

Suzanne L Ishaq

List of Publications by Year in descending order

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43
papers

2,679
citations

394421

19
h-index

315739

38
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47
all docs

47
docs citations

47
times ranked

3070
citing authors

#	ARTICLE	IF	CITATIONS
1	Fibrolitic rumen bacteria of camel and sheep and their applications in the bioconversion of barley straw to soluble sugars for biofuel production. <i>PLoS ONE</i> , 2022, 17, e0262304.	2.5	17
2	Twenty Important Research Questions in Microbial Exposure and Social Equity. <i>MSystems</i> , 2022, 7, e0124021.	3.8	14
3	Weed Communities in Winter Wheat: Responses to Cropping Systems under Different Climatic Conditions. <i>Sustainability</i> , 2022, 14, 6880.	3.2	0
4	Designing the Microbes and Social Equity Symposium: A Novel Interdisciplinary Virtual Research Conference Based on Achieving Group-Directed Outputs. <i>Challenges</i> , 2022, 13, 30.	1.7	1
5	Temporal Soil Bacterial Community Responses to Cropping Systems and Crop Identity in Dryland Agroecosystems of the Northern Great Plains. <i>Frontiers in Sustainable Food Systems</i> , 2021, 5, .	3.9	7
6	Adequacy of calcium and vitamin D reduces inflammation, β -catenin signaling, and dysbiotic <i>Parasutterella</i> bacteria in the colon of C57BL/6 mice fed a western-style diet. <i>Journal of Nutritional Biochemistry</i> , 2021, 92, 108613.	4.2	6
7	Bacterial transfer from <i>Pristionchus entomophagus</i> nematodes to the invasive ant <i>Myrmica rubra</i> and the potential for colony mortality in coastal Maine. <i>IScience</i> , 2021, 24, 102663.	4.1	4
8	Introducing the Microbes and Social Equity Working Group: Considering the Microbial Components of Social, Environmental, and Health Justice. <i>MSystems</i> , 2021, 6, e0047121.	3.8	45
9	It began on an ant hill in Maine: A story in multidisciplinary research. <i>IScience</i> , 2021, 24, 103411.	4.1	0
10	Review: Are there indigenous <i>Saccharomyces</i> in the digestive tract of livestock animal species? Implications for health, nutrition and productivity traits. <i>Animal</i> , 2020, 14, 22-30.	3.3	17
11	Building upon current knowledge and techniques of indoor microbiology to construct the next era of theory into microorganisms, health, and the built environment. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2020, 30, 219-235.	3.9	75
12	Soil bacterial communities of wheat vary across the growing season and among dryland farming systems. <i>Geoderma</i> , 2020, 358, 113989.	5.1	30
13	Dryland Cropping Systems, Weed Communities, and Disease Status Modulate the Effect of Climate Conditions on Wheat Soil Bacterial Communities. <i>MSphere</i> , 2020, 5, .	2.9	3
14	Viable bacterial communities on hospital window components in patient rooms. <i>PeerJ</i> , 2020, 8, e9580.	2.0	4
15	From one species to another: A review on the interaction between chemistry and microbiology in relation to cleaning in the built environment. <i>Indoor Air</i> , 2019, 29, 880-894.	4.3	22
16	Agroecosystem resilience is modified by management system via plant-soil feedbacks. <i>Basic and Applied Ecology</i> , 2019, 39, 1-9.	2.7	12
17	Monitored Indoor Environmental Quality of a Mass Timber Office Building: A Case Study. <i>Buildings</i> , 2019, 9, 142.	3.1	11
18	Pelleted-hay alfalfa feed increases sheep wether weight gain and rumen bacterial richness over loose-hay alfalfa feed. <i>PLoS ONE</i> , 2019, 14, e0215797.	2.5	19

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19	Framing the discussion of microorganisms as a facet of social equity in human health. PLoS Biology, 2019, 17, e3000536.	5.6	32
20	Zinc AA supplementation alters yearling ram rumen bacterial communities but zinc sulfate supplementation does not. Journal of Animal Science, 2019, 97, 687-697.	0.5	17
21	Accumulation of di-2-ethylhexyl phthalate from polyvinyl chloride flooring into settled house dust and the effect on the bacterial community. PeerJ, 2019, 7, e8147.	2.0	6
22	Biogeographical Differences in the Influence of Maternal Microbial Sources on the Early Successional Development of the Bovine Neonatal Gastrointestinal tract. Scientific Reports, 2018, 8, 3197.	3.3	133
23	Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection. Nature Biotechnology, 2018, 36, 359-367.	17.5	414
24	Colonic aberrant crypt formation accompanies an increase of opportunistic pathogenic bacteria in C57BL/6 mice fed a high-fat diet. Journal of Nutritional Biochemistry, 2018, 54, 18-27.	4.2	52
25	Null Mutations of Group A Streptococcus Orphan Kinase RocA: Selection in Mouse Infection and Comparison with CovS Mutations in Alteration of <i>In Vitro</i> and <i>In Vivo</i> Protease SpeB Expression and Virulence. Infection and Immunity, 2017, 85, .	2.2	16
26	Impact of Cropping Systems, Soil Inoculum, and Plant Species Identity on Soil Bacterial Community Structure. Microbial Ecology, 2017, 73, 417-434.	2.8	46
27	Ground Juniperus pinchotii and urea in supplements fed to Rambouillet ewe lambs Part 2: Ewe lamb rumen microbial communities. Journal of Animal Science, 2017, 95, 4587-4599.	0.5	15
28	An Investigation into Rumen Fungal and Protozoal Diversity in Three Rumen Fractions, during High-Fiber or Grain-Induced Sub-Acute Ruminal Acidosis Conditions, with or without Active Dry Yeast Supplementation. Frontiers in Microbiology, 2017, 8, 1943.	3.5	40
29	Feed efficiency phenotypes in lambs involve changes in ruminal, colonic, and small-intestine-located microbiota. Journal of Animal Science, 2017, 95, 2585.	0.5	42
30	Plant-microbial interactions in agriculture and the use of farming systems to improve diversity and productivity. AIMS Microbiology, 2017, 3, 335-353.	2.2	24
31	Colonic inflammation accompanies an increase of β -catenin signaling and Lachnospiraceae/Streptococcaceae bacteria in the hind gut of high-fat diet-fed mice. Journal of Nutritional Biochemistry, 2016, 35, 30-36.	4.2	136
32	Rumen and Cecum Microbiomes in Reindeer (<i>Rangifer tarandus tarandus</i>) Are Changed in Response to a Lichen Diet and May Affect Enteric Methane Emissions. PLoS ONE, 2016, 11, e0155213.	2.5	42
33	Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range. Scientific Reports, 2015, 5, 14567.	3.3	1,172
34	Toward the identification of methanogenic archaeal groups as targets of methane mitigation in livestock animals. Frontiers in Microbiology, 2015, 6, 776.	3.5	25
35	Fibrolitic Bacteria Isolated from the Rumen of North American Moose (<i>Alces alces</i>) and Their Use as a Probiotic in Neonatal Lambs. PLoS ONE, 2015, 10, e0144804.	2.5	22
36	Wild Ruminants. , 2015, , 37-45.		2

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37	High-throughput DNA sequencing of the moose rumen from different geographical locations reveals a core ruminal methanogenic archaeal diversity and a differential ciliate protozoal diversity. <i>Microbial Genomics</i> , 2015, 1, e000034.	2.0	15
38	Biodiversity of Human Gut Methanogens Varies With Concentration of Exhaled Breath Methane. <i>American Journal of Gastroenterology</i> , 2015, 110, S552-S553.	0.4	2
39	Terrestrial Vertebrate Animal Metagenomics, <i>Wild Ruminants.</i> , 2015, , 686-693.		0
40	High-Throughput DNA Sequencing of the Ruminal Bacteria from Moose (<i>Alces alces</i>) in Vermont, Alaska, and Norway. <i>Microbial Ecology</i> , 2014, 68, 185-195.	2.8	49
41	Design and Validation of Four New Primers for Next-Generation Sequencing To Target the 18S rRNA Genes of Gastrointestinal Ciliate Protozoa. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5515-5521.	3.1	36
42	Terrestrial Vertebrate Animal Metagenomics, <i>Wild Ruminants.</i> , 2013, , 1-10.		0
43	Insight into the bacterial gut microbiome of the North American moose (<i>Alces alces</i>). <i>BMC Microbiology</i> , 2012, 12, 212.	3.3	51