

Hooman Derakhshani

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

1,330
citations

471509

17
h-index

580821

25
g-index

25
all docs

25
docs citations

25
times ranked

1563
citing authors

#	ARTICLE	IF	CITATIONS
1	Invited review: Microbiota of the bovine udder: Contributing factors and potential implications for udder health and mastitis susceptibility. <i>Journal of Dairy Science</i> , 2018, 101, 10605-10625.	3.4	159
2	Development of Ruminal and Fecal Microbiomes Are Affected by Weaning But Not Weaning Strategy in Dairy Calves. <i>Frontiers in Microbiology</i> , 2016, 7, 582.	3.5	148
3	Induction of Subacute Ruminal Acidosis Affects the Ruminal Microbiome and Epithelium. <i>Frontiers in Microbiology</i> , 2016, 7, 701.	3.5	131
4	Review: Enhancing gastrointestinal health in dairy cows. <i>Animal</i> , 2018, 12, s399-s418.	3.3	116
5	Effects of grain feeding on microbiota in the digestive tract of cattle. <i>Animal Frontiers</i> , 2016, 6, 13-19.	1.7	97
6	An extended single-index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. <i>Journal of Basic Microbiology</i> , 2016, 56, 321-326.	3.3	93
7	Weaning age influences the severity of gastrointestinal microbiome shifts in dairy calves. <i>Scientific Reports</i> , 2017, 7, 198.	3.3	87
8	Linking Peripartal Dynamics of Ruminal Microbiota to Dietary Changes and Production Parameters. <i>Frontiers in Microbiology</i> , 2017, 7, 2143.	3.5	58
9	Co-fermentation of glucose, starch, and cellulose for mesophilic biohydrogen production. <i>International Journal of Hydrogen Energy</i> , 2014, 39, 20958-20967.	7.1	51
10	Composition of the teat canal and intramammary microbiota of dairy cows subjected to antimicrobial dry cow therapy and internal teat sealant. <i>Journal of Dairy Science</i> , 2018, 101, 10191-10205.	3.4	46
11	The Features of Fecal and Ileal Mucosa-Associated Microbiota in Dairy Calves during Early Infection with <i>Mycobacterium avium</i> Subspecies paratuberculosis. <i>Frontiers in Microbiology</i> , 2016, 7, 426.	3.5	44
12	Effect of live yeast <i>Saccharomyces cerevisiae</i> (Actisaf Sc 47) supplementation on the performance and hindgut microbiota composition of weanling pigs. <i>Scientific Reports</i> , 2018, 8, 5315.	3.3	44
13	Effect of live yeast <i>Saccharomyces cerevisiae</i> supplementation on the performance and cecum microbial profile of suckling piglets. <i>PLoS ONE</i> , 2019, 14, e0219557.	2.5	43
14	Association of bovine major histocompatibility complex (BoLA) gene polymorphism with colostrum and milk microbiota of dairy cows during the first week of lactation. <i>Microbiome</i> , 2018, 6, 203.	11.1	38
15	Composition and co-occurrence patterns of the microbiota of different niches of the bovine mammary gland: potential associations with mastitis susceptibility, udder inflammation, and teat-end hyperkeratosis. <i>Animal Microbiome</i> , 2020, 2, 11.	3.8	32
16	Associations between digital dermatitis lesion grades in dairy cattle and the quantities of four <i>Treponema</i> species. <i>Veterinary Research</i> , 2018, 49, 111.	3.0	28
17	Human milk fungi: environmental determinants and inter-kingdom associations with milk bacteria in the CHILD Cohort Study. <i>BMC Microbiology</i> , 2020, 20, 146.	3.3	28
18	Characterization of the rumen and fecal microbiome in bloated and non-bloated cattle grazing alfalfa pastures and subjected to bloat prevention strategies. <i>Scientific Reports</i> , 2019, 9, 4272.	3.3	20

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19	Identification and Quantification of Bovine Digital Dermatitis-Associated Microbiota across Lesion Stages in Feedlot Beef Cattle. <i>MSystems</i> , 2021, 6, e0070821.	3.8	19
20	Interrelationships of Fiber-Associated Anaerobic Fungi and Bacterial Communities in the Rumen of Bloat Cattle Grazing Alfalfa. <i>Microorganisms</i> , 2020, 8, 1543.	3.6	13
21	Significance of acclimatization for biohydrogen production from synthetic lignocellulose hydrolysate in continuous-flow systems. <i>International Journal of Hydrogen Energy</i> , 2016, 41, 14003-14014.	7.1	11
22	Completion of draft bacterial genomes by long-read sequencing of synthetic genomic pools. <i>BMC Genomics</i> , 2020, 21, 519.	2.8	11
23	Effect of <i>Propionibacterium acidipropionici</i> P169 on the rumen and faecal microbiota of beef cattle fed a maize-based finishing diet. <i>Beneficial Microbes</i> , 2017, 8, 785-799.	2.4	7
24	A Grain-Based SARA Challenge Affects the Composition of Epimural and Mucosa-Associated Bacterial Communities throughout the Digestive Tract of Dairy Cows. <i>Animals</i> , 2021, 11, 1658.	2.3	5
25	757 Associations between gut, mammary and vaginal microbiomes in dairy cows: Role in health and disease. <i>Journal of Animal Science</i> , 2017, 95, 366-366.	0.5	1