

Heather K Allen

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

5,991
citations

279798

23
h-index

168389

53
g-index

59
all docs

59
docs citations

59
times ranked

8158
citing authors

#	ARTICLE	IF	CITATIONS
1	Call of the wild: antibiotic resistance genes in natural environments. <i>Nature Reviews Microbiology</i> , 2010, 8, 251-259.	28.6	1,733
2	In-feed antibiotic effects on the swine intestinal microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1691-1696.	7.1	942
3	Functional metagenomics reveals diverse β -lactamases in a remote Alaskan soil. <i>ISME Journal</i> , 2009, 3, 243-251.	9.8	462
4	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. <i>ISME Journal</i> , 2014, 8, 1566-1576.	9.8	377
5	Meta-analysis To Define a Core Microbiota in the Swine Gut. <i>MSystems</i> , 2017, 2, .	3.8	240
6	Treatment, promotion, commotion: antibiotic alternatives in food-producing animals. <i>Trends in Microbiology</i> , 2013, 21, 114-119.	7.7	230
7	Finding alternatives to antibiotics. <i>Annals of the New York Academy of Sciences</i> , 2014, 1323, 91-100.	3.8	223
8	Intracellular Screen To Identify Metagenomic Clones That Induce or Inhibit a Quorum-Sensing Biosensor. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6335-6344.	3.1	191
9	Antibiotics in Feed Induce Prophages in Swine Fecal Microbiomes. <i>MBio</i> , 2011, 2, .	4.1	186
10	Collateral effects of antibiotics on mammalian gut microbiomes. <i>Gut Microbes</i> , 2012, 3, 463-467.	9.8	160
11	Carbadox has both temporary and lasting effects on the swine gut microbiota. <i>Frontiers in Microbiology</i> , 2014, 5, 276.	3.5	84
12	Resident Microbiota of the Gypsy Moth Midgut Harbors Antibiotic Resistance Determinants. <i>DNA and Cell Biology</i> , 2009, 28, 109-117.	1.9	79
13	Altered Egos: Antibiotic Effects on Food Animal Microbiomes. <i>Annual Review of Microbiology</i> , 2014, 68, 297-315.	7.3	79
14	Antibiotic resistance gene discovery in food-producing animals. <i>Current Opinion in Microbiology</i> , 2014, 19, 25-29.	5.1	77
15	Psychrotrophic Strain of <i>Xanthinobacterium lividum</i> from a Cold Alaskan Soil Produces Prodigiosin. <i>DNA and Cell Biology</i> , 2010, 29, 533-541.	1.9	75
16	Butyrate-Producing Bacteria, Including Mucin Degradars, from the Swine Intestinal Tract. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3879-3881.	3.1	75
17	Profiling the gastrointestinal microbiota in response to Salmonella: Low versus high Salmonella shedding in the natural porcine host. <i>Infection, Genetics and Evolution</i> , 2013, 16, 330-340.	2.3	71
18	Estimating population diversity with CatchAll. <i>Bioinformatics</i> , 2012, 28, 1045-1047.	4.1	65

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19	Pipeline for amplifying and analyzing amplicons of the V1-V3 region of the 16S rRNA gene. BMC Research Notes, 2016, 9, 380.	1.4	61
20	Dietary Resistant Potato Starch Alters Intestinal Microbial Communities and Their Metabolites, and Markers of Immune Regulation and Barrier Function in Swine. Frontiers in Immunology, 2019, 10, 1381.	4.8	56
21	The agricultural antibiotic carbadox induces phage-mediated gene transfer in Salmonella. Frontiers in Microbiology, 2014, 5, 52.	3.5	53
22	The In-Feed Antibiotic Carbadox Induces Phage Gene Transcription in the Swine Gut Microbiome. MBio, 2017, 8, .	4.1	37
23	Butyricoccus porcorum sp. nov., a butyrate-producing bacterium from swine intestinal tract. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1737-1742.	1.7	33
24	Toward Antibiotic Stewardship: Route of Antibiotic Administration Impacts the Microbiota and Resistance Gene Diversity in Swine Feces. Frontiers in Veterinary Science, 2020, 7, 255.	2.2	26
25	Weaning Age and Its Effect on the Development of the Swine Gut Microbiome and Resistome. MSystems, 2021, 6, e0068221.	3.8	26
26	Function and Phylogeny of Bacterial Butyryl Coenzyme A:Acetate Transferases and Their Diversity in the Proximal Colon of Swine. Applied and Environmental Microbiology, 2016, 82, 6788-6798.	3.1	24
27	Estimation of viral richness from shotgun metagenomes using a frequency count approach. Microbiome, 2013, 1, 5.	11.1	23
28	Investigating the dispersal of antibiotic resistance associated genes from manure application to soil and drainage waters in simulated agricultural farmland systems. PLoS ONE, 2019, 14, e0222470.	2.5	20
29	Paenibacillus 79R4, a potential rumen probiotic to enhance nitrite detoxification and methane mitigation in nitrate-treated ruminants. Science of the Total Environment, 2019, 671, 324-328.	8.0	19
30	Prophylactic Administration of Vector-Encoded Porcine Granulocyte-Colony Stimulating Factor Reduces Salmonella Shedding, Tonsil Colonization, and Microbiota Alterations of the Gastrointestinal Tract in Salmonella-Challenged Swine. Frontiers in Veterinary Science, 2016, 3, 66.	2.2	18
31	Porcine Response to a Multidrug-Resistant <i>Salmonella enterica</i> serovar I 4,[5],12:i:- Outbreak Isolate. Foodborne Pathogens and Disease, 2018, 15, 253-261.	1.8	18
32	Cattle intestinal microbiota shifts following Escherichia coli O157:H7 vaccination and colonization. PLoS ONE, 2019, 14, e0226099.	2.5	18
33	Outer membrane protein A (OmpA) of extraintestinal pathogenic Escherichia coli. BMC Research Notes, 2020, 13, 51.	1.4	18
34	Shifts in the nasal microbiota of swine in response to different dosing regimens of oxytetracycline administration. Veterinary Microbiology, 2019, 237, 108386.	1.9	17
35	Construction and validation of two metagenomic DNA libraries from Cerrado soil with high clay content. Biotechnology Letters, 2011, 33, 2169-2175.	2.2	16
36	Fecal microbiota changes associated with dehorning and castration stress primarily affects light-weight dairy calves. PLoS ONE, 2019, 14, e0210203.	2.5	16

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37	Chlortetracycline Enhances Tonsil Colonization and Fecal Shedding of Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhimurium DT104 without Major Alterations to the Porcine Tonsillar and Intestinal Microbiota. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	14
38	Isolation, characterization and strain selection of a <i>Paenibacillus</i> species for use as a probiotic to aid in ruminal methane mitigation, nitrate/nitrite detoxification and food safety. <i>Bioresource Technology</i> , 2018, 263, 358-364.	9.6	13
39	Telomerase Activity as a Potential Diagnostic Marker for Triage of Abnormal Pap Smears. <i>Journal of Lower Genital Tract Disease</i> , 2005, 9, 93-99.	1.9	12
40	Practical implications of erythromycin resistance gene diversity on surveillance and monitoring of resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	12
41	Fermentation products as feed additives mitigate some ill-effects of heat stress in pigs. <i>Journal of Animal Science</i> , 2017, 95, 279.	0.5	12
42	Complete Genome Sequence of the Multidrug-Resistant Neonatal Meningitis <i>Escherichia coli</i> Serotype O75:H5:K1 Strain mcjchv-1 (NMEC-O75). <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	11
43	A Response Regulator from a Soil Metagenome Enhances Resistance to the β -Lactam Antibiotic Carbenicillin in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2015, 10, e0120094.	2.5	9
44	Antimicrobial resistance in commensal <i>Escherichia coli</i> and <i>Enterococcus</i> spp. isolated from pigs subjected to different antimicrobial administration protocols. <i>Research in Veterinary Science</i> , 2021, 137, 174-185.	1.9	9
45	Diversity of Antibiotic Resistance genes and Transfer Elements-Quantitative Monitoring (DARTE-QM): a method for detection of antimicrobial resistance in environmental samples. <i>Communications Biology</i> , 2022, 5, 216.	4.4	7
46	Virus ecology and disturbances: impact of environmental disruption on the viruses of microorganisms. <i>Frontiers in Microbiology</i> , 2014, 5, 700.	3.5	6
47	Recto-Anal Junction (RA) and Fecal Microbiomes of Cattle Experimentally Challenged With <i>Escherichia coli</i> O157:H7. <i>Frontiers in Microbiology</i> , 2020, 11, 693.	3.5	6
48	Summer Workshop in Metagenomics: One Week Plus Eight Students Equals Gigabases of Cloned DNA. <i>Journal of Microbiology and Biology Education</i> , 2011, 12, 120-126.	1.0	5
49	Complete Genome Sequence of Avian Pathogenic <i>Escherichia coli</i> Strain APEC O2-211. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	5
50	That's disturbing! An exploration of the bacteriophage biology of change. <i>Frontiers in Microbiology</i> , 2013, 4, 295.	3.5	4
51	Effect of sole or combined administration of nitrate and 3-nitro-1-propionic acid on fermentation and <i>Salmonella</i> survivability in alfalfa-fed rumen cultures in vitro. <i>Bioresource Technology</i> , 2017, 229, 69-77.	9.6	4
52	ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS. , 2011, , .		4
53	Genomic Changes within a Subset of IncI2 Plasmids Associated with Dissemination of <i>mcr-1</i> Genes and Other Important Antimicrobial Resistance Determinants. <i>Antibiotics</i> , 2022, 11, 181.	3.7	3
54	Papillomavirus infection and telomerase activation. <i>Papillomavirus Report</i> , 2003, 14, 155-162.	0.2	1

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55	Escherichia coli resistance and gut microbiota profile in pigs raised with different antimicrobial administration in feed. , 0, , .		0