-577.	0.7	58
77	A new approach for the analysis of bacterial microarray-based Comparative Genomic Hybridization: insights from an empirical study. BMC Genomics, 2005, 6, 78.	1.2	29
78	Genome-wide Expression Analyses of Campylobacter jejuni NCTC11168 Reveals Coordinate Regulation of Motility and Virulence by flhA. Journal of Biological Chemistry, 2004, 279, 20327-20338.	1.6	190
79	Large-Scale Comparative Genomics Meta-Analysis of Campylobacter jejuni Isolates Reveals Low Level of Genome Plasticity. Journal of Clinical Microbiology, 2004, 42, 4566-4576.	1.8	103
80	The Genetic Bases for the Variation in the Lipo-oligosaccharide of the Mucosal Pathogen, Campylobacter jejuni. Journal of Biological Chemistry, 2002, 277, 327-337.	1.6	254