

Noelle R Noyes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/549910/publications.pdf>

Version: 2024-02-01

30
papers

1,934
citations

430874

18
h-index

477307

29
g-index

36
all docs

36
docs citations

36
times ranked

2513
citing authors

#	ARTICLE	IF	CITATIONS
1	Considerations and best practices in animal science 16S ribosomal RNA gene sequencing microbiome studies. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	36
2	The microbiome of common bedding materials before and after use on commercial dairy farms. <i>Animal Microbiome</i> , 2022, 4, 18.	3.8	8
3	Syotti: scalable bait design for DNA enrichment. <i>Bioinformatics</i> , 2022, 38, i177-i184.	4.1	3
4	AMR-meta: a <i>k</i> -mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. <i>GigaScience</i> , 2022, 11, .	6.4	8
5	A longitudinal investigation of the effects of age, dietary fiber type and level, and injectable antimicrobials on the fecal microbiome and antimicrobial resistance of finisher pigs. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	5
6	Beyond Antimicrobial Use: A Framework for Prioritizing Antimicrobial Resistance Interventions. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 313-332.	7.4	12
7	Investigating the cow skin and teat canal microbiomes of the bovine udder using different sampling and sequencing approaches. <i>Journal of Dairy Science</i> , 2021, 104, 644-661.	3.4	20
8	Metagenome SNP calling via read-colored de Bruijn graphs. <i>Bioinformatics</i> , 2021, 36, 5275-5281.	4.1	8
9	MEGARes 2.0: a database for classification of antimicrobial drug, biocide and metal resistance determinants in metagenomic sequence data. <i>Nucleic Acids Research</i> , 2020, 48, D561-D569.	14.5	227
10	Mobilization of Antibiotic Resistance: Are Current Approaches for Colocalizing Resistomes and Mobilomes Useful?. <i>Frontiers in Microbiology</i> , 2020, 11, 1376.	3.5	33
11	Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. <i>Communications Biology</i> , 2019, 2, 294.	4.4	31
12	Characterization of the Microbial Resistome in Conventional and "Raised Without Antibiotics" Beef and Dairy Production Systems. <i>Frontiers in Microbiology</i> , 2019, 10, 1980.	3.5	58
13	PrPC knockdown by liposome-siRNA-peptide complexes (LSPCs) prolongs survival and normal behavior of prion-infected mice immunotolerant to treatment. <i>PLoS ONE</i> , 2019, 14, e0219995.	2.5	16
14	Circulation of Plasmids Harboring Resistance Genes to Quinolones and/or Extended-Spectrum Cephalosporins in Multiple <i>Salmonella enterica</i> Serotypes from Swine in the United States. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	16
15	A Cautionary Report for Pathogen Identification Using Shotgun Metagenomics; A Comparison to Aerobic Culture and Polymerase Chain Reaction for <i>Salmonella enterica</i> Identification. <i>Frontiers in Microbiology</i> , 2019, 10, 2499.	3.5	27
16	Metagenomics of Meat and Poultry. , 2019, , 939-962.		0
17	Genome Sequence of <i>Listeria innocua</i> Strain MEZLIS26, Isolated from a Goat in South Africa. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	6
18	Impact of sequencing depth on the characterization of the microbiome and resistome. <i>Scientific Reports</i> , 2018, 8, 5890.	3.3	174

#	ARTICLE	IF	CITATIONS
19	Investigating Effects of Tulathromycin Metaphylaxis on the Fecal Resistome and Microbiome of Commercial Feedlot Cattle Early in the Feeding Period. <i>Frontiers in Microbiology</i> , 2018, 9, 1715.	3.5	78
20	Effects of Ceftiofur and Chlortetracycline on the Resistomes of Feedlot Cattle. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	50
21	A Comparative Study of Serum Biochemistry, Metabolome and Microbiome Parameters of Clinically Healthy, Normal Weight, Overweight, and Obese Companion Dogs. <i>Topics in Companion Animal Medicine</i> , 2018, 33, 126-135.	0.9	58
22	Associations between sexual habits, menstrual hygiene practices, demographics and the vaginal microbiome as revealed by Bayesian network analysis. <i>PLoS ONE</i> , 2018, 13, e0191625.	2.5	92
23	MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580.	14.5	328
24	Succinct colored de Bruijn graphs. <i>Bioinformatics</i> , 2017, 33, 3181-3187.	4.1	99
25	Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3059-3071.	1.8	19
26	Enrichment allows identification of diverse, rare elements in metagenomic resistome-virulome sequencing. <i>Microbiome</i> , 2017, 5, 142.	11.1	78
27	Resistome diversity in cattle and the environment decreases during beef production. <i>ELife</i> , 2016, 5, e13195.	6.0	126
28	Characterization of the resistome in manure, soil and wastewater from dairy and beef production systems. <i>Scientific Reports</i> , 2016, 6, 24645.	3.3	112
29	Use of Metagenomic Shotgun Sequencing Technology To Detect Foodborne Pathogens within the Microbiome of the Beef Production Chain. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2433-2443.	3.1	132
30	Antimicrobial Resistance in <i>Escherichia coli</i> Recovered from Feedlot Cattle and Associations with Antimicrobial Use. <i>PLoS ONE</i> , 2015, 10, e0143995.	2.5	57