

James L Bono

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.

88
papers

1,942
citations

24
h-index

42
g-index

92
ext. papers

2,409
ext. citations

4.4
avg, IF

4.55
L-index

#	Paper	IF	Citations
88	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013 , 14, R101	18.3	286
87	Animal-to-animal variation in fecal microbial diversity among beef cattle. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 4858-62	4.8	118
86	Greater diversity of Shiga toxin-encoding bacteriophage insertion sites among Escherichia coli O157:H7 isolates from cattle than in those from humans. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 671-9	4.8	95
85	Shiga-toxigenic Escherichia coli O157 in agricultural fair livestock, United States. <i>Emerging Infectious Diseases</i> , 2006 , 12, 780-6	10.2	85
84	Biofilm formation by Shiga toxin-producing Escherichia coli O157:H7 and Non-O157 strains and their tolerance to sanitizers commonly used in the food processing environment. <i>Journal of Food Protection</i> , 2012 , 75, 1418-28	2.5	80
83	Virulence-associated and antibiotic resistance genes of microbial populations in cattle feces analyzed using a metagenomic approach. <i>Journal of Microbiological Methods</i> , 2011 , 84, 278-82	2.8	71
82	Variable tick protein in two genomic groups of the relapsing fever spirochete Borrelia hermsii in western North America. <i>Infection and Immunity</i> , 2005 , 73, 6647-58	3.7	63
81	Outer surface protein A protects Lyme disease spirochetes from acquired host immunity in the tick vector. <i>Infection and Immunity</i> , 2008 , 76, 5228-37	3.7	61
80	Association of Escherichia coli O157:H7 tir polymorphisms with human infection. <i>BMC Infectious Diseases</i> , 2007 , 7, 98	4	58
79	Effect of proximity to a cattle feedlot on Escherichia coli O157:H7 contamination of leafy greens and evaluation of the potential for airborne transmission. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1101-10	4.8	55
78	Bgp, a secreted glycosaminoglycan-binding protein of Borrelia burgdorferi strain N40, displays nucleosidase activity and is not essential for infection of immunodeficient mice. <i>Infection and Immunity</i> , 2006 , 74, 3016-20	3.7	50
77	Phylogeny of Shiga toxin-producing Escherichia coli O157 isolated from cattle and clinically ill humans. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2047-62	8.3	47
76	Support vector machine applied to predict the zoonotic potential of E. coli O157 cattle isolates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11312-11317 ^{11.5}	11.5	44
75	Comparative genomics of the Campylobacter lari group. <i>Genome Biology and Evolution</i> , 2014 , 6, 3252-663.9	3.9	44
74	Phylogenetic classification of Escherichia coli O157:H7 strains of human and bovine origin using a novel set of nucleotide polymorphisms. <i>Genome Biology</i> , 2009 , 10, R56	18.3	42
73	Characterization of Escherichia coli O157:H7 strains isolated from supershedding cattle. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 4294-303	4.8	37
72	Prevalence and enumeration of Escherichia coli O157:H7 and Salmonella in U.S. abattoirs that process fewer than 1000 head of cattle per day. <i>Journal of Food Protection</i> , 2009 , 72, 1272-8	2.5	35

71	Genomic signatures of <i>Mannheimia haemolytica</i> that associate with the lungs of cattle with respiratory disease, an integrative conjugative element, and antibiotic resistance genes. <i>BMC Genomics</i> , 2016 , 17, 982	4.5	33
70	Evaluation of real time PCR assays for the detection and enumeration of enterohemorrhagic <i>Escherichia coli</i> directly from cattle feces. <i>Journal of Microbiological Methods</i> , 2014 , 105, 72-9	2.8	30
69	Association of nucleotide polymorphisms within the O-antigen gene cluster of <i>Escherichia coli</i> O26, O45, O103, O111, O121, and O145 with serogroups and genetic subtypes. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6689-703	4.8	28
68	Comparison of effects of antimicrobial interventions on multidrug-resistant <i>Salmonella</i> , susceptible <i>Salmonella</i> , and <i>Escherichia coli</i> O157:H7. <i>Journal of Food Protection</i> , 2008 , 71, 2177-81	2.5	27
67	Diverse genetic markers concordantly identify bovine origin <i>Escherichia coli</i> O157 genotypes underrepresented in human disease. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 361-5	4.8	26
66	Distribution of Shiga-toxigenic <i>Escherichia coli</i> O157 in the gastrointestinal tract of naturally O157-shedding cattle at necropsy. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5278-81	4.8	26
65	Large genomic differences between <i>Moraxella bovoculi</i> isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. <i>Veterinary Research</i> , 2016 , 47, 31	3.8	24
64	Evaluation of a real-time PCR kit for detecting <i>Escherichia coli</i> O157 in bovine fecal samples. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 1855-7	4.8	24
63	Evolution of a zoonotic pathogen: investigating prophage diversity in enterohaemorrhagic O157 by long-read sequencing. <i>Microbial Genomics</i> , 2016 , 2, e000096	4.4	21
62	Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing <i>Escherichia coli</i> O104. <i>BMC Microbiology</i> , 2015 , 15, 83	4.5	20
61	Bacterial community analysis of beef cattle feedlots reveals that pen surface is distinct from feces. <i>Foodborne Pathogens and Disease</i> , 2011 , 8, 647-9	3.8	20
60	Short-term evolution of Shiga toxin-producing O157:H7 between two food-borne outbreaks. <i>Microbial Genomics</i> , 2016 , 2, e000084	4.4	20
59	Shiga toxin sub-type 2a increases the efficiency of <i>Escherichia coli</i> O157 transmission between animals and restricts epithelial regeneration in bovine enteroids. <i>PLoS Pathogens</i> , 2019 , 15, e1008003	7.6	19
58	Complete Genome Sequence for the Shellfish Pathogen <i>Vibrio coralliilyticus</i> RE98 Isolated from a Shellfish Hatchery. <i>Genome Announcements</i> , 2014 , 2,		19
57	Characterization of <i>Escherichia coli</i> O157:H7 strains from contaminated raw beef trim during "high event periods". <i>Applied and Environmental Microbiology</i> , 2014 , 80, 506-14	4.8	19
56	International comparison of clinical, bovine, and environmental <i>Escherichia coli</i> O157 isolates on the basis of Shiga toxin-encoding bacteriophage insertion site genotypes. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7447-50	4.8	19
55	Genome Sequence of the Thermotolerant Foodborne Pathogen Serovar Senftenberg ATCC 43845 and Phylogenetic Analysis of Loci Encoding Increased Protein Quality Control Mechanisms. <i>MSystems</i> , 2017 , 2,	7.6	18
54	Disinfectant and antibiotic susceptibility profiles of <i>Escherichia coli</i> O157:H7 strains from cattle carcasses, feces, and hides and ground beef from the United States. <i>Journal of Food Protection</i> , 2013 , 76, 6-17	2.5	18

53	Lineage and genogroup-defining single nucleotide polymorphisms of Escherichia coli O157:H7. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 7036-41	4.8	17
52	Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of Escherichia coli O157:H7. <i>Clinical Infectious Diseases</i> , 2019 , 69, 428-437	11.6	16
51	Comparative Genomic Analysis Identifies a Campylobacter Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , 2017 , 9, 1843-1858	3.9	14
50	Dual-serotype biofilm formation by shiga toxin-producing Escherichia coli O157:H7 and O26:H11 strains. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 6341-4	4.8	14
49	Comparison of whole genome sequences from human and non-human Escherichia coli O26 strains. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015 , 5, 21	5.9	12
48	Comparative genomics of Salmonella enterica serovar Montevideo reveals lineage-specific gene differences that may influence ecological niche association. <i>Microbial Genomics</i> , 2018 , 4,	4.4	12
47	Comparative Genomics of All Three Campylobacter sputorum Biovars and a Novel Cattle-Associated C. sputorum Clade. <i>Genome Biology and Evolution</i> , 2017 , 9, 1513-1518	3.9	11
46	Disinfectant and Antimicrobial Susceptibility Profiles of the Big Six Non-O157 Shiga Toxin-Producing Escherichia coli Strains from Food Animals and Humans. <i>Journal of Food Protection</i> , 2016 , 79, 1355-70	2.5	11
45	Sequence of Colonization Determines the Composition of Mixed Biofilms by Escherichia coli O157:H7 and O111:H8 Strains. <i>Journal of Food Protection</i> , 2015 , 78, 1554-9	2.5	10
44	Genomic-based identification of environmental and clinical Listeria monocytogenes strains associated with an abortion outbreak in beef heifers. <i>BMC Veterinary Research</i> , 2020 , 16, 70	2.7	8
43	Complete Genome Sequence of a Colistin Resistance Gene (mcr-1)-Bearing Isolate of Escherichia coli from the United States. <i>Genome Announcements</i> , 2016 , 4,		7
42	Closed Genome and Comparative Phylogenetic Analysis of the Clinical Multidrug Resistant Shigella sonnei Strain 866. <i>Genome Biology and Evolution</i> , 2018 , 10, 2241-2247	3.9	7
41	First Closed Genome Sequence of Campylobacter fetus subsp. venerealis bv. intermedius. <i>Genome Announcements</i> , 2014 , 2,		7
40	Molecular serotyping of Escherichia coli O111:H8. <i>Journal of Microbiological Methods</i> , 2007 , 69, 381-3	2.8	7
39	Complete Genome Sequence of the Larval Shellfish Pathogen Vibrio tubiashii Type Strain ATCC 19109. <i>Genome Announcements</i> , 2014 , 2,		6
38	Genotyping Escherichia coli O157:H7 for its ability to cause disease in humans. <i>Current Protocols in Microbiology</i> , 2009 , Chapter 5, Unit 5A.3	7.1	6
37	Canonical Single Nucleotide Polymorphisms (SNPs) for High-Resolution Subtyping of Shiga-Toxin Producing Escherichia coli (STEC) O157:H7. <i>PLoS ONE</i> , 2015 , 10, e0131967	3.7	6
36	Complete Genome Sequence of UV-Resistant Campylobacter jejuni RM3194, Including an 81.08-Kilobase Plasmid. <i>Genome Announcements</i> , 2016 , 4,		6

35	Complete Genome Sequence of <i>Campylobacter jejuni</i> RM1285, a Rod-Shaped Morphological Variant. <i>Genome Announcements</i> , 2015 , 3,		5
34	Genome Sequences of Eight Shiga Toxin-Producing <i>Escherichia coli</i> Strains Isolated from a Produce-Growing Region in California. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	5
33	Complete Closed Genome Sequences of a <i>Mannheimia haemolytica</i> Serotype A1 Leukotoxin Deletion Mutant and Its Wild-Type Parent Strain. <i>Genome Announcements</i> , 2015 , 3,		4
32	Complete Genome Sequence of the <i>Campylobacter ureolyticus</i> Clinical Isolate RIGS 9880. <i>Genome Announcements</i> , 2015 , 3,		4
31	Complete Closed Genome Sequences of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serotypes Anatum, Montevideo, Typhimurium, and Newport, Isolated from Beef, Cattle, and Humans. <i>Genome Announcements</i> , 2016 , 4,		4
30	Occurrence of O157:H7 in Pest Flies Captured in Leafy Greens Plots Grown Near a Beef Cattle Feedlot. <i>Journal of Food Protection</i> , 2019 , 82, 1300-1307	2-5	4
29	Complete Closed Genome Sequences of Four <i>Mannheimia varigena</i> Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014 , 2,		4
28	Closed Genome Sequences of Seven Isolates from Beef Calves with Bovine Respiratory Disease Complex. <i>Genome Announcements</i> , 2017 , 5,		4
27	Locus of Heat Resistance (LHR) in Meat-Borne <i>Escherichia coli</i> : Screening and Genetic Characterization. <i>Applied and Environmental Microbiology</i> , 2021 , 87,	4-8	4
26	Complete Genome Sequence of the <i>Arcobacter molluscorum</i> Type Strain LMG 25693. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	4
25	Closed Genome Sequence of <i>Escherichia coli</i> K-12 Group Strain C600. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1-3	3
24	Complete, Closed Genome Sequences of 10 <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Typhimurium Strains Isolated from Human and Bovine Sources. <i>Genome Announcements</i> , 2016 , 4,		3
23	Complete Genome Sequence of the <i>Arcobacter bivalviorum</i> Type Strain LMG 26154. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	3
22	Complete Genome Sequences of the <i>Arcobacter cryaerophilus</i> Strains ATCC 43158 and ATCC 49615. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	3
21	Complete Genome Sequence of the <i>Arcobacter mytili</i> Type Strain LMG 24559. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1-3	3
20	Pathogenomes of Atypical Non-shigatoxigenic NSF/SF O157:H7/NM: Comprehensive Phylogenomic Analysis Using Closed Genomes. <i>Frontiers in Microbiology</i> , 2020 , 11, 619	5-7	2
19	Complete Genome Sequence of the Type Strain ATCC 51209. <i>Genome Announcements</i> , 2017 , 5,		2
18	Complete and Closed Genome Sequences of 10 <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Anatum Isolates from Human and Bovine Sources. <i>Genome Announcements</i> , 2016 , 4,		2

17	Greater Diversity of Shiga Toxin-Encoding Bacteriophage Insertion Sites among Escherichia coli O157:H7 Isolates from Cattle than in Those from Humans. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 554-554	4.8	2
16	Prophage-dependent recombination drives genome structural variation and phenotypic heterogeneity in Escherichia coli O157:H7		2
15	Differences between predicted outer membrane proteins of genotype 1 and 2 Mannheimia haemolytica. <i>BMC Microbiology</i> , 2020 , 20, 250	4.5	2
14	A Computational Method to Quantify the Effects of Slipped Strand Mispairing on Bacterial Tetranucleotide Repeats. <i>Scientific Reports</i> , 2019 , 9, 18087	4.9	2
13	Closed Genome Sequences and Antibigrams of 16 Isolates from Bovine Respiratory Disease Complex Cases and Apparently Healthy Controls. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	2
12	Complete Genome Sequence of the Type Strain LMG 24588. <i>Genome Announcements</i> , 2017 , 5,		1
11	Complete Genome Sequence of the Hippuricase-Positive Type Strain LMG 24591. <i>Genome Announcements</i> , 2017 , 5,		1
10	Genome Sequence of a Urease-Positive Campylobacter lari Strain. <i>Genome Announcements</i> , 2015 , 3,		1
9	Complete Closed Genome Sequence of the Extremely Heat-Resistant Strain Escherichia coli AW1.7. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0050221	1.3	1
8	Rapid estimation of Salmonella enterica contamination level in ground beef - Application of the time-to-positivity method using a combination of molecular detection and direct plating. <i>Food Microbiology</i> , 2021 , 93, 103615	6	1
7	Draft Genome Sequences of Seven Strains of Shiga Toxin-Producing Escherichia coli O111 with Variation in Their Sensitivity to Novobiocin. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1
6	Complete Genome Sequence of the Arcobacter ellisii Type Strain LMG 26155. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1
5	Complete Genome Sequence of the Arcobacter halophilus Type Strain CCUG 53805. <i>Microbiology Resource Announcements</i> , 2018 , 7,	1.3	1
4	Rates of evolutionary change of resident Escherichia coli O157:H7 differ within the same ecological niche.. <i>BMC Genomics</i> , 2022 , 23, 275	4.5	0
3	Complete Genome Sequencing of Four Arcobacter Species Reveals a Diverse Suite of Mobile Elements. <i>Genome Biology and Evolution</i> , 2020 , 12, 3850-3856	3.9	
2	Genomic analysis of shiga toxin-containing Escherichia coli O157:H7 isolated from Argentinean cattle. <i>PLoS ONE</i> , 2021 , 16, e0258753	3.7	
1	Reply to Baba and Kanamori. <i>Clinical Infectious Diseases</i> , 2020 , 71, 1353-1355	11.6	