

Trevor W Alexander

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,676
citations

218677

26
h-index

315739

38
g-index

50
all docs

50
docs citations

50
times ranked

1262
citing authors

#	ARTICLE	IF	CITATIONS
1	The nasal viromes of cattle on arrival at western Canadian feedlots and their relationship to development of bovine respiratory disease. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2209-2218.	3.0	18
2	Quantifying fluorescent glycan uptake to elucidate strain-level variability in foraging behaviors of rumen bacteria. <i>Microbiome</i> , 2021, 9, 23.	11.1	16
3	Genetic relatedness and antimicrobial resistance in respiratory bacteria from beef calves sampled from spring processing to 40 days after feedlot entry. <i>Veterinary Microbiology</i> , 2020, 240, 108478.	1.9	12
4	Progression of nasopharyngeal and tracheal bacterial microbiotas of feedlot cattle during development of bovine respiratory disease. <i>Veterinary Microbiology</i> , 2020, 248, 108826.	1.9	22
5	Assessment of Metagenomic Sequencing and qPCR for Detection of Influenza D Virus in Bovine Respiratory Tract Samples. <i>Viruses</i> , 2020, 12, 814.	3.3	10
6	Topography of the respiratory tract bacterial microbiota in cattle. <i>Microbiome</i> , 2020, 8, 91.	11.1	38
7	Analysis of Active Site Architecture and Reaction Product Linkage Chemistry Reveals a Conserved Cleavage Substrate for an Endo-alpha-mannanase within Diverse Yeast Mannans. <i>Journal of Molecular Biology</i> , 2020, 432, 1083-1097.	4.2	16
8	Intranasal Bacterial Therapeutics Reduce Colonization by the Respiratory Pathogen <i>Mannheimia haemolytica</i> in Dairy Calves. <i>MSystems</i> , 2020, 5, .	3.8	33
9	A Sensitive and Accurate Recombinase Polymerase Amplification Assay for Detection of the Primary Bacterial Pathogens Causing Bovine Respiratory Disease. <i>Frontiers in Veterinary Science</i> , 2020, 7, 208.	2.2	16
10	Respiratory Bacterial Microbiota in Cattle. <i>Veterinary Clinics of North America - Food Animal Practice</i> , 2020, 36, 297-320.	1.2	36
11	The role of the bovine respiratory bacterial microbiota in health and disease. <i>Animal Health Research Reviews</i> , 2020, 21, 168-171.	3.1	11
12	Draft Genome Sequences of 14 <i>Lactobacillus</i> , <i>Enterococcus</i> , and <i>Staphylococcus</i> Isolates from the Nasopharynx of Healthy Feedlot Cattle. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
13	Development of Bacterial Therapeutics against the Bovine Respiratory Pathogen <i>Mannheimia haemolytica</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	29
14	Evaluation of the Nasopharyngeal Microbiota in Beef Cattle Transported to a Feedlot, With a Focus on Lactic Acid-Producing Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 1988.	3.5	22
15	Antibiotic treatment in feedlot cattle: a longitudinal study of the effect of oxytetracycline and tulathromycin on the fecal and nasopharyngeal microbiota. <i>Microbiome</i> , 2019, 7, 86.	11.1	69
16	Lower Respiratory Tract Microbiome and Resistome of Bovine Respiratory Disease Mortalities. <i>Microbial Ecology</i> , 2019, 78, 446-456.	2.8	46
17	Respiratory viruses identified in western Canadian beef cattle by metagenomic sequencing and their association with bovine respiratory disease. <i>Transboundary and Emerging Diseases</i> , 2019, 66, 1379-1386.	3.0	59
18	Comparison of the nasopharyngeal bacterial microbiota of beef calves raised without the use of antimicrobials between healthy calves and those diagnosed with bovine respiratory disease. <i>Veterinary Microbiology</i> , 2019, 231, 56-62.	1.9	33

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19	Long-term and legacy effects of manure application on soil microbial community composition. <i>Biology and Fertility of Soils</i> , 2018, 54, 269-283.	4.3	82
20	In silico identification and high throughput screening of antigenic proteins as candidates for a <i>Mannheimia haemolytica</i> vaccine. <i>Veterinary Immunology and Immunopathology</i> , 2018, 195, 19-24.	1.2	4
21	Injectable antimicrobials in commercial feedlot cattle and their effect on the nasopharyngeal microbiota and antimicrobial resistance. <i>Veterinary Microbiology</i> , 2018, 214, 140-147.	1.9	47
22	Fecal microbiota of lambs fed purple prairie clover (<i>Dalea purpurea</i> Vent.) and alfalfa (<i>Medicago</i>) Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 6	2.2	26
23	Evolution of the nasopharyngeal bacterial microbiota of beef calves from spring processing to 40 days after feedlot arrival. <i>Veterinary Microbiology</i> , 2018, 225, 139-148.	1.9	30
24	Variability in Characterizing <i>Escherichia coli</i> from Cattle Feces: A Cautionary Tale. <i>Microorganisms</i> , 2018, 6, 74.	3.6	5
25	Challenges of a one-health approach to the development of alternatives to antibiotics. <i>Animal Frontiers</i> , 2018, 8, 10-20.	1.7	19
26	Distinct bacterial metacommunities inhabit the upper and lower respiratory tracts of healthy feedlot cattle and those diagnosed with bronchopneumonia. <i>Veterinary Microbiology</i> , 2018, 221, 105-113.	1.9	65
27	Effects of transportation to and co-mingling at an auction market on nasopharyngeal and tracheal bacterial communities of recently weaned beef cattle. <i>Veterinary Microbiology</i> , 2018, 223, 126-133.	1.9	31
28	A novel multiplex PCR-electronic microarray assay for rapid and simultaneous detection of bovine respiratory and enteric pathogens. <i>Journal of Virological Methods</i> , 2018, 261, 51-62.	2.1	21
29	Inclusion of Red Osier Dogwood in High-Forage and High-Grain Diets Affected in Vitro Rumen Fermentation. <i>Annals of Animal Science</i> , 2018, 18, 453-467.	1.6	9
30	The nasopharyngeal microbiota of beef cattle before and after transport to a feedlot. <i>BMC Microbiology</i> , 2017, 17, 70.	3.3	69
31	Metagenomic Sequencing of Bronchoalveolar Lavage Samples from Feedlot Cattle Mortalities Associated with Bovine Respiratory Disease. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
32	Prevalence and antimicrobial susceptibility of <i>Mannheimia haemolytica</i> , <i>Pasteurella multocida</i> , and <i>Histophilus somni</i> isolated from the lower respiratory tract of healthy feedlot cattle and those diagnosed with bovine respiratory disease. <i>Veterinary Microbiology</i> , 2017, 208, 118-125.	1.9	98
33	Upper and lower respiratory tract microbiota in horses: bacterial communities associated with health and mild asthma (inflammatory airway disease) and effects of dexamethasone. <i>BMC Microbiology</i> , 2017, 17, 184.	3.3	49
34	The Type of Forage Substrate Preparation Included as Substrate in a RUSITEC System Affects the Ruminal Microbiota and Fermentation Characteristics. <i>Frontiers in Microbiology</i> , 2017, 8, 704.	3.5	44
35	Incubation Temperature, But Not Pequi Oil Supplementation, Affects Methane Production, and the Ruminal Microbiota in a Rumen Simulation Technique (Rusitec) System. <i>Frontiers in Microbiology</i> , 2017, 8, 1076.	3.5	24
36	Changes in bacterial community composition of <i>Escherichia coli</i> O157:H7 super-shedder cattle occur in the lower intestine. <i>PLoS ONE</i> , 2017, 12, e0170050.	2.5	25

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37	The nasopharyngeal microbiota in feedlot cattle and its role in respiratory health. <i>Animal Frontiers</i> , 2016, 6, 44-50.	1.7	47
38	Effect of Co-Composting Cattle Manure with Construction and Demolition Waste on the Archaeal, Bacterial, and Fungal Microbiota, and on Antimicrobial Resistance Determinants. <i>PLoS ONE</i> , 2016, 11, e0157539.	2.5	54
39	Influence of Season and Feedlot Location on Prevalence and Virulence Factors of Seven Serogroups of <i>Escherichia coli</i> in Feces of Western-Canadian Slaughter Cattle. <i>PLoS ONE</i> , 2016, 11, e0159866.	2.5	56
40	Evolution of the nasopharyngeal microbiota of beef cattle from weaning to 40 days after arrival at a feedlot. <i>Veterinary Microbiology</i> , 2016, 187, 75-81.	1.9	70
41	Monitoring Seven Potentially Pathogenic <i>Escherichia coli</i> Serogroups in a Closed Herd of Beef Cattle from Weaning to Finishing Phases. <i>Foodborne Pathogens and Disease</i> , 2016, 13, 661-667.	1.8	20
42	Comparative Genomic Analysis of <i>Mannheimia haemolytica</i> from Bovine Sources. <i>PLoS ONE</i> , 2016, 11, e0149520.	2.5	41
43	The nasopharyngeal microbiota of feedlot cattle. <i>Scientific Reports</i> , 2015, 5, 15557.	3.3	64
44	The nasopharyngeal microbiota of feedlot cattle that develop bovine respiratory disease. <i>Veterinary Microbiology</i> , 2015, 180, 90-95.	1.9	88
45	Susceptibility to tulathromycin in <i>Mannheimia haemolytica</i> isolated from feedlot cattle over a 3-year period. <i>Frontiers in Microbiology</i> , 2013, 4, 297.	3.5	28
46	A multiplex polymerase chain reaction assay for the identification of <i>Mannheimia haemolytica</i> , <i>Mannheimia glucosida</i> and <i>Mannheimia ruminalis</i> . <i>Veterinary Microbiology</i> , 2008, 130, 165-175.	1.9	35
47	Impact of feed processing and mixed ruminal culture on the fate of recombinant EPSP synthase and endogenous canola plant DNA. <i>FEMS Microbiology Letters</i> , 2002, 214, 263-269.	1.8	28