

James L Bono

List of Publications by Year in descending order

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89
papers

2,613
citations

218592

26
h-index

206029

48
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92
all docs

92
docs citations

92
times ranked

3144
citing authors

#	ARTICLE	IF	CITATIONS
1	Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , 2013, 14, R101.	13.9	378
2	Animal-to-Animal Variation in Fecal Microbial Diversity among Beef Cattle. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4858-4862.	1.4	146
3	Greater Diversity of Shiga Toxin-Encoding Bacteriophage Insertion Sites among <i>Escherichia coli</i> O157:H7 Isolates from Cattle than in Those from Humans. <i>Applied and Environmental Microbiology</i> , 2007, 73, 671-679.	1.4	117
4	Biofilm Formation by Shiga Toxin-Producing <i>Escherichia coli</i> 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, 1418-1428.	0.8	116
5	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, 278-282.	0.7	103
6	Shiga-toxigenic <i>Escherichia coli</i> O157 in Agricultural Fair Livestock, United States. <i>Emerging Infectious Diseases</i> , 2006, 12, 780-786.	2.0	97
7	Variable Tick Protein in Two Genomic Groups of the Relapsing Fever Spirochete <i>Borrelia hermsii</i> in Western North America. <i>Infection and Immunity</i> , 2005, 73, 6647-6658.	1.0	70
8	Outer Surface Protein A Protects Lyme Disease Spirochetes from Acquired Host Immunity in the Tick Vector. <i>Infection and Immunity</i> , 2008, 76, 5228-5237.	1.0	69
9	Comparative Genomics of the <i>Campylobacter lari</i> Group. <i>Genome Biology and Evolution</i> , 2014, 6, 3252-3266.	1.1	69
10	Effect of Proximity to a Cattle Feedlot on <i>Escherichia coli</i> O157:H7 Contamination of Leafy Greens and Evaluation of the Potential for Airborne Transmission. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1101-1110.	1.4	67
11	Association of <i>Escherichia coli</i> O157:H7 tir polymorphisms with human infection. <i>BMC Infectious Diseases</i> , 2007, 7, 98.	1.3	64
12	Bgp, a Secreted Glycosaminoglycan-Binding Protein of <i>Borrelia burgdorferi</i> Strain N40, Displays Nucleosidase Activity and Is Not Essential for Infection of Immunodeficient Mice. <i>Infection and Immunity</i> , 2006, 74, 3016-3020.	1.0	55
13	Support vector machine applied to predict the zoonotic potential of <i>E. coli</i> O157 cattle isolates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11312-11317.	3.3	55
14	Phylogeny of Shiga Toxin-Producing <i>Escherichia coli</i> O157 Isolated from Cattle and Clinically Ill Humans. <i>Molecular Biology and Evolution</i> , 2012, 29, 2047-2062.	3.5	53
15	Phylogenetic classification of <i>Escherichia coli</i> O157:H7 strains of human and bovine origin using a novel set of nucleotide polymorphisms. <i>Genome Biology</i> , 2009, 10, R56.	13.9	47
16	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.	1.2	46
17	Evolution of a zoonotic pathogen: investigating prophage diversity in enterohaemorrhagic <i>Escherichia coli</i> O157 by long-read sequencing. <i>Microbial Genomics</i> , 2016, 2, e000096.	1.0	46
18	Characterization of <i>Escherichia coli</i> O157:H7 Strains Isolated from Supershedding Cattle. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4294-4303.	1.4	45

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19	Short-term evolution of Shiga toxin-producing <i>Escherichia coli</i> O157:H7 between two food-borne outbreaks. <i>Microbial Genomics</i> , 2016, 2, e000084.	1.0	45
20	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, 72-79.	0.7	42
21	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.	2.1	42
22	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, 2177-2181.	0.8	41
23	Prevalence and Enumeration of <i>Escherichia coli</i> O157:H7 and <i>Salmonella</i> in U.S. Abattoirs that Process Fewer than 1,000 Head of Cattle per Day. <i>Journal of Food Protection</i> , 2009, 72, 1272-1278.	0.8	38
24	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.	1.1	38
25	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, 361-365.	1.4	35
26	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, 5278-5281.	1.4	29
27	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, 6689-6703.	1.4	28
28	Genotyping <i>Escherichia coli</i> O157:H7 for Its Ability to Cause Disease in Humans. <i>Current Protocols in Microbiology</i> , 2009, 14, Unit 5A.3.	6.5	27
29	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.	0.8	27
30	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, 506-514.	1.4	26
31	Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of <i>Escherichia coli</i> O157:H7. <i>Clinical Infectious Diseases</i> , 2019, 69, 428-437.	2.9	26
32	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, 1855-1857.	1.4	25
33	Complete Genome Sequence for the Shellfish Pathogen <i>Vibrio coralliilyticus</i> RE98 Isolated from a Shellfish Hatchery. <i>Genome Announcements</i> , 2014, 2, .	0.8	25
34	Genome Sequence of the Thermotolerant Foodborne Pathogen <i>Salmonella enterica</i> Serovar Senftenberg ATCC 43845 and Phylogenetic Analysis of Loci Encoding Increased Protein Quality Control Mechanisms. <i>MSystems</i> , 2017, 2, .	1.7	25
35	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.	1.3	24
36	Bacterial Community Analysis of Beef Cattle Feedlots Reveals That Pen Surface Is Distinct from Feces. <i>Foodborne Pathogens and Disease</i> , 2011, 8, 647-649.	0.8	23

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37	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, 7447-7450.	1.4	21
38	Closed Genome Sequence of <i>Escherichia coli</i> K-12 Group Strain C600. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	21
39	Complete Genome Sequence of UV-Resistant <i>Campylobacter jejuni</i> RM3194, Including an 81.08-Kilobase Plasmid. <i>Genome Announcements</i> , 2016, 4, .	0.8	20
40	Comparative Genomic Analysis Identifies a <i>Campylobacter</i> Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , 2017, 9, 1843-1858.	1.1	20
41	Lineage and Genogroup-Defining Single Nucleotide Polymorphisms of <i>Escherichia coli</i> O157:H7. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7036-7041.	1.4	19
42	Comparative genomics of <i>Salmonella enterica</i> serovar Montevideo reveals lineage-specific gene differences that may influence ecological niche association. <i>Microbial Genomics</i> , 2018, 4, .	1.0	19
43	Comparison of whole genome sequences from human and non-human <i>Escherichia coli</i> O26 strains. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 21.	1.8	15
44	Comparative Genomics of All Three <i>Campylobacter sputorum</i> Biovars and a Novel Cattle-Associated <i>C. sputorum</i> Clade. <i>Genome Biology and Evolution</i> , 2017, 9, 1513-1518.	1.1	15
45	Dual-Serotype Biofilm Formation by Shiga Toxin-Producing <i>Escherichia coli</i> O157:H7 and O26:H11 Strains. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6341-6344.	1.4	14
46	Disinfectant and Antimicrobial Susceptibility Profiles of the Big Six Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> Strains from Food Animals and Humans. <i>Journal of Food Protection</i> , 2016, 79, 1355-1370.	0.8	14
47	Genomic-based identification of environmental and clinical <i>Listeria monocytogenes</i> strains associated with an abortion outbreak in beef heifers. <i>BMC Veterinary Research</i> , 2020, 16, 70.	0.7	14
48	Sequence of Colonization Determines the Composition of Mixed Biofilms by <i>Escherichia coli</i> O157:H7 and O111:H8 Strains. <i>Journal of Food Protection</i> , 2015, 78, 1554-1559.	0.8	13
49	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, .	0.3	11
50	Pathogenomes of Atypical Non-shigatoxigenic <i>Escherichia coli</i> NSF/SF O157:H7/NM: Comprehensive Phylogenomic Analysis Using Closed Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 619.	1.5	11
51	Closed Genome and Comparative Phylogenetic Analysis of the Clinical Multidrug Resistant <i>Shigella sonnei</i> Strain 866. <i>Genome Biology and Evolution</i> , 2018, 10, 2241-2247.	1.1	10
52	First Closed Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> bv. <i>intermedius</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	9
53	Complete Genome Sequence of a Colistin Resistance Gene (<i>mcr-1</i>)-Bearing Isolate of <i>Escherichia coli</i> from the United States. <i>Genome Announcements</i> , 2016, 4, .	0.8	9
54	Differences between predicted outer membrane proteins of genotype 1 and <i>Mannheimia haemolytica</i> . <i>BMC Microbiology</i> , 2020, 20, 250.	1.3	9

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55	Genome structural variation in <i>Escherichia coli</i> O157:H7. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
56	Complete Genome Sequence of the Larval Shellfish Pathogen <i>Vibrio tubiashii</i> Type Strain ATCC 19109. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
57	Occurrence of <i>Escherichia coli</i> 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.	0.8	8
58	Locus of Heat Resistance (LHR) in Meat-Borne <i>Escherichia coli</i> : Screening and Genetic Characterization. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	8
59	Canonical Single Nucleotide Polymorphisms (SNPs) for High-Resolution Subtyping of Shiga-Toxin Producing <i>Escherichia coli</i> (STEC) O157:H7. <i>PLoS ONE</i> , 2015, 10, e0131967.	1.1	8
60	Molecular serotyping of <i>Escherichia coli</i> O111:H8. <i>Journal of Microbiological Methods</i> , 2007, 69, 381-383.	0.7	7
61	Complete Closed Genome Sequences of Four <i>Mannheimia varigena</i> Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
62	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, .	0.8	6
63	Complete Genome Sequence of the <i>Arcobacter molluscorum</i> Type Strain LMG 25693. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	6
64	Complete Genome Sequence of <i>Campylobacter jejuni</i> RM1285, a Rod-Shaped Morphological Variant. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
65	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, .	0.8	5
66	Complete Genome Sequence of the <i>Campylobacter ureolyticus</i> Clinical Isolate RIGS 9880. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
67	Closed Genome Sequences of Seven <i>Histophilus somni</i> Isolates from Beef Calves with Bovine Respiratory Disease Complex. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
68	Complete Genome Sequence of the <i>Arcobacter bivalviorum</i> Type Strain LMG 26154. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	5
69	A Computational Method to Quantify the Effects of Slipped Strand Mispairing on Bacterial Tetranucleotide Repeats. <i>Scientific Reports</i> , 2019, 9, 18087.	1.6	5
70	Complete Genome Sequences of the <i>Arcobacter cryaerophilus</i> Strains ATCC 43158 T and ATCC 49615. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
71	Complete Genome Sequence of the <i>Arcobacter mytili</i> Type Strain LMG 24559. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
72	Genomic analysis of shiga toxin-containing <i>Escherichia coli</i> O157:H7 isolated from Argentinean cattle. <i>PLoS ONE</i> , 2021, 16, e0258753.	1.1	4

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73	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, .	0.8	3
74	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, .	0.8	3
75	Complete Genome Sequence of the <i>Campylobacter helveticus</i> Type Strain ATCC 51209. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
76	Rapid estimation of <i>Salmonella enterica</i> 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.	2.1	3
77	Rates of evolutionary change of resident <i>Escherichia coli</i> O157:H7 differ within the same ecological niche. <i>BMC Genomics</i> , 2022, 23, 275.	1.2	3
78	Closed Genome Sequences and Antibiograms of 16 <i>Pasteurella multocida</i> Isolates from Bovine Respiratory Disease Complex Cases and Apparently Healthy Controls. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	2
79	Complete Closed Genome Sequence of the Extremely Heat-Resistant Strain <i>Escherichia coli</i> AW1.7. <i>Microbiology Resource Announcements</i> , 2021, 10, e0050221.	0.3	2
80	Genome Sequence of a Urease-Positive <i>Campylobacter lari</i> Strain. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
81	Complete Genome Sequence of the Hippuricase-Positive <i>Campylobacter avium</i> Type Strain LMG 24591. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
82	Complete Genome Sequence of the <i>Campylobacter cuniculorum</i> Type Strain LMG 24588. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
83	Draft Genome Sequences of Seven Strains of Shiga Toxin-Producing <i>Escherichia coli</i> O111 with Variation in Their Sensitivity to Novobiocin. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
84	Complete Genome Sequence of the <i>Arcobacter ellisii</i> Type Strain LMG 26155. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
85	Complete Genome Sequence of the <i>Arcobacter halophilus</i> Type Strain CCUG 53805. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	1
86	Complete Genome Sequence of the <i>Arcobacter suis</i> Type Strain LMG 26152. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	0
87	Complete Genome Sequences of Three Shiga Toxin-Producing <i>Escherichia coli</i> O111:H8 Strains Exhibiting an Aggregation Phenotype. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
88	Reply to Baba and Kanamori. <i>Clinical Infectious Diseases</i> , 2020, 71, 1353-1355.	2.9	0
89	Complete Genome Sequencing of Four <i>Arcobacter</i> Species Reveals a Diverse Suite of Mobile Elements. <i>Genome Biology and Evolution</i> , 2020, 12, 3850-3856.	1.1	0