

# James L Bono

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/69959/james-l-bono-publications-by-year.pdf>

**Version:** 2024-04-27

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.

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 | Rates of evolutionary change of resident Escherichia coli O157:H7 differ within the same ecological niche.. <i>BMC Genomics</i> , <b>2022</b> , 23, 275  | 4.5  | 0         |
| 87 | Genomic analysis of shiga toxin-containing Escherichia coli O157:H7 isolated from Argentinean cattle. <i>PLoS ONE</i> , <b>2021</b> , 16, e0258753   | 3.7  |           |
| 86 | Locus of Heat Resistance (LHR) in Meat-Borne Escherichia coli: Screening and Genetic Characterization. <i>Applied and Environmental Microbiology</i> , <b>2021</b> , 87,   | 4.8  | 4         |
| 85 | Complete Closed Genome Sequence of the Extremely Heat-Resistant Strain Escherichia coli AW1.7. <i>Microbiology Resource Announcements</i> , <b>2021</b> , 10, e0050221   | 1.3  | 1         |
| 84 | 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> , <b>2021</b> , 93, 103615 | 6    | 1         |
| 83 | Genomic-based identification of environmental and clinical Listeria monocytogenes strains associated with an abortion outbreak in beef heifers. <i>BMC Veterinary Research</i> , <b>2020</b> , 16, 70  | 2.7  | 8         |
| 82 | Complete Genome Sequencing of Four Arcobacter Species Reveals a Diverse Suite of Mobile Elements. <i>Genome Biology and Evolution</i> , <b>2020</b> , 12, 3850-3856  | 3.9  |           |
| 81 | Pathogenomes of Atypical Non-shigatoxigenic NSF/SF O157:H7/NM: Comprehensive Phylogenomic Analysis Using Closed Genomes. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 619  | 5.7  | 2         |
| 80 | Reply to Baba and Kanamori. <i>Clinical Infectious Diseases</i> , <b>2020</b> , 71, 1353-1355  | 11.6 |           |
| 79 | Differences between predicted outer membrane proteins of genotype 1 and 2 Mannheimia haemolytica. <i>BMC Microbiology</i> , <b>2020</b> , 20, 250  | 4.5  | 2         |
| 78 | Shiga toxin sub-type 2a increases the efficiency of Escherichia coli O157 transmission between animals and restricts epithelial regeneration in bovine enteroids. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1008003                         | 7.6  | 19        |
| 77 | Closed Genome Sequence of Escherichia coli K-12 Group Strain C600. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,   | 1.3  | 3         |
| 76 | Occurrence of O157:H7 in Pest Flies Captured in Leafy Greens Plots Grown Near a Beef Cattle Feedlot. <i>Journal of Food Protection</i> , <b>2019</b> , 82, 1300-1307   | 2.5  | 4         |
| 75 | A Computational Method to Quantify the Effects of Slipped Strand Mispairing on Bacterial Tetranucleotide Repeats. <i>Scientific Reports</i> , <b>2019</b> , 9, 18087   | 4.9  | 2         |
| 74 | Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of Escherichia coli O157:H7. <i>Clinical Infectious Diseases</i> , <b>2019</b> , 69, 428-437                                    | 11.6 | 16        |
| 73 | Closed Genome and Comparative Phylogenetic Analysis of the Clinical Multidrug Resistant Shigella sonnei Strain 866. <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 2241-2247  | 3.9  | 7         |
| 72 | Comparative genomics of Salmonella enterica serovar Montevideo reveals lineage-specific gene differences that may influence ecological niche association. <i>Microbial Genomics</i> , <b>2018</b> , 4,                                       | 4.4  | 12        |

|    |  |     |    |
|----|--|-----|----|
| 71 | Complete Genome Sequence of the <i>Arcobacter bivalviorum</i> Type Strain LMG 26154. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,   | 1.3 | 3  |
| 70 | 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> , <b>2018</b> , 7,  | 1.3 | 5  |
| 69 | 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> , <b>2018</b> , 7,                                   | 1.3 | 1  |
| 68 | Complete Genome Sequence of the <i>Arcobacter ellisii</i> Type Strain LMG 26155. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,   | 1.3 | 1  |
| 67 | Complete Genome Sequence of the <i>Arcobacter molluscorum</i> Type Strain LMG 25693. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,   | 1.3 | 4  |
| 66 | Closed Genome Sequences and Antibigrams of 16 Isolates from Bovine Respiratory Disease Complex Cases and Apparently Healthy Controls. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,  | 1.3 | 2  |
| 65 | Complete Genome Sequences of the <i>Arcobacter cryaerophilus</i> Strains ATCC 43158 and ATCC 49615. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,  | 1.3 | 3  |
| 64 | Complete Genome Sequence of the <i>Arcobacter halophilus</i> Type Strain CCUG 53805. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,   | 1.3 | 1  |
| 63 | Complete Genome Sequence of the <i>Arcobacter mytili</i> Type Strain LMG 24559. <i>Microbiology Resource Announcements</i> , <b>2018</b> , 7,  | 1.3 | 3  |
| 62 | Complete Genome Sequence of the Type Strain LMG 24588. <i>Genome Announcements</i> , <b>2017</b> , 5,  |     | 1  |
| 61 | Complete Genome Sequence of the Type Strain ATCC 51209. <i>Genome Announcements</i> , <b>2017</b> , 5,   |     | 2  |
| 60 | Comparative Genomic Analysis Identifies a <i>Campylobacter</i> Clade Deficient in Selenium Metabolism. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 1843-1858  | 3.9 | 14 |
| 59 | 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> , <b>2017</b> , 9, 1513-1518   | 3.9 | 11 |
| 58 | 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> , <b>2017</b> , 2,                              | 7.6 | 18 |
| 57 | Closed Genome Sequences of Seven Isolates from Beef Calves with Bovine Respiratory Disease Complex. <i>Genome Announcements</i> , <b>2017</b> , 5,   |     | 4  |
| 56 | Complete Genome Sequence of the Hippuricase-Positive Type Strain LMG 24591. <i>Genome Announcements</i> , <b>2017</b> , 5,   |     | 1  |
| 55 | 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> , <b>2016</b> , 113, 11312-11317 <sup>11.5</sup> |     | 44 |
| 54 | 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> , <b>2016</b> , 4,  |     | 7  |

|    |  |     |    |
|----|--|-----|----|
| 53 | Complete, Closed Genome Sequences of 10 Salmonella enterica subsp. enterica Serovar Typhimurium Strains Isolated from Human and Bovine Sources. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 3  |
| 52 | Complete and Closed Genome Sequences of 10 Salmonella enterica subsp. enterica Serovar Anatum Isolates from Human and Bovine Sources. <i>Genome Announcements</i> , <b>2016</b> , 4,   |     | 2  |
| 51 | Complete Closed Genome Sequences of Salmonella enterica subsp. enterica Serotypes Anatum, Montevideo, Typhimurium, and Newport, Isolated from Beef, Cattle, and Humans. <i>Genome Announcements</i> , <b>2016</b> , 4,                           |     | 4  |
| 50 | Large genomic differences between Moraxella bovoculi isolates acquired from the eyes of cattle with infectious bovine keratoconjunctivitis versus the deep nasopharynx of asymptomatic cattle. <i>Veterinary Research</i> , <b>2016</b> , 47, 31 | 3.8 | 24 |
| 49 | Short-term evolution of Shiga toxin-producing O157:H7 between two food-borne outbreaks. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000084   | 4.4 | 20 |
| 48 | Evolution of a zoonotic pathogen: investigating prophage diversity in enterohaemorrhagic O157 by long-read sequencing. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000096  | 4.4 | 21 |
| 47 | Complete Genome Sequence of UV-Resistant Campylobacter jejuni RM3194, Including an 81.08-Kilobase Plasmid. <i>Genome Announcements</i> , <b>2016</b> , 4,  |     | 6  |
| 46 | Genomic signatures of Mannheimia haemolytica that associate with the lungs of cattle with respiratory disease, an integrative conjugative element, and antibiotic resistance genes. <i>BMC Genomics</i> , <b>2016</b> , 17, 982                  | 4.5 | 33 |
| 45 | 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> , <b>2016</b> , 79, 1355-70                        | 2.5 | 11 |
| 44 | Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing Escherichia coli O104. <i>BMC Microbiology</i> , <b>2015</b> , 15, 83       | 4.5 | 20 |
| 43 | Complete Closed Genome Sequences of a Mannheimia haemolytica Serotype A1 Leukotoxin Deletion Mutant and Its Wild-Type Parent Strain. <i>Genome Announcements</i> , <b>2015</b> , 3,  |     | 4  |
| 42 | Complete Genome Sequence of the Campylobacter ureolyticus Clinical Isolate RIGS 9880. <i>Genome Announcements</i> , <b>2015</b> , 3,   |     | 4  |
| 41 | Complete Genome Sequence of Campylobacter jejuni RM1285, a Rod-Shaped Morphological Variant. <i>Genome Announcements</i> , <b>2015</b> , 3,  |     | 5  |
| 40 | Genome Sequence of a Urease-Positive Campylobacter lari Strain. <i>Genome Announcements</i> , <b>2015</b> , 3,   |     | 1  |
| 39 | Comparison of whole genome sequences from human and non-human Escherichia coli O26 strains. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2015</b> , 5, 21  | 5.9 | 12 |
| 38 | Sequence of Colonization Determines the Composition of Mixed Biofilms by Escherichia coli O157:H7 and O111:H8 Strains. <i>Journal of Food Protection</i> , <b>2015</b> , 78, 1554-9  | 2.5 | 10 |
| 37 | 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> , <b>2015</b> , 81, 1101-10           | 4.8 | 55 |
| 36 | Canonical Single Nucleotide Polymorphisms (SNPs) for High-Resolution Subtyping of Shiga-Toxin Producing Escherichia coli (STEC) O157:H7. <i>PLoS ONE</i> , <b>2015</b> , 10, e0131967  | 3.7 | 6  |

|    |  |      |     |
|----|--|------|-----|
| 35 | 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> , <b>2014</b> , 105, 72-9  | 2.8  | 30  |
| 34 | Complete Closed Genome Sequences of Four <i>Mannheimia varigena</i> Isolates from Cattle with Shipping Fever. <i>Genome Announcements</i> , <b>2014</b> , 2,   |      | 4   |
| 33 | First Closed Genome Sequence of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> bv. <i>intermedius</i> . <i>Genome Announcements</i> , <b>2014</b> , 2,  |      | 7   |
| 32 | Complete Genome Sequence of the Larval Shellfish Pathogen <i>Vibrio tubiashii</i> Type Strain ATCC 19109. <i>Genome Announcements</i> , <b>2014</b> , 2,   |      | 6   |
| 31 | Complete Genome Sequence for the Shellfish Pathogen <i>Vibrio coralliilyticus</i> RE98 Isolated from a Shellfish Hatchery. <i>Genome Announcements</i> , <b>2014</b> , 2,  |      | 19  |
| 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> , <b>2014</b> , 80, 506-14  | 4.8  | 19  |
| 29 | Comparative genomics of the <i>Campylobacter lari</i> group. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 3252-663.9   |      | 44  |
| 28 | 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> , <b>2013</b> , 76, 6-17                  | 2.5  | 18  |
| 27 | Lineage and genogroup-defining single nucleotide polymorphisms of <i>Escherichia coli</i> O157:H7. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 7036-41   | 4.8  | 17  |
| 26 | Reducing assembly complexity of microbial genomes with single-molecule sequencing. <i>Genome Biology</i> , <b>2013</b> , 14, R101  | 18.3 | 286 |
| 25 | Characterization of <i>Escherichia coli</i> O157:H7 strains isolated from supershedding cattle. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 4294-303   | 4.8  | 37  |
| 24 | 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> , <b>2012</b> , 78, 6689-703 | 4.8  | 28  |
| 23 | Phylogeny of Shiga toxin-producing <i>Escherichia coli</i> O157 isolated from cattle and clinically ill humans. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 2047-62   | 8.3  | 47  |
| 22 | 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> , <b>2012</b> , 75, 1418-28          | 2.5  | 80  |
| 21 | Dual-serotype biofilm formation by shiga toxin-producing <i>Escherichia coli</i> O157:H7 and O26:H11 strains. <i>Applied and Environmental Microbiology</i> , <b>2012</b> , 78, 6341-4   | 4.8  | 14  |
| 20 | Virulence-associated and antibiotic resistance genes of microbial populations in cattle feces analyzed using a metagenomic approach. <i>Journal of Microbiological Methods</i> , <b>2011</b> , 84, 278-82  | 2.8  | 71  |
| 19 | Bacterial community analysis of beef cattle feedlots reveals that pen surface is distinct from feces. <i>Foodborne Pathogens and Disease</i> , <b>2011</b> , 8, 647-9  | 3.8  | 20  |
| 18 | Diverse genetic markers concordantly identify bovine origin <i>Escherichia coli</i> O157 genotypes underrepresented in human disease. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 361-5  | 4.8  | 26  |

|    |  |      |     |
|----|--|------|-----|
| 17 | 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> , <b>2010</b> , 76, 5278-81  | 4.8  | 26  |
| 16 | Animal-to-animal variation in fecal microbial diversity among beef cattle. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 4858-62   | 4.8  | 118 |
| 15 | Prevalence and enumeration of <i>Escherichia coli</i> O157:H7 and <i>Salmonella</i> in U.S. abattoirs that process fewer than 1000 head of cattle per day. <i>Journal of Food Protection</i> , <b>2009</b> , 72, 1272-8                                      | 2.5  | 35  |
| 14 | Genotyping <i>Escherichia coli</i> O157:H7 for its ability to cause disease in humans. <i>Current Protocols in Microbiology</i> , <b>2009</b> , Chapter 5, Unit 5A.3   | 7.1  | 6   |
| 13 | 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> , <b>2009</b> , 10, R56   | 18.3 | 42  |
| 12 | 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> , <b>2008</b> , 74, 7447-50 | 4.8  | 19  |
| 11 | 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> , <b>2008</b> , 74, 554-554                      | 4.8  | 2   |
| 10 | Outer surface protein A protects Lyme disease spirochetes from acquired host immunity in the tick vector. <i>Infection and Immunity</i> , <b>2008</b> , 76, 5228-37  | 3.7  | 61  |
| 9  | 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> , <b>2008</b> , 71, 2177-81                           | 2.5  | 27  |
| 8  | Association of <i>Escherichia coli</i> O157:H7 tir polymorphisms with human infection. <i>BMC Infectious Diseases</i> , <b>2007</b> , 7, 98  | 4    | 58  |
| 7  | 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> , <b>2007</b> , 73, 671-9                        | 4.8  | 95  |
| 6  | Molecular serotyping of <i>Escherichia coli</i> O111:H8. <i>Journal of Microbiological Methods</i> , <b>2007</b> , 69, 381-3   | 2.8  | 7   |
| 5  | 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> , <b>2006</b> , 74, 3016-20            | 3.7  | 50  |
| 4  | Shiga-toxigenic <i>Escherichia coli</i> O157 in agricultural fair livestock, United States. <i>Emerging Infectious Diseases</i> , <b>2006</b> , 12, 780-6  | 10.2 | 85  |
| 3  | 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> , <b>2005</b> , 73, 6647-58  | 3.7  | 63  |
| 2  | Evaluation of a real-time PCR kit for detecting <i>Escherichia coli</i> O157 in bovine fecal samples. <i>Applied and Environmental Microbiology</i> , <b>2004</b> , 70, 1855-7   | 4.8  | 24  |
| 1  | Prophage-dependent recombination drives genome structural variation and phenotypic heterogeneity in <i>Escherichia coli</i> O157:H7  |      | 2   |