Hooman Derakhshani

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/516612/publications.pdf

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	A Grain-Based SARA Challenge Affects the Composition of Epimural and Mucosa-Associated Bacterial Communities throughout the Digestive Tract of Dairy Cows. Animals, 2021, 11, 1658.	2.3	5
2	Identification and Quantification of Bovine Digital Dermatitis-Associated Microbiota across Lesion Stages in Feedlot Beef Cattle. MSystems, 2021, 6, e0070821.	3.8	19
3	Interrelationships of Fiber-Associated Anaerobic Fungi and Bacterial Communities in the Rumen of Bloated Cattle Grazing Alfalfa. Microorganisms, 2020, 8, 1543.	3.6	13
4	Completion of draft bacterial genomes by long-read sequencing of synthetic genomic pools. BMC Genomics, 2020, 21, 519.	2.8	11
5	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. Animal Microbiome, 2020, 2, 11.	3.8	32
6	Human milk fungi: environmental determinants and inter-kingdom associations with milk bacteria in the CHILD Cohort Study. BMC Microbiology, 2020, 20, 146.	3.3	28
7	Effect of live yeast Saccharomyces cerevisiae supplementation on the performance and cecum microbial profile of suckling piglets. PLoS ONE, 2019, 14, e0219557.	2.5	43
8	Characterization of the rumen and fecal microbiome in bloated and non-bloated cattle grazing alfalfa pastures and subjected to bloat prevention strategies. Scientific Reports, 2019, 9, 4272.	3.3	20
9	Effect of live yeast Saccharomyces cerevisiae (Actisaf Sc 47) supplementation on the performance and hindgut microbiota composition of weanling pigs. Scientific Reports, 2018, 8, 5315.	3.3	44
10	Association of bovine major histocompatibility complex (BoLA) gene polymorphism with colostrum and milk microbiota of dairy cows during the first week of lactation. Microbiome, 2018, 6, 203.	11.1	38
11	Associations between digital dermatitis lesion grades in dairy cattle and the quantities of four Treponema species. Veterinary Research, 2018, 49, 111.	3.0	28
12	Invited review: Microbiota of the bovine udder: Contributing factors and potential implications for udder health and mastitis susceptibility. Journal of Dairy Science, 2018, 101, 10605-10625.	3.4	159
13	Composition of the teat canal and intramammary microbiota of dairy cows subjected to antimicrobial dry cow therapy and internal teat sealant. Journal of Dairy Science, 2018, 101, 10191-10205.	3.4	46
14	Review: Enhancing gastrointestinal health in dairy cows. Animal, 2018, 12, s399-s418.	3.3	116
15	Weaning age influences the severity of gastrointestinal microbiome shifts in dairy calves. Scientific Reports, 2017, 7, 198.	3.3	87
16	Effect of Propionibacterium acidipropionici P169 on the rumen and faecal microbiota of beef cattle fed a maize-based finishing diet. Beneficial Microbes, 2017, 8, 785-799.	2.4	7
17	757 Associations between gut, mammary and vaginal microbiomes in dairy cows: Role in health and disease. Journal of Animal Science, 2017, 95, 366-366.	0.5	1
18	Linking Peripartal Dynamics of Ruminal Microbiota to Dietary Changes and Production Parameters. Frontiers in Microbiology, 2017, 7, 2143.	3.5	58

#	ARTICLE	IF	CITATIONS
19	The Features of Fecal and Ileal Mucosa-Associated Microbiota in Dairy Calves during Early Infection with Mycobacterium avium Subspecies paratuberculosis. Frontiers in Microbiology, 2016, 7, 426.	3.5	44
20	Development of Ruminal and Fecal Microbiomes Are Affected by Weaning But Not Weaning Strategy in Dairy Calves. Frontiers in Microbiology, 2016, 7, 582.	3.5	148
21	Induction of Subacute Ruminal Acidosis Affects the Ruminal Microbiome and Epithelium. Frontiers in Microbiology, 2016, 7, 701.	3.5	131
22	Significance of acclimatization for biohydrogen production from synthetic lignocellulose hydrolysate in continuous-flow systems. International Journal of Hydrogen Energy, 2016, 41, 14003-14014.	7.1	11
23	Effects of grain feeding on microbiota in the digestive tract of cattle. Animal Frontiers, 2016, 6, 13-19.	1.7	97
24	An extended singleâ€index multiplexed 16S rRNA sequencing for microbial community analysis on MiSeq illumina platforms. Journal of Basic Microbiology, 2016, 56, 321-326.	3.3	93
25	Co-fermentation of glucose, starch, and cellulose for mesophilic biohydrogen production. International Journal of Hydrogen Energy, 2014, 39, 20958-20967.	7.1	51