

Eduardo N Taboada

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1616091/eduardo-n-taboada-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Systematic Evaluation of Whole-Genome Sequencing Based Prediction of Antimicrobial Resistance in and. <i>Frontiers in Microbiology</i> , 2021 , 12, 776967	5.7	1
81	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	
80	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
79	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
78	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
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	4.5	0
76	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	3.1	5
75	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
74	"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
73	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,	4.8	8
72	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	3.7	8
71	Salmonella, <i>Campylobacter</i> , <i>Clostridium difficile</i> , and anti-microbial resistant <i>Escherichia coli</i> in the faeces of sympatric meso-mammals in southern Ontario, Canada. <i>Zoonoses and Public Health</i> , 2019 , 66, 406-416	2.9	9
70	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
69	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
68	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
67	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
66	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	2.9	4

65	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
64	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
63	Frequent Implication of Multistress-Tolerant <i>Campylobacter jejuni</i> in Human Infections. <i>Emerging Infectious Diseases</i> , 2018 , 24, 1037-1044	10.2	18
62	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	3.2	6
61	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
60	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,	4.4	25
59	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
58	The EpiQuant Framework for Computing Epidemiological Concordance of Microbial Subtyping Data. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 1334-1349	9.7	2
57	Whole-Genome Sequencing in Epidemiology of <i>Campylobacter jejuni</i> Infections. <i>Journal of Clinical Microbiology</i> , 2017 , 55, 1269-1275	9.7	56
56	Prevalence and diversity of waterborne <i>Arcobacter butzleri</i> in southwestern Alberta, Canada. <i>Canadian Journal of Microbiology</i> , 2017 , 63, 330-340	3.2	6
55	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
54	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	5.8	32
53	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	4.3	7
52	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
51	SNVPhyl: a single nucleotide variant phylogenomics pipeline for microbial genomic epidemiology. <i>Microbial Genomics</i> , 2017 , 3, e000116	4.4	77
50	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	2.9	7
49	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	2.9	4
48	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

47	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
46	A Genome-Wide Association Study to Identify Diagnostic Markers for Human Pathogenic Strains. <i>Frontiers in Microbiology</i> , 2017 , 8, 1224	5.7	27
45	Efficacy of wastewater treatment on <i>Arcobacter butzleri</i> density and strain diversity. <i>Water Research</i> , 2016 , 105, 291-296	12.5	15
44	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
43	SuperPhy: predictive genomics for the bacterial pathogen <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2016 , 16, 65	4.5	9
42	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, 1082-8	9.7	25
41	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
40	Monomorphic genotypes within a generalist lineage of show signs of global dispersion. <i>Microbial Genomics</i> , 2016 , 2, e000088	4.4	19
39	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	2.8	9
38	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
37	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
36	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
35	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
34	Comparative variation within the genome of <i>Campylobacter jejuni</i> NCTC 11168 in human and murine hosts. <i>PLoS ONE</i> , 2014 , 9, e88229	3.7	23
33	Current methods for molecular typing of <i>Campylobacter</i> species. <i>Journal of Microbiological Methods</i> , 2013 , 95, 24-31	2.8	52
32	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
31	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
30	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	3.7	23

29	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, 506-13	2.8	35
28	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
27	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
26	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	9.7	41
25	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
24	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
23	Identification of <i>Salmonella enterica</i> species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 2151-61	4.5	9
22	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
21	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
20	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
19	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
18	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
17	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	31
16	Genotypic characterization and prevalence of virulence factors among Canadian <i>Escherichia coli</i> O157:H7 strains. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 4314-23	4.8	46
15	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, 6606-15	4.8	29
14	Genome evolution in major <i>Escherichia coli</i> O157:H7 lineages. <i>BMC Genomics</i> , 2007 , 8, 121	4.5	123
13	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	4.5	33
12	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

11	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
10	Studying bacterial genome dynamics using microarray-based comparative genomic hybridization. <i>Methods in Molecular Biology</i> , 2007 , 396, 223-53	1.4	7
9	Comparative genomics profiling of clinical isolates of <i>Aeromonas salmonicida</i> using DNA microarrays. <i>BMC Genomics</i> , 2006 , 7, 43	4.5	21
8	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
7	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
6	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
5	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
4	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
3	Rapid and accurate SNP genotyping of clonal bacterial pathogens with BioHansel		1
2	Rapid Identification of Stable Clusters in Bacterial Populations Using the Adjusted Wallace Coefficient		3
1	The Integrated Rapid Infectious Disease Analysis (IRIDA) Platform		13