

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	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
2	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
3	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
4	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
5	Genome evolution in major Escherichia coli O157:H7 lineages. BMC Genomics, 2007, 8, 121.	1.2	138
6	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. Microbial Genomics, 2017, 3, e000116.	1.0	119
7	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
8	Whole-Genome Sequencing in Epidemiology of Campylobacter jejuni Infections. Journal of Clinical Microbiology, 2017, 55, 1269-1275.	1.8	97
9	A Systematic Review Characterizing On-Farm Sources of Campylobacter spp. for Broiler Chickens. PLoS ONE, 2014, 9, e104905.	1.1	96
10	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
11	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. Frontiers in Microbiology, 2017, 8, 909.	1.5	87
12	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
13	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
14	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
15	Evaluation of MALDI-TOF mass spectroscopy methods for determination of Escherichia coli pathotypes. Journal of Microbiological Methods, 2013, 94, 180-191.	0.7	66
16	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
17	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
18	Spatial and Temporal Drivers of Zoonotic Pathogen Contamination of an Agricultural Watershed. Journal of Environmental Quality, 2012, 41, 242-252.	1.0	59

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19	Transcriptional and translational expression patterns associated with immobilized growth of <i>Campylobacter jejuni</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 567-577.	0.7	58
20	Current methods for molecular typing of <i>Campylobacter</i> species. <i>Journal of Microbiological Methods</i> , 2013, 95, 24-31.	0.7	57
21	Comparison of Molecular Typing Methods Useful for Detecting Clusters of <i>Campylobacter jejuni</i> and <i>C. coli</i> Isolates through Routine Surveillance. <i>Journal of Clinical Microbiology</i> , 2012, 50, 798-809.	1.8	52
22	The occurrence and sources of <i>Campylobacter</i> spp., <i>Salmonella</i> enterica and <i>Escherichia coli</i> O157:H7 in the Salmon River, British Columbia, Canada. <i>Journal of Water and Health</i> , 2010, 8, 374-386.	1.1	51
23	Methodologies towards the development of an oligonucleotide microarray for determination of <i>Salmonella</i> serotypes. <i>Journal of Microbiological Methods</i> , 2007, 70, 261-271.	0.7	49
24	Epidemiology of antimicrobial resistant <i>Campylobacter</i> spp. isolated from retail meats in Canada. <i>International Journal of Food Microbiology</i> , 2017, 253, 43-47.	2.1	49
25	Genotypic Characterization and Prevalence of Virulence Factors among Canadian <i>Escherichia coli</i> O157:H7 Strains. <i>Applied and Environmental Microbiology</i> , 2008, 74, 4314-4323.	1.4	48
26	Development of a comparative genomic fingerprinting assay for rapid and high resolution genotyping of <i>Arcobacter butzleri</i> . <i>BMC Microbiology</i> , 2015, 15, 94.	1.3	48
27	Comprehensive assessment of the quality of <i>Salmonella</i> whole genome sequence data available in public sequence databases using the <i>Salmonella</i> in silico Typing Resource (SISTR). <i>Microbial Genomics</i> , 2018, 4, .	1.0	46
28	An enhanced technique combining pre-enrichment and passive filtration increases the isolation efficiency of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> from water and animal fecal samples. <i>Journal of Microbiological Methods</i> , 2012, 91, 506-513.	0.7	43
29	A Genome-Wide Association Study to Identify Diagnostic Markers for Human Pathogenic <i>Campylobacter jejuni</i> Strains. <i>Frontiers in Microbiology</i> , 2017, 8, 1224.	1.5	40
30	Comparative genomic analysis of <i>Campylobacter jejuni</i> associated with Guillain-Barré and Miller Fisher syndromes: neuropathogenic and enteritis-associated isolates can share high levels of genomic similarity. <i>BMC Genomics</i> , 2007, 8, 359.	1.2	36
31	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , 2017, 26, 4497-4508.	2.0	36
32	Comparative genomic assessment of Multi-Locus Sequence Typing: rapid accumulation of genomic heterogeneity among clonal isolates of <i>Campylobacter jejuni</i> . <i>BMC Evolutionary Biology</i> , 2008, 8, 229.	3.2	34
33	Comparative Variation within the Genome of <i>Campylobacter jejuni</i> NCTC 11168 in Human and Murine Hosts. <i>PLoS ONE</i> , 2014, 9, e88229.	1.1	34
34	Comparative Detection and Quantification of <i>Arcobacter butzleri</i> in Stools from Diarrheic and Nondiarrheic People in Southwestern Alberta, Canada. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1082-1088.	1.8	32
35	Frequent Implication of Multistress-Tolerant <i>Campylobacter jejuni</i> in Human Infections. <i>Emerging Infectious Diseases</i> , 2018, 24, 1037-1044.	2.0	32
36	A Framework for Assessing the Concordance of Molecular Typing Methods and the True Strain Phylogeny of <i>Campylobacter jejuni</i> and <i>C. coli</i> Using Draft Genome Sequence Data. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 57.	1.8	31

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37	Detection of Genetic Diversity in <i>Campylobacter jejuni</i> Isolated from a Commercial Turkey Flock Using <i>flaA</i> Typing, MLST Analysis and Microarray Assay. <i>PLoS ONE</i> , 2013, 8, e51582.	1.1	31
38	Monomorphic genotypes within a generalist lineage of <i>Campylobacter jejuni</i> show signs of global dispersion. <i>Microbial Genomics</i> , 2016, 2, e000088.	1.0	31
39	Rapid Determination of <i>Escherichia coli</i> O157:H7 Lineage Types and Molecular Subtypes by Using Comparative Genomic Fingerprinting. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6606-6615.	1.4	30
40	Genome-wide identification of geographical segregated genetic markers in <i>Salmonella enterica</i> serovar Typhimurium variant 4,[5],12:i:-. <i>Scientific Reports</i> , 2018, 8, 15251.	1.6	30
41	A new approach for the analysis of bacterial microarray-based Comparative Genomic Hybridization: insights from an empirical study. <i>BMC Genomics</i> , 2005, 6, 78.	1.2	29
42	Genomic insights from whole genome sequencing of four clonal outbreak <i>Campylobacter jejuni</i> assessed within the global <i>C. jejuni</i> population. <i>BMC Genomics</i> , 2016, 17, 990.	1.2	28
43	Comparative genomics profiling of clinical isolates of <i>Aeromonas salmonicida</i> using DNA microarrays. <i>BMC Genomics</i> , 2006, 7, 43.	1.2	27
44	Subtype-Specific Selection for Resistance to Fluoroquinolones but Not to Tetracyclines Is Evident in <i>Campylobacter jejuni</i> Isolates from Beef Cattle in Confined Feeding Operations in Southern Alberta, Canada. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	24
45	Subtyping of a Large Collection of Historical <i>Listeria monocytogenes</i> Strains from Ontario, Canada, by an Improved Multilocus Variable-Number Tandem-Repeat Analysis (MLVA). <i>Applied and Environmental Microbiology</i> , 2013, 79, 6472-6480.	1.4	21
46	Extensive characterization of <i>Campylobacter jejuni</i> chicken isolates to uncover genes involved in the ability to compete for gut colonization. <i>BMC Microbiology</i> , 2015, 15, 97.	1.3	21
47	Efficacy of wastewater treatment on <i>Arcobacter butzleri</i> density and strain diversity. <i>Water Research</i> , 2016, 105, 291-296.	5.3	20
48	Genomics-Based Molecular Epidemiology of <i>Campylobacter jejuni</i> Isolates from Feedlot Cattle and from People in Alberta, Canada. <i>Journal of Clinical Microbiology</i> , 2009, 47, 410-420.	1.8	19
49	SuperPhy: predictive genomics for the bacterial pathogen <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2016, 16, 65.	1.3	18
50	Epidemiology of <i>Campylobacter</i> , <i>Salmonella</i> and antimicrobial resistant <i>Escherichia coli</i> in free-living Canada geese (<i>Branta canadensis</i>) from three sources in southern Ontario. <i>Zoonoses and Public Health</i> , 2018, 65, 873-886.	0.9	18
51	Epidemiology, Relative Invasive Ability, Molecular Characterization, and Competitive Performance of <i>Campylobacter jejuni</i> Strains in the Chicken Gut. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7959-7966.	1.4	17
52	<i>Salmonella</i> , <i>Campylobacter</i> , <i>Clostridium difficile</i> , and antimicrobial resistant <i>Escherichia coli</i> in the faeces of sympatric mesomammals in southern Ontario, Canada. <i>Zoonoses and Public Health</i> , 2019, 66, 406-416.	0.9	14
53	Systematic Evaluation of Whole-Genome Sequencing Based Prediction of Antimicrobial Resistance in <i>Campylobacter jejuni</i> and <i>C. coli</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 776967.	1.5	14
54	Genomic Regions Conserved in Lineage II <i>Escherichia coli</i> O157:H7 Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 3271-3280.	1.4	13

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55	Molecular Epidemiology of <i>Campylobacter jejuni</i> Human and Chicken Isolates from Two Health Units. <i>Foodborne Pathogens and Disease</i> , 2014, 11, 150-155.	0.8	13
56	Rates of fluoroquinolone resistance in domestically acquired <i>Campylobacter jejuni</i> are increasing in people living within a model study location in Canada. <i>Canadian Journal of Microbiology</i> , 2021, 67, 37-52.	0.8	13
57	Evaluation of real-time PCR assays and standard curve optimisation for enhanced accuracy in quantification of <i>Campylobacter</i> environmental water isolates. <i>Journal of Microbiological Methods</i> , 2016, 129, 70-77.	0.7	12
58	Generalizability and comparability of prevalence estimates in the wild bird literature: methodological and epidemiological considerations. <i>Animal Health Research Reviews</i> , 2020, 21, 89-95.	1.4	12
59	Identification of <i>Salmonella enterica</i> species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2151-2161.	1.0	10
60	Molecular and Statistical Analysis of <i>Campylobacter</i> spp. and Antimicrobial Resistant <i>Campylobacter</i> Carriage in Wildlife and Livestock from Ontario Farms. <i>Zoonoses and Public Health</i> , 2017, 64, 194-203.	0.9	10
61	A strain comparison of <i>Campylobacter</i> isolated from retail poultry and human clinical cases in Atlantic Canada. <i>PLoS ONE</i> , 2019, 14, e0215928.	1.1	10
62	Clinically Relevant <i>Campylobacter jejuni</i> Subtypes Are Readily Found and Transmitted within the Cattle Production Continuum but Present a Limited Foodborne Risk. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	10
63	Therapeutic administration of enrofloxacin in mice does not select for fluoroquinolone resistance in <i>Campylobacter jejuni</i> . <i>Canadian Journal of Microbiology</i> , 2018, 64, 681-694.	0.8	9
64	Enhanced microbiological surveillance reveals that temporal case clusters contribute to the high rates of campylobacteriosis in a model agroecosystem. <i>International Journal of Medical Microbiology</i> , 2019, 309, 232-244.	1.5	9
65	Tetracycline Resistant <i>Campylobacter jejuni</i> Subtypes Emanating from Beef Cattle Administered Non-Therapeutic Chlorotetracycline are Longitudinally Transmitted within the Production Continuum but are Not Detected in Ground Beef. <i>Microorganisms</i> , 2020, 8, 23.	1.6	9
66	These Aren't the Strains You're Looking for: Recovery Bias of Common <i>Campylobacter jejuni</i> Subtypes in Mixed Cultures. <i>Frontiers in Microbiology</i> , 2020, 11, 541.	1.5	9
67	Prevalence and diversity of waterborne <i>Arcobacter butzleri</i> in southwestern Alberta, Canada. <i>Canadian Journal of Microbiology</i> , 2017, 63, 330-340.	0.8	8
68	Comparative genomic fingerprinting of <i>Campylobacter</i> : application in routine public health surveillance and epidemiological investigations. <i>Epidemiology and Infection</i> , 2017, 145, 299-309.	1.0	8
69	Studying Bacterial Genome Dynamics Using Microarray-Based Comparative Genomic Hybridization. <i>Methods in Molecular Biology</i> , 2007, 396, 223-253.	0.4	7
70	Cluster Analysis of <i>Campylobacter jejuni</i> Genotypes Isolated from Small and Medium-Sized Mammalian Wildlife and Bovine Livestock from Ontario Farms. <i>Zoonoses and Public Health</i> , 2017, 64, 185-193.	0.9	6
71	<i>Campylobacter jejuni</i> Strain Dynamics in a Raccoon (<i>Procyon lotor</i>) Population in Southern Ontario, Canada: High Prevalence and Rapid Subtype Turnover. <i>Frontiers in Veterinary Science</i> , 2020, 7, 27.	0.9	6
72	A repeated cross-sectional study of the epidemiology of <i>Campylobacter</i> and antimicrobial resistant Enterobacteriaceae in free-living Canada geese in Guelph, Ontario, Canada. <i>Zoonoses and Public Health</i> , 2019, 66, 60-72.	0.9	5

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73	Analysis of <i>Campylobacter jejuni</i> Subtype Distribution in the Chicken Broiler Production Continuum: a Longitudinal Examination To Identify Primary Contamination Points. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	5
74	Carriage of <i>Campylobacter</i> , <i>Salmonella</i> , and Antimicrobial-Resistant, Nonspecific <i>Escherichia coli</i> by Waterfowl Species Collected from Three Sources in Southern Ontario, Canada. <i>Journal of Wildlife Diseases</i> , 2019, 55, 917.	0.3	4
75	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. <i>Microbial Genomics</i> , 2021, 7, .	1.0	4
76	Clinical Metagenomics Is Increasingly Accurate and Affordable to Detect Enteric Bacterial Pathogens in Stool. <i>Microorganisms</i> , 2022, 10, 441.	1.6	4
77	<i>Campylobacter coli</i> isolated in Brazil typed by core genome Multilocus Sequence Typing shows high genomic diversity in a global context. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105018.	1.0	3
78	The EpiQuant Framework for Computing Epidemiological Concordance of Microbial Subtyping Data. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1334-1349.	1.8	2
79	Epidemiology of <i>Campylobacter jejuni</i> in raccoons (<i>Procyon lotor</i>) on swine farms and in conservation areas in southern Ontario. <i>Zoonoses and Public Health</i> , 2021, 68, 19-28.	0.9	1
80	Carriage of , , and Antimicrobial-Resistant, Nonspecific by Waterfowl Species Collected from Three Sources in Southern Ontario, Canada. <i>Journal of Wildlife Diseases</i> , 2019, 55, 917-922.	0.3	1