Lance B Price

List of Publications by Year
in descending order

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89 papers	8,087 citations	36303 51 h-index	49909 87 g-index
91 all docs	91 docs citations	91 times ranked	9652 citing authors

#	Article	IF	Citations
1	Staphylococcus aureus CC398: Host Adaptation and Emergence of Methicillin Resistance in Livestock. MBio, 2012, 3, .	4.1	638
2	Industrial Food Animal Production, Antimicrobial Resistance, and Human Health. Annual Review of Public Health, 2008, 29, 151-169.	17.4	480
3	The Epidemic of Extended-Spectrum-Î²-Lactamase-Producing Escherichia coli ST131 Is Driven by a Single Highly Pathogenic Subclone, H 30-Rx. MBio, 2013, 4, e00377-13.	4.1	380
4	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	4.1	289
5	Population Genetics of Vibrio cholerae from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. MBio, 2011, 2, e00157-11.	4.1	268
6	Quantitative Microbial Ecology through Stable Isotope Probing. Applied and Environmental Microbiology, 2015, 81, 7570-7581.	3.1	242
7	Multidrug-Resistant Staphylococcus aureus in US Meat and Poultry. Clinical Infectious Diseases, 2011, 52, 1227-1230.	5.8	238
8	The Effects of Circumcision on the Penis Microbiome. PLoS ONE, 2010, 5, e8422.	2.5	216
9	Community Analysis of Chronic Wound Bacteria Using 16S rRNA Gene-Based Pyrosequencing: Impact of Diabetes and Antibiotics on Chronic Wound Microbiota. PLoS ONE, 2009, 4, e6462.	2.5	199
10	Identification and Characterization of Variable-Number Tandem Repeats in the Yersinia pestis Genome. Journal of Clinical Microbiology, 2001, 39, 3179-3185.	3.9	198
11	Staphylococcus aureus and the ecology of the nasal microbiome. Science Advances, 2015, 1, e1400216.	10.3	189
12	Escherichia coli ST131- H 22 as a Foodborne Uropathogen. MBio, 2018, 9, .	4.1	184
13	Phylogeography of Francisella tularensis : Global Expansion of a Highly Fit Clone. Journal of Bacteriology, 2009, 191, 2474-2484.	2.2	176
14	Large energetic adaptations of elderly muscle to resistance and endurance training. Journal of Applied Physiology, 2001, 90, 1663-1670.	2.5	168
15	Phylogenetic organization of bacterial activity. ISME Journal, 2016, 10, 2336-2340.	9.8	150
16	Linking soil bacterial biodiversity and soil carbon stability. ISME Journal, 2015, 9, 1477-1480.	9.8	147
17	Male Circumcision Significantly Reduces Prevalence and Load of Genital Anaerobic Bacteria. MBio, 2013, 4, e00076.	4.1	130
18	Livestock-Associated Methicillin and Multidrug Resistant Staphylococcus aureus Is Present among Industrial, Not Antibiotic-Free Livestock Operation Workers in North Carolina. PLoS ONE, 2013, 8, e67641.	2.5	130

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19	Fluoroquinolone-Resistant Campylobacter Isolates from Conventional and Antibiotic-Free Chicken Products. Environmental Health Perspectives, 2005, 113, 557-560.	6.0	124
20	The Persistence of Fluoroquinolone-ResistantCampylobacterin Poultry Production. Environmental Health Perspectives, 2007, 115, 1035-1039.	6.0	114
21	Molecular Epidemiology of Escherichia coli Sequence Type 131 and Its H30 and H30-Rx Subclones among Extended-Spectrum-Î²-Lactamase-Positive and -Negative E. coli Clinical Isolates from the Chicago Region, 2007 to 2010. Antimicrobial Agents and Chemotherapy, 2013, 57, 6385-6388.	3.2	112
22	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. MBio, 2014, 5, e01721.	4.1	112
23	Origin and Evolution of European Community-Acquired Methicillin-Resistant Staphylococcus aureus. MBio, 2014, 5, e01044-14.	4.1	112
24	In Vitro Selection and Characterization of Bacillus anthracis Mutants with High-Level Resistance to Ciprofloxacin. Antimicrobial Agents and Chemotherapy, 2003, 47, 2362-2365.	3.2	111
25	IntermingledKlebsiella pneumoniaePopulations Between Retail Meats and Human Urinary Tract Infections. Clinical Infectious Diseases, 2015, 61, 892-899.	5.8	104
26	Antibiotic resistant enterococci and staphylococci isolated from flies collected near confined poultry feeding operations. Science of the Total Environment, 2009, 407, 2701-2710.	8.0	103
27	Foodborne urinary tract infections: a new paradigm for antimicrobial-resistant foodborne illness. Frontiers in Microbiology, 2013, 4, 29.	3.5	103
28	Separate F-Type Plasmids Have Shaped the Evolution of the H 30 Subclone of Escherichia coli Sequence Type 131. MSphere, 2016, 1, .	2.9	98
29	Penile Microbiota and Female Partner Bacterial Vaginosis in Rakai, Uganda. MBio, 2015, 6, e00589.	4.1	96
30	Combating Global Antibiotic Resistance: Emerging One Health Concerns in Lower- and Middle-Income Countries. Clinical Infectious Diseases, 2018, 66, 963-969.	5.8	95
31	Evidence for Human Adaptation and Foodborne Transmission of Livestock-Associated Methicillin-ResistantStaphylococcus aureus: Table 1.. Clinical Infectious Diseases, 2016, 63, 1349-1352.	5.8	89
32	Elevated Risk of Carrying Gentamicin-Resistant Escherichia coli among U.S. Poultry Workers. Environmental Health Perspectives, 2007, 115, 1738-1742.	6.0	87
33	Genetic Diversity in the Protective Antigen Gene of Bacillus anthracis. Journal of Bacteriology, 1999, 181, 2358-2362.	2.2	85
34	Fate of antimicrobial-resistant enterococci and staphylococci and resistance determinants in stored poultry litter. Environmental Research, 2009, 109, 682-689.	7.5	84
35	Arsenic: A Roadblock to Potential Animal Waste Management Solutions. Environmental Health Perspectives, 2005, 113, 1123-1124.	6.0	82
36	Rapid Differentiation between Livestock-Associated and Livestock-Independent Staphylococcus aureus CC398 Clades. PLoS ONE, 2013, 8, e79645.	2.5	78

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37	Emergence of Livestock-Associated Methicillin-Resistant Staphylococcus aureus Bloodstream Infections in Denmark. Clinical Infectious Diseases, 2017, 65, 1072-1076.	5.8	78
38	Industrial Food Animal Production and Community Health. Current Environmental Health Reports, 2015, 2, 259-271.	6.7	74
39	The Semen Microbiome and Its Relationship with Local Immunology and Viral Load in HIV Infection. PLoS Pathogens, 2014, 10, e1004262.	4.7	73
40	Medical therapy reduces microbiota diversity and evenness in surgically recalcitrant chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2013, 3, 775-781.	2.8	71
41	Colonizing opportunistic pathogens (COPs): The beasts in all of us. PLoS Pathogens, 2017, 13, e1006369.	4.7	71
42	Multidrug-Resistant and Methicillin-ResistantStaphylococcus aureus(MRSA) in Hog Slaughter and Processing Plant Workers and Their Community in North Carolina (USA). Environmental Health Perspectives, 2014, 122, 471-477.	6.0	68
43	Recent Research Examining Links Among Klebsiella pneumoniae from Food, Food Animals, and Human Extraintestinal Infections. Current Environmental Health Reports, 2016, 3, 128-135.	6.7	68
44	Animal production and antimicrobial resistance in the clinic. Lancet, The, 2016, 387, e1-e3.	13.7	67
45	Foodâ€animal production and the spread of antibiotic resistance: the role of ecology. Frontiers in Ecology and the Environment, 2017, 15, 309-318.	4.0	64
46	Predictive Diagnostics for Escherichia coli Infections Based on the Clonal Association of Antimicrobial Resistance and Clinical Outcome. Journal of Clinical Microbiology, 2013, 51, 2991-2999.	3.9	62
47	Household Clustering of Escherichia coli Sequence Type 131 Clinical and Fecal Isolates According to Whole Genome Sequence Analysis. Open Forum Infectious Diseases, 2016, 3, ofw129.	0.9	62
48	Penile Anaerobic Dysbiosis as a Risk Factor for HIV Infection. MBio, 2017, 8, .	4.1	62
49	Halocin S8: a 36-Amino-Acid Microhalocin from the Haloarchaeal Strain S8a. Journal of Bacteriology, 2000, 182, 4951-4958.	2.2	61
50	Primary Severe Acute Respiratory Syndrome Coronavirus Infection Limits Replication but Not Lung Inflammation upon Homologous Rechallenge. Journal of Virology, 2012, 86, 4234-4244.	3.4	58
51	Clonal Dissemination of Enterobacter cloacae Harboring bla _{KPC-3} in the Upper Midwestern United States. Antimicrobial Agents and Chemotherapy, 2015, 59, 7723-7734.	3.2	58
52	Diversity and Population Overlap between Avian and Human Escherichia coli Belonging to Sequence Type 95. MSphere, 2019, 4, .	2.9	57
53	Role of Homologous Recombination in Adaptive Diversification of Extraintestinal Escherichia coli. Journal of Bacteriology, 2013, 195, 231-242.	2.2	50
54	Macroscale spatial variation in chronic wound microbiota: A crossâ€sectional study. Wound Repair and Regeneration, 2011, 19, 80-88.	3.0	49

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55	Complete Genome Sequence of the Epidemic and Highly Virulent CTX-M-15-Producing H 30-Rx Subclone of Escherichia coli ST131. Genome Announcements, 2013, 1, .	0.8	42
56	An ecological perspective on U.S. industrial poultry production: the role of anthropogenic ecosystems on the emergence of drug-resistant bacteria from agricultural environments. Current Opinion in Microbiology, 2011, 14, 244-250.	5.1	41
57	Ominous projections for global antibiotic use in food-animal production. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5554-5555.	7.1	40
58	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of Staphylococcus aureus. PLoS ONE, 2015, 10, e0130955.	2.5	40
59	Impact of saline irrigation and topical corticosteroids on the postsurgical sinonasal microbiota. International Forum of Allergy and Rhinology, 2015, 5, 185-190.	2.8	37
60	External Societal Costs of Antimicrobial Resistance in Humans Attributable to Antimicrobial Use in Livestock. Annual Review of Public Health, 2020, 41, 141-157.	17.4	35
61	Genome Sequence of Staphylococcus aureus Strain 11819-97, an ST80-IV European Community-Acquired Methicillin-Resistant Isolate. Journal of Bacteriology, 2012, 194, 1625-1626.	2.2	31
62	A Framework to Reduce Infectious Disease Risk from Urban Poultry in the United States. Public Health Reports, 2015, 130, 380-391.	2.5	31
63	vrrB, a Hypervariable Open Reading Frame in Bacillus anthracis. Journal of Bacteriology, 2000, 182, 3989-3997.	2.2	27
64	Arsenic Resistance in Campylobacter spp. Isolated from Retail Poultry Products. Applied and Environmental Microbiology, 2006, 72, 3069-3071.	3.1	27
65	Rapid Identification of Genetic Modifications in Bacillus anthracis Using Whole Genome Draft Sequences Generated by 454 Pyrosequencing. PLoS ONE, 2010, 5, e12397.	2.5	27
66	Genome Sequence of â€œCandidatus Microthrix parvicellaâ€•Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. Journal of Bacteriology, 2012, 194, 6670-6671.	2.2	27
67	Contrasting rRNA gene abundance patterns for aquatic fungi and bacteria in response to leaf-litter chemistry. Freshwater Science, 2013, 32, 663-672.	1.8	26
68	Prevalence of potentially neuropathic Campylobacter jejuni strains on commercial broiler chicken products. International Journal of Food Microbiology, 2011, 145, 395-399.	4.7	25
69	Neurologic Symptoms and Neuropathologic Antibodies in Poultry Workers Exposed to Campylobacter jejuni. Journal of Occupational and Environmental Medicine, 2007, 49, 748-755.	1.7	24
70	Molecular Investigations of a Locally Acquired Case of Melioidosis in Southern AZ, USA. PLoS Neglected Tropical Diseases, 2011, 5, e1347.	3.0	23
71	Antimicrobial-resistant Bacteria: An Unrecognized Work-related Risk in Food Animal Production. Safety and Health at Work, 2012, 3, 85-91.	0.6	22
72	Staphylococcus aureus Nasal Carriage among Beefpacking Workers in a Midwestern United States Slaughterhouse. PLoS ONE, 2016, 11, e0148789.	2.5	22

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73	Emergence of Enteroaggregative Escherichia coli within the ST131 Lineage as a Cause of Extraintestinal Infections. MBio, 2020, 11, .	4.1	22
74	Defining Wound Microbial Flora: Molecular Microbiology Opening New Horizons. Archives of Dermatology, 2009, 145, 1193-5.	1.4	20
75	Effects of concentrated poultry operations and cropland manure application on antibiotic resistant Escherichia coli and nutrient pollution in Chesapeake Bay watersheds. Science of the Total Environment, 2020, 735, 139401.	8.0	19
76	Whole-Genome Analysis of Recurrent Staphylococcus aureus t571/ST398 Infection in Farmer, Iowa, USA. Emerging Infectious Diseases, 2018, 24, 153-154.	4.3	17
77	Contamination of Retail Meat Samples with Multidrug-Resistant Organisms in Relation to Organic and Conventional Production and Processing: A Cross-Sectional Analysis of Data from the United States National Antimicrobial Resistance Monitoring System, 2012â€“2017. Environmental Health Perspectives, 2021, 129, 57004.	6.0	17
78	Social, cultural and economic aspects of antimicrobial resistance. Bulletin of the World Health Organization, 2020, 98, 823-823A.	3.3	16
79	Internal and Flanking Sequence from AFLP Fragments Using Ligation-Mediated Suppression PCR. BioTechniques, 1999, 26, 905-912.	1.8	15
80	Genomic differences between nasal Staphylococcus aureus from hog slaughterhouse workers and their communities. PLoS ONE, 2018, 13, e0193820.	2.5	11
81	End non-essential use of antimicrobials in livestock. BMJ: British Medical Journal, 2018, 360, k259.	2.3	7
82	The Effect of Antiretroviral Therapy Initiation on the Vaginal Microbiome in HIV-Infected Women. Open Forum Infectious Diseases, 2019, 6, ofz328.	0.9	7
83	Policy reforms for antibiotic use claims in livestock. Science, 2022, 376, 130-132.	12.6	7
84	Genital Anaerobic Bacterial Overgrowth and the PrePex Male Circumcision Device, Rakai, Uganda. Journal of Infectious Diseases, 2016, 214, 595-598.	4.0	6
85	An exploratory study of dog park visits as a risk factor for exposure to drug-resistant extra-intestinal pathogenic E. coli (ExPEC). BMC Research Notes, 2015, 8, 137.	1.4	5
86	Getting ahead of antibiotic-resistant Staphylococcus aureus in U.S. hogs. Environmental Research, 2021, 196, 110954.	7.5	3
87	Integrating sample similarities into latent class analysis: a treeâ€structured shrinkage approach. Biometrics, 2023, 79, 264-279.	1.4	3
88	Bacterial Whack-a-Mole: Reconsidering the Public Health Relevance of Using Carbadox in Food Animals. MBio, 2017, 8, .	4.1	1
89	Draft Whole-Genome Sequences of Ciprofloxacin-Resistant Derivatives of a Bacillus anthracis Î”ANR Strain Lacking pXO1 and pXO2 Plasmids. Microbiology Resource Announcements, 2020, 9, .	0.6	0