Heather K Allen

List of Publications by Year in descending order

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		279798	168389
55	5,991	23	53
papers	citations	h-index	g-index
59	59	59	8158
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Genomic Changes within a Subset of Incl2 Plasmids Associated with Dissemination of mcr-1 Genes and Other Important Antimicrobial Resistance Determinants. Antibiotics, 2022, 11, 181.	3.7	3
2	Diversity of Antibiotic Resistance genes and Transfer Elements-Quantitative Monitoring (DARTE-QM): a method for detection of antimicrobial resistance in environmental samples. Communications Biology, 2022, 5, 216.	4.4	7
3	Antimicrobial resistance in commensal Escherichia coli and Enterococcus spp. isolated from pigs subjected to different antimicrobial administration protocols. Research in Veterinary Science, 2021, 137, 174-185.	1.9	9
4	Weaning Age and Its Effect on the Development of the Swine Gut Microbiome and Resistome. MSystems, 2021, 6, e0068221.	3.8	26
5	Recto-Anal Junction (RAJ) and Fecal Microbiomes of Cattle Experimentally Challenged With Escherichia coli O157:H7. Frontiers in Microbiology, 2020, 11, 693.	3.5	6
6	Outer membrane protein A (OmpA) of extraintestinal pathogenic Escherichia coli. BMC Research Notes, 2020, 13, 51.	1.4	18
7	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
8	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
9	Shifts in the nasal microbiota of swine in response to different dosing regimens of oxytetracycline administration. Veterinary Microbiology, 2019, 237, 108386.	1.9	17
10	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
11	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
12	Fecal microbiota changes associated with dehorning and castration stress primarily affects light-weight dairy calves. PLoS ONE, 2019, 14, e0210203.	2,5	16
13	Cattle intestinal microbiota shifts following Escherichia coli O157:H7 vaccination and colonization. PLoS ONE, 2019, 14, e0226099.	2.5	18
14	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. Applied and Environmental Microbiology, 2019, 85, .	3.1	14
15	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
16	Practical implications of erythromycin resistance gene diversity on surveillance and monitoring of resistance. FEMS Microbiology Ecology, 2018, 94, .	2.7	12
17	Isolation, characterization and strain selection of a Paenibacillus species for use as a probiotic to aid in ruminal methane mitigation, nitrate/nitrite detoxification and food safety. Bioresource Technology, 2018, 263, 358-364.	9.6	13
18	Complete Genome Sequence of the Multidrug-Resistant Neonatal Meningitis Escherichia coli Serotype O75:H5:K1 Strain mcjchv-1 (NMEC-O75). Microbiology Resource Announcements, 2018, 7, .	0.6	11

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19	Complete Genome Sequence of Avian Pathogenic Escherichia coli Strain APEC O2-211. Microbiology Resource Announcements, 2018, 7, .	0.6	5
20	Butyricicoccus 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
21	Effect of sole or combined administration of nitrate and 3-nitro-1-propionic acid on fermentation and Salmonella survivability in alfalfa-fed rumen cultures in vitro. Bioresource Technology, 2017, 229, 69-77.	9.6	4
22	Meta-analysis To Define a Core Microbiota in the Swine Gut. MSystems, 2017, 2, .	3.8	240
23	The In-Feed Antibiotic Carbadox Induces Phage Gene Transcription in the Swine Gut Microbiome. MBio, 2017, 8, .	4.1	37
24	Fermentation products as feed additives mitigate some ill-effects of heat stress in pigs. Journal of Animal Science, 2017, 95, 279.	0.5	12
25	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
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	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
28	A Response Regulator from a Soil Metagenome Enhances Resistance to the \hat{I}^2 -Lactam Antibiotic Carbenicillin in Escherichia coli. PLoS ONE, 2015, 10, e0120094.	2.5	9
29	Virus ecology and disturbances: impact of environmental disruption on the viruses of microorganisms. Frontiers in Microbiology, 2014, 5, 700.	3.5	6
30	Carbadox has both temporary and lasting effects on the swine gut microbiota. Frontiers in Microbiology, 2014, 5, 276.	3.5	84
31	Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. ISME Journal, 2014, 8, 1566-1576.	9.8	377
32	Antibiotic resistance gene discovery in food-producing animals. Current Opinion in Microbiology, 2014, 19, 25-29.	5.1	77
33	Finding alternatives to antibiotics. Annals of the New York Academy of Sciences, 2014, 1323, 91-100.	3.8	223
34	Altered Egos: Antibiotic Effects on Food Animal Microbiomes. Annual Review of Microbiology, 2014, 68, 297-315.	7.3	79
35	The agricultural antibiotic carbadox induces phage-mediated gene transfer in Salmonella. Frontiers in Microbiology, 2014, 5, 52.	3.5	53
36	Estimation of viral richness from shotgun metagenomes using a frequency count approach. Microbiome, 2013, 1, 5.	11.1	23

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37	Profiling the gastrointestinal microbiota in response to Salmonella: Low versus high Salmonella shedding in the natural porcine host. Infection, Genetics and Evolution, 2013, 16, 330-340.	2.3	71
38	Treatment, promotion, commotion: antibiotic alternatives in food-producing animals. Trends in Microbiology, 2013, 21, 114-119.	7.7	230
39	Butyrate-Producing Bacteria, Including Mucin Degraders, from the Swine Intestinal Tract. Applied and Environmental Microbiology, 2013, 79, 3879-3881.	3.1	75
40	That's disturbing! An exploration of the bacteriophage biology of change. Frontiers in Microbiology, 2013, 4, 295.	3.5	4
41	Estimating population diversity with CatchAll. Bioinformatics, 2012, 28, 1045-1047.	4.1	65
42	In-feed antibiotic effects on the swine intestinal microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1691-1696.	7.1	942
43	Collateral effects of antibiotics on mammalian gut microbiomes. Gut Microbes, 2012, 3, 463-467.	9.8	160
44	Summer Workshop in Metagenomics: One Week Plus Eight Students Equals Gigabases of Cloned DNA. Journal of Microbiology and Biology Education, 2011, 12, 120-126.	1.0	5
45	Construction and validation of two metagenomic DNA libraries from Cerrado soil with high clay content. Biotechnology Letters, 2011, 33, 2169-2175.	2.2	16
46	Antibiotics in Feed Induce Prophages in Swine Fecal Microbiomes. MBio, 2011, 2, .	4.1	186
46	Antibiotics in Feed Induce Prophages in Swine Fecal Microbiomes. MBio, 2011, 2, . ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS., 2011,,.	4.1	186
		28.6	
47	ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS., 2011,,. Call of the wild: antibiotic resistance genes in natural environments. Nature Reviews Microbiology,		4
47	ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS., 2011,,. Call of the wild: antibiotic resistance genes in natural environments. Nature Reviews Microbiology, 2010, 8, 251-259. Psychrotrophic Strain of in Janthinobacterium lividum in the country of the c	28.6	1,733
48	ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS., 2011,,. Call of the wild: antibiotic resistance genes in natural environments. Nature Reviews Microbiology, 2010, 8, 251-259. Psychrotrophic Strain of < i > Janthinobacterium lividum < / i > from a Cold Alaskan Soil Produces Prodigiosin. DNA and Cell Biology, 2010, 29, 533-541. Functional metagenomics reveals diverse β-lactamases in a remote Alaskan soil. ISME Journal, 2009, 3,	28.6	4 1,733 75
47 48 49 50	ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS., 2011,, Call of the wild: antibiotic resistance genes in natural environments. Nature Reviews Microbiology, 2010, 8, 251-259. Psychrotrophic Strain of (i) Janthinobacterium lividum (i) from a Cold Alaskan Soil Produces Prodigiosin. DNA and Cell Biology, 2010, 29, 533-541. Functional metagenomics reveals diverse β-lactamases in a remote Alaskan soil. ISME Journal, 2009, 3, 243-251. Resident Microbiota of the Gypsy Moth Midgut Harbors Antibiotic Resistance Determinants. DNA and	28.6 1.9 9.8	4 1,733 75 462
47 48 49 50	ESTIMATING POPULATION DIVERSITY WITH UNRELIABLE LOW FREQUENCY COUNTS., 2011, ,. Call of the wild: antibiotic resistance genes in natural environments. Nature Reviews Microbiology, 2010, 8, 251-259. Psychrotrophic Strain of (i) Janthinobacterium lividum (li) from a Cold Alaskan Soil Produces Prodigiosin. DNA and Cell Biology, 2010, 29, 533-541. Functional metagenomics reveals diverse β-lactamases in a remote Alaskan soil. ISME Journal, 2009, 3, 243-251. Resident Microbiota of the Cypsy Moth Midgut Harbors Antibiotic Resistance Determinants. DNA and Cell Biology, 2009, 28, 109-117. Telomerase Activity as a Potential Diagnostic Marker for Triage of Abnormal Pap Smears. Journal of	28.6 1.9 9.8	4 1,733 75 462 79

ARTICLE IF CITATIONS

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