

Le Luo Guan

List of Publications by Year in descending order

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156
papers

9,494
citations

31976

53
h-index

46799

89
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159
all docs

159
docs citations

159
times ranked

8348
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
2	Assessment of the Microbial Ecology of Ruminant Methanogens in Cattle with Different Feed Efficiencies. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6524-6533.	3.1	280
3	Metatranscriptomic Profiling Reveals Linkages between the Active Rumen Microbiome and Feed Efficiency in Beef Cattle. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	258
4	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	3.5	255
5	Linkage of microbial ecology to phenotype: correlation of rumen microbial ecology to cattle's feed efficiency. <i>FEMS Microbiology Letters</i> , 2008, 288, 85-91.	1.8	251
6	Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. <i>Microbiome</i> , 2019, 7, 92.	11.1	230
7	Taxonomic Identification of Commensal Bacteria Associated with the Mucosa and Digesta throughout the Gastrointestinal Tracts of Preweaned Calves. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2021-2028.	3.1	202
8	Development and physiology of the rumen and the lower gut: Targets for improving gut health. <i>Journal of Dairy Science</i> , 2016, 99, 4955-4966.	3.4	190
9	The Gut Microbiome and Its Potential Role in the Development and Function of Newborn Calf Gastrointestinal Tract. <i>Frontiers in Veterinary Science</i> , 2015, 2, 36.	2.2	178
10	Characterization of Variation in Rumen Methanogenic Communities under Different Dietary and Host Feed Efficiency Conditions, as Determined by PCR-Denaturing Gradient Gel Electrophoresis Analysis. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3776-3786.	3.1	173
11	Impact of Feed Efficiency and Diet on Adaptive Variations in the Bacterial Community in the Rumen Fluid of Cattle. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1203-1214.	3.1	166
12	Multi-omics reveals that the rumen microbiome and its metabolome together with the host metabolome contribute to individualized dairy cow performance. <i>Microbiome</i> , 2020, 8, 64.	11.1	165
13	Understanding host-microbial interactions in rumen: searching the best opportunity for microbiota manipulation. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 8.	5.3	153
14	Comparative metagenomic and metatranscriptomic analyses reveal the breed effect on the rumen microbiome and its associations with feed efficiency in beef cattle. <i>Microbiome</i> , 2019, 7, 6.	11.1	150
15	Metabolomics of Four Biofluids from Dairy Cows: Potential Biomarkers for Milk Production and Quality. <i>Journal of Proteome Research</i> , 2015, 14, 1287-1298.	3.7	139
16	Selection of Aptamers against Live Bacterial Cells. <i>Analytical Chemistry</i> , 2008, 80, 7812-7819.	6.5	131
17	Probiotic preparation VSL#3 induces remission in children with mild to moderate acute ulcerative colitis: A pilot study. <i>Inflammatory Bowel Diseases</i> , 2009, 15, 760-768.	1.9	119
18	From pre- to postweaning: Transformation of the young calf's gastrointestinal tract. <i>Journal of Dairy Science</i> , 2017, 100, 5984-5995.	3.4	119

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19	Detection and Identification of <i>Lactobacillus</i> Species in Crops of Broilers of Different Ages by Using PCR-Denaturing Gradient Gel Electrophoresis and Amplified Ribosomal DNA Restriction Analysis. <i>Applied and Environmental Microbiology</i> , 2003, 69, 6750-6757.	3.1	117
20	Characterization of microRNA expression in bovine adipose tissues: a potential regulatory mechanism of subcutaneous adipose tissue development. <i>BMC Molecular Biology</i> , 2010, 11, 29.	3.0	112
21	The Role of the Gut Microbiome in Cattle Production and Health: Driver or Passenger?. <i>Annual Review of Animal Biosciences</i> , 2020, 8, 199-220.	7.4	111
22	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2021, 9, 137.	11.1	110
23	Changes in Bacterial Diversity Associated with Epithelial Tissue in the Beef Cow Rumen during the Transition to a High-Grain Diet. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5770-5781.	3.1	109
24	Understanding the gut microbiome of dairy calves: Opportunities to improve early-life gut health. <i>Journal of Dairy Science</i> , 2017, 100, 5996-6005.	3.4	101
25	Correlation of Particular Bacterial PCR-Denaturing Gradient Gel Electrophoresis Patterns with Bovine Ruminal Fermentation Parameters and Feed Efficiency Traits. <i>Applied and Environmental Microbiology</i> , 2010, 76, 6338-6350.	3.1	99
26	Assessment of Rumen Microbiota from a Large Dairy Cattle Cohort Reveals the Pan and Core Bacteriomes Contributing to Varied Phenotypes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	97
27	Regulation of rumen development in neonatal ruminants through microbial metagenomes and host transcriptomes. <i>Genome Biology</i> , 2019, 20, 172.	8.8	94
28	MicroRNA regulation in mammalian adipogenesis. <i>Experimental Biology and Medicine</i> , 2011, 236, 997-1004.	2.4	93
29	Transcriptome profiling of the rumen epithelium of beef cattle differing in residual feed intake. <i>BMC Genomics</i> , 2016, 17, 592.	2.8	93
30	Lipid metabolism, adipocyte depot physiology and utilization of meat animals as experimental models for metabolic research. <i>International Journal of Biological Sciences</i> , 2010, 6, 691-699.	6.4	89
31	Variation of bacterial communities and expression of Toll-like receptor genes in the rumen of steers differing in susceptibility to subacute ruminal acidosis. <i>Veterinary Microbiology</i> , 2012, 159, 451-459.	1.9	88
32	Regional and age dependent changes in gene expression of Toll-like receptors and key antimicrobial defence molecules throughout the gastrointestinal tract of dairy calves. <i>Veterinary Immunology and Immunopathology</i> , 2012, 146, 18-26.	1.2	86
33	Effect of Exogenous Siderophores on Iron Uptake Activity of Marine Bacteria under Iron-Limited Conditions. <i>Applied and Environmental Microbiology</i> , 2001, 67, 1710-1717.	3.1	84
34	Heat-treated colostrum feeding promotes beneficial bacteria colonization in the small intestine of neonatal calves. <i>Journal of Dairy Science</i> , 2015, 98, 8044-8053.	3.4	83
35	Potential Regulatory Role of MicroRNAs in the Development of Bovine Gastrointestinal Tract during Early Life. <i>PLoS ONE</i> , 2014, 9, e92592.	2.5	78
36	Perspectives on Super-Shedding of <i>Escherichia coli</i> O157:H7 by Cattle. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 89-103.	1.8	78

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37	MicroRNAs in bovine adipogenesis: genomic context, expression and function. <i>BMC Genomics</i> , 2014, 15, 137.	2.8	77
38	The Bovine Metabolome. <i>Metabolites</i> , 2020, 10, 233.	2.9	77
39	Linking perturbations to temporal changes in diversity, stability, and compositions of neonatal calf gut microbiota: prediction of diarrhea. <i>ISME Journal</i> , 2020, 14, 2223-2235.	9.8	77
40	Identification of a putative quantitative trait nucleotide in guanylate binding protein 5 for host response to PRRS virus infection. <i>BMC Genomics</i> , 2015, 16, 412.	2.8	75
41	Characterization of bovine miRNAs by sequencing and bioinformatics analysis. <i>BMC Molecular Biology</i> , 2009, 10, 90.	3.0	73
42	Antarctic Krill 454 Pyrosequencing Reveals Chaperone and Stress Transcriptome. <i>PLoS ONE</i> , 2011, 6, e15919.	2.5	73
43	Influence of Sire Breed on the Interplay among Rumen Microbial Populations Inhabiting the Rumen Liquid of the Progeny in Beef Cattle. <i>PLoS ONE</i> , 2013, 8, e58461.	2.5	70
44	Assessment of microbiome changes after rumen transfaunation: implications on improving feed efficiency in beef cattle. <i>Microbiome</i> , 2018, 6, 62.	11.1	70
45	Adipogenesis of bovine perimuscular preadipocytes. <i>Biochemical and Biophysical Research Communications</i> , 2008, 366, 54-59.	2.1	67
46	Gene co-expression network analysis identifies porcine genes associated with variation in Salmonella shedding. <i>BMC Genomics</i> , 2014, 15, 452.	2.8	65
47	Egg ovotransferrin-derived ACE inhibitory peptide IRW increases ACE2 but decreases proinflammatory genes expression in mesenteric artery of spontaneously hypertensive rats. <i>Molecular Nutrition and Food Research</i> , 2015, 59, 1735-1744.	3.3	65
48	Transcriptome analysis reveals regional and temporal differences in mucosal immune system development in the small intestine of neonatal calves. <i>BMC Genomics</i> , 2016, 17, 602.	2.8	62
49	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 987.	3.5	61
50	Shift of hindgut microbiota and microbial short chain fatty acids profiles in dairy calves from birth to pre-weaning. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	61
51	Serum metabolome profiling revealed potential biomarkers for milk protein yield in dairy cows. <i>Journal of Proteomics</i> , 2018, 184, 54-61.	2.4	60
52	Allied Industry Approaches to Alter Intramuscular Fat Content and Composition in Beef Animals. <i>Journal of Food Science</i> , 2010, 75, R1-8.	3.1	59
53	Distinct commensal bacteria associated with ingesta and mucosal epithelium in the gastrointestinal tracts of calves and chickens. <i>FEMS Microbiology Ecology</i> , 2012, 79, 337-347.	2.7	59
54	Characterization of bovine ruminal epithelial bacterial communities using 16S rRNA sequencing, PCR-DGGE, and qRT-PCR analysis. <i>Veterinary Microbiology</i> , 2012, 155, 72-80.	1.9	59

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55	Effects of Flavonoid-rich Plant Extracts on <i>In vitro</i> Ruminal Methanogenesis, Microbial Populations and Fermentation Characteristics. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 530-537.	2.4	58
56	Bacterial Growth Stimulation with Exogenous Siderophore and Synthetic N-Acyl Homoserine Lactone Autoinducers under Iron-Limited and Low-Nutrient Conditions. <i>Applied and Environmental Microbiology</i> , 2000, 66, 2797-2803.	3.1	57
57	Dissect the mode of action of probiotics in affecting host-microbial interactions and immunity in food producing animals. <i>Veterinary Immunology and Immunopathology</i> , 2018, 205, 35-48.	1.2	57
58	Effects of dietary physical or nutritional factors on morphology of rumen papillae and transcriptome changes in lactating dairy cows based on three different forage-based diets. <i>BMC Genomics</i> , 2017, 18, 353.	2.8	55
59	Systematic microRNAome profiling reveals the roles of microRNAs in milk protein metabolism and quality: insights on low-quality forage utilization. <i>Scientific Reports</i> , 2016, 6, 21194.	3.3	54
60	Skeletal Muscle Stem Cells from Animals I. <i>Basic Cell Biology</i> . <i>International Journal of Biological Sciences</i> , 2010, 6, 465-474.	6.4	53
61	Factors influencing ruminal bacterial community diversity and composition and microbial fibrolytic enzyme abundance in lactating dairy cows with a focus on the role of active dry yeast. <i>Journal of Dairy Science</i> , 2017, 100, 4377-4393.	3.4	53
62	Gene expression patterns of bovine perimuscular preadipocytes during adipogenesis. <i>Biochemical and Biophysical Research Communications</i> , 2008, 366, 346-351.	2.1	48
63	Altered microRNA expression and pre-mRNA splicing events reveal new mechanisms associated with early stage <i>Mycobacterium avium</i> subspecies paratuberculosis infection. <i>Scientific Reports</i> , 2016, 6, 24964.	3.3	47
64	Altered MicroRNA Expression in Bovine Subcutaneous and Visceral Adipose Tissues from Cattle under Different Diet. <i>PLoS ONE</i> , 2012, 7, e40605.	2.5	46
65	Comparative miRNAome analysis revealed different miRNA expression profiles in bovine sera and exosomes. <i>BMC Genomics</i> , 2016, 17, 630.	2.8	45
66	Increasing gene discovery and coverage using RNA-seq of globin RNA reduced porcine blood samples. <i>BMC Genomics</i> , 2014, 15, 954.	2.8	43
67	Gut microbiome and omics: a new definition to ruminant production and health. <i>Animal Frontiers</i> , 2016, 6, 8-12.	1.7	43
68	Strategies to improve the efficiency of beef cattle production. <i>Canadian Journal of Animal Science</i> , 2021, 101, 1-19.	1.5	42
69	Roles of small RNAs in the effects of nutrition on apoptosis and spermatogenesis in the adult testis. <i>Scientific Reports</i> , 2015, 5, 10372.	3.3	41
70	The Development of Microbiota and Metabolome in Small Intestine of Sika Deer (<i>Cervus nippon</i>) from Birth to Weaning. <i>Frontiers in Microbiology</i> , 2018, 9, 4.	3.5	41
71	Taxonomic and Functional Compositions of the Small Intestinal Microbiome in Neonatal Calves Provide a Framework for Understanding Early Life Gut Health. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	41
72	Mucosal changes in a long-term bovine intestinal segment model following removal of ingesta and microflora. <i>Gut Microbes</i> , 2011, 2, 134-144.	9.8	39

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73	Gene-expression profiling of calves 6 and 9 months after inoculation with <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> . <i>Veterinary Research</i> , 2014, 45, 96.	3.0	39
74	Short communication: The effect of heat treatment of bovine colostrum on the concentration of oligosaccharides in colostrum and in the intestine of neonatal male Holstein calves. <i>Journal of Dairy Science</i> , 2018, 101, 401-407.	3.4	37
75	Effect of a butyrate-fortified milk replacer on gastrointestinal microbiota and products of fermentation in artificially reared dairy calves at weaning. <i>Scientific Reports</i> , 2018, 8, 14901.	3.3	37
76	Colostrum feeding shapes the hindgut microbiota of dairy calves during the first 12 h of life. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	36
77	Detection, Characterization, and In Vitro and In Vivo Expression of Genes Encoding S-Proteins in <i>Lactobacillus gallinarum</i> Strains Isolated from Chicken Crops. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6633-6643.	3.1	35
78	Comparative analysis on gene expression profiles in cattle subcutaneous fat tissues. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2008, 3, 251-256.	1.0	34
79	Feeding colostrum or a 1:1 colostrum:milk mixture for 3 days postnatal increases small intestinal development and minimally influences plasma glucagon-like peptide-2 and serum insulin-like growth factor-1 concentrations in Holstein bull calves. <i>Journal of Dairy Science</i> , 2020, 103, 4236-4251.	3.4	34
80	Genome-wide whole blood microRNAome and transcriptome analyses reveal miRNA-mRNA regulated host response to foodborne pathogen <i>Salmonella</i> infection in swine. <i>Scientific Reports</i> , 2015, 5, 12620.	3.3	33
81	Survey of rumen microbiota of domestic grazing yak during different growth stages revealed novel maturation patterns of four key microbial groups and their dynamic interactions. <i>Animal Microbiome</i> , 2020, 2, 23.	3.8	33
82	Methanogen prevalence throughout the gastrointestinal tract of pre-weaned dairy calves. <i>Gut Microbes</i> , 2014, 5, 628-638.	9.8	32
83	Genetic architecture of gene expression underlying variation in host response to porcine reproductive and respiratory syndrome virus infection. <i>Scientific Reports</i> , 2017, 7, 46203.	3.3	32
84	Implication and challenges of direct-fed microbial supplementation to improve ruminant production and health. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 109.	5.3	32
85	Mucosal dendritic cell subpopulations in the small intestine of newborn calves. <i>Developmental and Comparative Immunology</i> , 2011, 35, 1040-1051.	2.3	31
86	Gene expression profiling and putative biomarkers of calves 3 months after infection with <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> . <i>Veterinary Immunology and Immunopathology</i> , 2014, 160, 107-117.	1.2	31
87	Air-Dried Brown Seaweed, <i>Ascophyllum nodosum</i> , Alters the Rumen Microbiome in a Manner That Changes Rumen Fermentation Profiles and Lowers the Prevalence of Foodborne Pathogens. <i>MSphere</i> , 2018, 3, .	2.9	31
88	Noncoding RNAs: Regulatory Molecules of Host-Microbiome Crosstalk. <i>Trends in Microbiology</i> , 2021, 29, 713-724.	7.7	31
89	Investigating temporal microbial dynamics in the rumen of beef calves raised on two farms during early life. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	30
90	Transcriptome analysis of subcutaneous adipose tissues in beef cattle using 3â€² digital gene expression-tag profiling1. <i>Journal of Animal Science</i> , 2012, 90, 171-183.	0.5	28

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91	Multi-omics reveals functional genomic and metabolic mechanisms of milk production and quality in dairy cows. <i>Bioinformatics</i> , 2020, 36, 2530-2537.	4.1	28
92	Cellular and Molecular Implications of Mature Adipocyte Dedifferentiation. <i>Journal of Genomics</i> , 2013, 1, 5-12.	0.9	27
93	MicroRNA expression profiles across blood and different tissues in cattle. <i>Scientific Data</i> , 2019, 6, 190013.	5.3	26
94	Understanding the role of rumen epithelial host-microbe interactions in cattle feed efficiency. <i>Animal Nutrition</i> , 2022, 10, 41-53.	5.1	25
95	Bioinformatic analyses in early host response to Porcine Reproductive and Respiratory Syndrome virus (PRRSV) reveals pathway differences between pigs with alternate genotypes for a major host response QTL. <i>BMC Genomics</i> , 2016, 17, 196.	2.8	24
96	Symposium review: Mining metagenomic and metatranscriptomic data for clues about microbial metabolic functions in ruminants. <i>Journal of Dairy Science</i> , 2018, 101, 5605-5618.	3.4	24
97	Interactions of the Hindgut Mucosa-Associated Microbiome with Its Host Regulate Shedding of <i>Escherichia coli</i> O157:H7 by Cattle. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	24
98	Landscape of multi-tissue global gene expression reveals the regulatory signatures of feed efficiency in beef cattle. <i>Bioinformatics</i> , 2019, 35, 1712-1719.	4.1	23
99	Early supplementation of <i>Saccharomyces cerevisiae</i> boulardii CNCM I-1079 in newborn dairy calves increases IgA production in the intestine at 1 week of age. <i>Journal of Dairy Science</i> , 2020, 103, 8615-8628.	3.4	23
100	InÂvitro evaluation of effects of gut region and fiber structure on the intestinal dominant bacterial diversity and functional bacterial species. <i>Anaerobe</i> , 2014, 28, 168-177.	2.1	22
101	Functional changes in mRNA expression and alternative pre-mRNA splicing associated with the effects of nutrition on apoptosis and spermatogenesis in the adult testis. <i>BMC Genomics</i> , 2017, 18, 64.	2.8	22
102	Model systems to analyze the role of miRNAs and commensal microflora in bovine mucosal immune system development. <i>Molecular Immunology</i> , 2015, 66, 57-67.	2.2	21
103	Longitudinal blood transcriptomic analysis to identify molecular regulatory patterns of bovine respiratory disease in beef cattle. <i>Genomics</i> , 2020, 112, 3968-3977.	2.9	21
104	Effects of seaweed extracts on in vitro rumen fermentation characteristics, methane production, and microbial abundance. <i>Scientific Reports</i> , 2021, 11, 24092.	3.3	21
105	Comparative analysis of gene expression profiles in ruminal tissue from Holstein dairy cows fed high or low concentrate diets. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2010, 5, 274-279.	1.0	20
106	Metatranscriptomic Profiling Reveals the Effect of Breed on Active Rumen Eukaryotic Composition in Beef Cattle With Varied Feed Efficiency. <i>Frontiers in Microbiology</i> , 2020, 11, 367.	3.5	20
107	Prewaning to postweaning rumen papillae structural growth, ruminal fermentation characteristics, and acute-phase proteins in calves. <i>Journal of Dairy Science</i> , 2021, 104, 3632-3645.	3.4	20
108	Expansion of ruminant-specific microRNAs shapes target gene expression divergence between ruminant and non-ruminant species. <i>BMC Genomics</i> , 2013, 14, 609.	2.8	19

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109	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. <i>Journal of Dairy Science</i> , 2021, 104, 1928-1950.	3.4	19
110	Age-related changes in the distribution and frequency of myeloid and T cell populations in the small intestine of calves. <i>Cellular Immunology</i> , 2011, 271, 428-437.	3.0	18
111	Characterization of fecal branched-chain fatty acid profiles and their associations with fecal microbiota in diarrheic and healthy dairy calves. <i>Journal of Dairy Science</i> , 2021, 104, 2290-2301.	3.4	18
112	Comparative Transcriptomic Analysis of Rectal Tissue from Beef Steers Revealed Reduced Host Immunity in <i>Escherichia coli</i> O157:H7 Super-Shedders. <i>PLoS ONE</i> , 2016, 11, e0151284.	2.5	18
113	Metatranscriptomic analyses reveal ruminal pH regulates fiber degradation and fermentation by shifting the microbial community and gene expression of carbohydrate-active enzymes. <i>Animal Microbiome</i> , 2021, 3, 32.	3.8	17
114	MicroRNA Buffering and Altered Variance of Gene Expression in Response to <i>Salmonella</i> Infection. <i>PLoS ONE</i> , 2014, 9, e94352.	2.5	17
115	A review of the resistome within the digestive tract of livestock. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 121.	5.3	17
116	Elucidation of Molecular Mechanisms of Physiological Variations between Bovine Subcutaneous and Visceral Fat Depots under Different Nutritional Regimes. <i>PLoS ONE</i> , 2013, 8, e83211.	2.5	16
117	Feeding colostrum or a 1:1 colostrum:whole milk mixture for 3 days after birth increases serum immunoglobulin G and apparent immunoglobulin G persistency in Holstein bulls. <i>Journal of Dairy Science</i> , 2020, 103, 11833-11843.	3.4	16
118	Gene expression alterations in Rocky Mountain elk infected with chronic wasting disease. <i>Prion</i> , 2012, 6, 282-301.	1.8	15
119	Nutrition affects Sertoli cell function but not Sertoli cell numbers in sexually mature male sheep. <i>Reproduction, Fertility and Development</i> , 2016, 28, 1152.	0.4	15
120	Host mechanisms involved in cattle <i>Escherichia coli</i> O157 shedding: a fundamental understanding for reducing foodborne pathogen in food animal production. <i>Scientific Reports</i> , 2017, 7, 7630.	3.3	15
121	Whole-Blood Transcriptome Analysis of Feedlot Cattle With and Without Bovine Respiratory Disease. <i>Frontiers in Genetics</i> , 2021, 12, 627623.	2.3	15
122	Microbial interaction-driven community differences as revealed by network analysis. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6000-6008.	4.1	15
123	Microarray Analysis of Differentially Expressed Genes from Peyer's Patches of Cattle Orally Challenged with Bovine Spongiform Encephalopathy. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2009, 72, 1008-1013.	2.3	14
124	Gene Expression in the Medulla Following Oral Infection of Cattle with Bovine Spongiform Encephalopathy. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2011, 74, 110-126.	2.3	14
125	Feedomics: Promises for food security with sustainable food animal production. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 107, 130-141.	11.4	14
126	Ruminal resistome of dairy cattle is individualized and the resistotypes are associated with milking traits. <i>Animal Microbiome</i> , 2021, 3, 18.	3.8	14

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127	Gene co-expression and alternative splicing analysis of key metabolic tissues to unravel the regulatory signatures of fatty acid composition in cattle. <i>RNA Biology</i> , 2021, 18, 854-862.	3.1	13
128	Longitudinal assessment revealed the shifts in rumen and colon mucosal-attached microbiota of dairy calves during weaning transition. <i>Journal of Dairy Science</i> , 2021, 104, 5948-5963.	3.4	13
129	Rumen and Hindgut Bacteria Are Potential Indicators for Mastitis of Mid-Lactating Holstein Dairy Cows. <i>Microorganisms</i> , 2020, 8, 2042.	3.6	12
130	Short communication: Odd-chain and branched-chain fatty acid concentrations in bovine colostrum and transition milk and their stability under heating and freezing treatments. <i>Journal of Dairy Science</i> , 2020, 103, 11483-11489.	3.4	12
131	Functional Genomics Approach for Identification of Molecular Processes Underlying Neurodegenerative Disorders in Prion Diseases. <i>Current Genomics</i> , 2012, 13, 369-378.	1.6	11
132	Comparative Microbiome Analysis Reveals the Ecological Relationships Between Rumen Methanogens, Acetogens, and Their Hosts. <i>Frontiers in Microbiology</i> , 2020, 11, 1311.	3.5	11
133	The effect of neomycin inclusion in milk replacer on the health, growth, and performance of male Holstein calves during preweaning. <i>Journal of Dairy Science</i> , 2021, 104, 8188-8201.	3.4	10
134	Identifying active rumen epithelial associated bacteria and archaea in beef cattle divergent in feed efficiency using total RNA-seq. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100064.	2.3	10
135	Accelerated discovery of novel glycoside hydrolases using targeted functional profiling and selective pressure on the rumen microbiome. <i>Microbiome</i> , 2021, 9, 229.	11.1	10
136	Effects of replacing inorganic salts of trace minerals with organic trace minerals in pre- and postpartum diets on feeding behavior, rumen fermentation, and performance of dairy cows. <i>Journal of Dairy Science</i> , 2022, 105, 6693-6709.	3.4	10
137	Arteriovenous blood metabolomics: An efficient method to determine the key metabolic pathway for milk synthesis in the intra-mammary gland. <i>Scientific Reports</i> , 2018, 8, 5598.	3.3	9
138	Taxonomic and functional assessment using metatranscriptomics reveals the effect of Angus cattle on rumen microbial signatures. <i>Animal</i> , 2020, 14, 731-744.	3.3	9
139	Abundance and Expression of Shiga Toxin Genes in <i>Escherichia coli</i> at the Recto-Anal Junction Relates to Host Immune Genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 633573.	3.9	9
140	Effect of colostrum feeding strategies on the expression of neuroendocrine genes and active gut mucosa-attached bacterial populations in neonatal calves. <i>Journal of Dairy Science</i> , 2020, 103, 8629-8642.	3.4	8
141	The potential for mitigation of methane emissions in ruminants through the application of metagenomics, metabolomics, and other -OMICS technologies. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	8
142	Genome wide transcriptome analysis provides bases on colonic mucosal immune system development affected by colostrum feeding strategies in neonatal calves. <i>BMC Genomics</i> , 2018, 19, 635.	2.8	7
143	Expressions of resistome is linked to the key functions and stability of active rumen microbiome. <i>Animal Microbiome</i> , 2022, 4, .	3.8	7
144	MicroRNAomes of Cattle Intestinal Tissues Revealed Possible miRNA Regulated Mechanisms Involved in <i>Escherichia coli</i> O157 Fecal Shedding. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 634505.	3.9	6

#	ARTICLE	IF	CITATIONS
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146	Rumen microbiota and its relation to fermentation in lactose-fed calves. <i>Journal of Dairy Science</i> , 2021, 104, 10744-10752.	3.4	5
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155	Terrestrial Vertebrate Animal Metagenomics, Domesticated Bovinae. , 2013, , 1-12.		1
156	Transcriptome analysis revealed that delaying first colostrum feeding postponed ileum immune system development of neonatal calves. <i>Genomics</i> , 2021, 113, 4116-4125.	2.9	1