

Eduardo N Taboada

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

82

papers

2,728

citations

29

h-index

50

g-index

88

ext. papers

3,415

ext. citations

4.6

avg, IF

4.86

L-index

#	Paper	IF	Citations
82	The Salmonella In Silico Typing Resource (SISTR): An Open Web-Accessible Tool for Rapidly Typing and Subtyping Draft Salmonella Genome Assemblies. <i>PLoS ONE</i> , 2016 , 11, e0147101	3.7	235
81	The genetic bases for the variation in the lipo-oligosaccharide of the mucosal pathogen, <i>Campylobacter jejuni</i> . Biosynthesis of sialylated ganglioside mimics in the core oligosaccharide. <i>Journal of Biological Chemistry</i> , 2002 , 277, 327-37	5.4	215
80	Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. <i>BMC Bioinformatics</i> , 2010 , 11, 461	3.6	200
79	Genome-wide expression analyses of <i>Campylobacter jejuni</i> NCTC11168 reveals coordinate regulation of motility and virulence by flhA. <i>Journal of Biological Chemistry</i> , 2004 , 279, 20327-38	5.4	162
78	Genome evolution in major <i>Escherichia coli</i> O157:H7 lineages. <i>BMC Genomics</i> , 2007 , 8, 121	4.5	123
77	Large-scale comparative genomics meta-analysis of <i>Campylobacter jejuni</i> isolates reveals low level of genome plasticity. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 4566-76	9.7	102
76	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. <i>Microbial Genomics</i> , 2017 , 3, e000116	4.4	77
75	Molecular subtypes of <i>Campylobacter</i> spp., <i>Salmonella enterica</i> , and <i>Escherichia coli</i> O157:H7 isolated from faecal and surface water samples in the Oldman River watershed, Alberta, Canada. <i>Water Research</i> , 2011 , 45, 1247-57	12.5	75
74	A systematic review characterizing on-farm sources of <i>Campylobacter</i> spp. for broiler chickens. <i>PLoS ONE</i> , 2014 , 9, e104905	3.7	67
73	In silico genomic analyses reveal three distinct lineages of <i>Escherichia coli</i> O157:H7, one of which is associated with hyper-virulence. <i>BMC Genomics</i> , 2009 , 10, 287	4.5	59
72	Development and validation of a comparative genomic fingerprinting method for high-resolution genotyping of <i>Campylobacter jejuni</i> . <i>Journal of Clinical Microbiology</i> , 2012 , 50, 788-97	9.7	59
71	Whole-Genome Sequencing in Epidemiology of <i>Campylobacter jejuni</i> Infections. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 1269-1275	9.7	56
70	Transcriptional and translational expression patterns associated with immobilized growth of <i>Campylobacter jejuni</i> . <i>Microbiology (United Kingdom)</i> , 2006 , 152, 567-577	2.9	55
69	The Validation and Implications of Using Whole Genome Sequencing as a Replacement for Traditional Serotyping for a National Reference Laboratory. <i>Frontiers in Microbiology</i> , 2017 , 8, 1044	5.7	54
68	Evaluation of MALDI-TOF mass spectroscopy methods for determination of <i>Escherichia coli</i> pathotypes. <i>Journal of Microbiological Methods</i> , 2013 , 94, 180-91	2.8	53
67	Current methods for molecular typing of <i>Campylobacter</i> species. <i>Journal of Microbiological Methods</i> , 2013 , 95, 24-31	2.8	52
66	The occurrence and sources of <i>Campylobacter</i> spp., <i>Salmonella enterica</i> and <i>Escherichia coli</i> O157:H7 in the Salmon River, British Columbia, Canada. <i>Journal of Water and Health</i> , 2010 , 8, 374-86	2.2	47

65	Genotypic characterization and prevalence of virulence factors among Canadian Escherichia coli O157:H7 strains. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 4314-23	4.8	46
64	Methodologies towards the development of an oligonucleotide microarray for determination of Salmonella serotypes. <i>Journal of Microbiological Methods</i> , 2007 , 70, 261-71	2.8	46
63	Integrating Whole-Genome Sequencing Data Into Quantitative Risk Assessment of Foodborne Antimicrobial Resistance: A Review of Opportunities and Challenges. <i>Frontiers in Microbiology</i> , 2019 , 10, 1107	5.7	42
62	Spatial and temporal drivers of zoonotic pathogen contamination of an agricultural watershed. <i>Journal of Environmental Quality</i> , 2012 , 41, 242-52	3.4	42
61	Comparison of molecular typing methods useful for detecting clusters of Campylobacter jejuni and C. coli isolates through routine surveillance. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 798-809	9.7	41
60	Food Safety in the Age of Next Generation Sequencing, Bioinformatics, and Open Data Access. <i>Frontiers in Microbiology</i> , 2017 , 8, 909	5.7	40
59	Source attribution of human campylobacteriosis at the point of exposure by combining comparative exposure assessment and subtype comparison based on comparative genomic fingerprinting. <i>PLoS ONE</i> , 2017 , 12, e0183790	3.7	35
58	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. <i>Journal of Microbiological Methods</i> , 2012 , 91, 506-13	2.8	35
57	Comparative genomic analysis of Campylobacter jejuni 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	4.5	33
56	Epidemiology of antimicrobial resistant Campylobacter spp. isolated from retail meats in Canada. <i>International Journal of Food Microbiology</i> , 2017 , 253, 43-47	5.8	32
55	Comparative genomic assessment of Multi-Locus Sequence Typing: rapid accumulation of genomic heterogeneity among clonal isolates of Campylobacter jejuni. <i>BMC Evolutionary Biology</i> , 2008 , 8, 229	3	31
54	Rapid determination of Escherichia coli O157:H7 lineage types and molecular subtypes by using comparative genomic fingerprinting. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 6606-15	4.8	29
53	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	4.5	29
52	A Genome-Wide Association Study to Identify Diagnostic Markers for Human Pathogenic Strains. <i>Frontiers in Microbiology</i> , 2017 , 8, 1224	5.7	27
51	Comparative Detection and Quantification of Arcobacter butzleri in Stools from Diarrheic and Nondiarrheic People in Southwestern Alberta, Canada. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1082-8	9.7	25
50	Comprehensive assessment of the quality of Salmonella whole genome sequence data available in public sequence databases using the Salmonella in silico Typing Resource (SISTR). <i>Microbial Genomics</i> , 2018 , 4,	4.4	25
49	Detection of genetic diversity in Campylobacter jejuni isolated from a commercial turkey flock using flaA typing, MLST analysis and microarray assay. <i>PLoS ONE</i> , 2013 , 8, e51582	3.7	23
48	Comparative variation within the genome of Campylobacter jejuni NCTC 11168 in human and murine hosts. <i>PLoS ONE</i> , 2014 , 9, e88229	3.7	23

47	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	5.9	22
46	Comparative genomics profiling of clinical isolates of <i>Aeromonas salmonicida</i> using DNA microarrays. <i>BMC Genomics</i> , 2006 , 7, 43	4.5	21
45	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	5.7	20
44	Monomorphic genotypes within a generalist lineage of show signs of global dispersion. <i>Microbial Genomics</i> , 2016 , 2, e000088	4.4	19
43	Frequent Implication of Multistress-Tolerant <i>Campylobacter jejuni</i> in Human Infections. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1037-1044	10.2	18
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	4.5	17
41	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	4.5	16
40	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	4.5	16
39	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, 410-20	9.7	16
38	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	4.9	16
37	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,	4.8	15
36	Efficacy of wastewater treatment on <i>Arcobacter butzleri</i> density and strain diversity. <i>Water Research</i> , 2016 , 105, 291-296	12.5	15
35	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, 6472-80	4.8	15
34	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, 7959-66	4.8	15
33	The Integrated Rapid Infectious Disease Analysis (IRIDA) Platform		13
32	Molecular epidemiology of <i>Campylobacter jejuni</i> human and chicken isolates from two health units. <i>Foodborne Pathogens and Disease</i> , 2014 , 11, 150-5	3.8	12
31	Genomic regions conserved in lineage II <i>Escherichia coli</i> O157:H7 strains. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3271-80	4.8	12
30	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	2.9	10

29	Salmonella, Campylobacter, Clostridium difficile, and anti-microbial resistant Escherichia coli in the faeces of sympatric meso-mammals in southern Ontario, Canada. <i>Zoonoses and Public Health</i> , 2019 , 66, 406-416	2.9	9
28	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	2.1	9
27	SuperPhy: predictive genomics for the bacterial pathogen Escherichia coli. <i>BMC Microbiology</i> , 2016 , 16, 65	4.5	9
26	Identification of Salmonella enterica species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 2151-61	4.5	9
25	Evaluation of real-time PCR assays and standard curve optimisation for enhanced accuracy in quantification of Campylobacter environmental water isolates. <i>Journal of Microbiological Methods</i> , 2016 , 129, 70-77	2.8	9
24	A strain comparison of Campylobacter isolated from retail poultry and human clinical cases in Atlantic Canada. <i>PLoS ONE</i> , 2019 , 14, e0215928	3.7	8
23	Clinically Relevant Campylobacter jejuni 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,	4.8	8
22	Comparative genomic fingerprinting of Campylobacter: application in routine public health surveillance and epidemiological investigations. <i>Epidemiology and Infection</i> , 2017 , 145, 299-309	4.3	7
21	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	3.7	7
20	Molecular and Statistical Analysis of Campylobacter spp. and Antimicrobial-Resistant Campylobacter Carriage in Wildlife and Livestock from Ontario Farms. <i>Zoonoses and Public Health</i> , 2017 , 64, 194-203	2.9	7
19	Studying bacterial genome dynamics using microarray-based comparative genomic hybridization. <i>Methods in Molecular Biology</i> , 2007 , 396, 223-53	1.4	7
18	Rates of fluoroquinolone resistance in domestically acquired are increasing in people living within a model study location in Canada. <i>Canadian Journal of Microbiology</i> , 2021 , 67, 37-52	3.2	7
17	Prevalence and diversity of waterborne Arcobacter butzleri in southwestern Alberta, Canada. <i>Canadian Journal of Microbiology</i> , 2017 , 63, 330-340	3.2	6
16	Therapeutic administration of enrofloxacin in mice does not select for fluoroquinolone resistance in Campylobacter jejuni. <i>Canadian Journal of Microbiology</i> , 2018 , 64, 681-694	3.2	6
15	Strain Dynamics in a Raccoon () Population in Southern Ontario, Canada: High Prevalence and Rapid Subtype Turnover. <i>Frontiers in Veterinary Science</i> , 2020 , 7, 27	3.1	5
14	"These Aren't the Strains You're Looking for": Recovery Bias of Common Subtypes in Mixed Cultures. <i>Frontiers in Microbiology</i> , 2020 , 11, 541	5.7	4
13	Cluster Analysis of Campylobacter jejuni 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	2.9	4
12	A repeated cross-sectional study of the epidemiology of Campylobacter and antimicrobial resistant Enterobacteriaceae in free-living Canada geese in Guelph, Ontario, Canada. <i>Zoonoses and Public Health</i> , 2019 , 66, 60-72	2.9	4

11	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	1.3	3
10	Rapid Identification of Stable Clusters in Bacterial Populations Using the Adjusted Wallace Coefficient		3
9	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,	4.8	3
8	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
7	The EpiQuant Framework for Computing Epidemiological Concordance of Microbial Subtyping Data. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 1334-1349	9.7	2
6	Tetracycline Resistant Subtypes Emanating from Beef Cattle Administered Non-Therapeutic Chlortetracycline are Longitudinally Transmitted within the Production Continuum but are Not Detected in Ground Beef. <i>Microorganisms</i> , 2019 , 8,	4.9	2
5	Systematic Evaluation of Whole-Genome Sequencing Based Prediction of Antimicrobial Resistance in and. <i>Frontiers in Microbiology</i> , 2021 , 12, 776967	5.7	1
4	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel		1
3	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	1.3	1
2	<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	4.5	0
1	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	2.9	