

Le Luo Guan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6424791/publications.pdf>

Version: 2024-02-01

156
papers

9,494
citations

31976

53
h-index

46799

89
g-index

159
all docs

159
docs citations

159
times ranked

8348
citing authors

#	ARTICLE	IF	CITATIONS
1	Translational multi-omics microbiome research for strategies to improve cattle production and health. <i>Emerging Topics in Life Sciences</i> , 2022, , .	2.6	3
2	Breed dependent regulatory mechanisms of beneficial and non-beneficial fatty acid profiles in subcutaneous adipose tissue in cattle with divergent feed efficiency. <i>Scientific Reports</i> , 2022, 12, 4612.	3.3	3
3	Understanding the role of rumen epithelial host-microbe interactions in cattle feed efficiency. <i>Animal Nutrition</i> , 2022, 10, 41-53.	5.1	25
4	Expressions of resistome is linked to the key functions and stability of active rumen microbiome. <i>Animal Microbiome</i> , 2022, 4, .	3.8	7
5	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
6	Strategies to improve the efficiency of beef cattle production. <i>Canadian Journal of Animal Science</i> , 2021, 101, 1-19.	1.5	42
7	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
8	Genomics for Food Security With Efficient and Sustainable Livestock Production. , 2021, , 229-244.		1
9	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
10	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
11	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
12	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
13	Whole-Blood Transcriptome Analysis of Feedlot Cattle With and Without Bovine Respiratory Disease. <i>Frontiers in Genetics</i> , 2021, 12, 627623.	2.3	15
14	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
15	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
16	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
17	Integrative network analysis revealed molecular mechanisms of urine urea output in lactating dairy cows: Potential solutions to reduce environmental nitrate contamination. <i>Genomics</i> , 2021, 113, 1522-1533.	2.9	2
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Assessing Dietary Effects on the Rumen Microbiome: Different Sequencing Methods Tell Different Stories. <i>Veterinary Sciences</i> , 2021, 8, 138.	1.7	3
22	Noncoding RNAs: Regulatory Molecules of Host-Microbiome Crosstalk. <i>Trends in Microbiology</i> , 2021, 29, 713-724.	7.7	31
23	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
24	Rumen microbiota and its relation to fermentation in lactose-fed calves. <i>Journal of Dairy Science</i> , 2021, 104, 10744-10752.	3.4	5
25	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
26	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
27	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
28	Microbial interaction-driven community differences as revealed by network analysis. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6000-6008.	4.1	15
29	Distinctive roles between rumen epimural and content bacterial communities on beef cattle feed efficiency: A combined analysis. <i>Current Research in Microbial Sciences</i> , 2021, 2, 100085.	2.3	5
30	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
31	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
32	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
33	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
34	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
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Rumen and Hindgut Bacteria Are Potential Indicators for Mastitis of Mid-Lactating Holstein Dairy Cows. <i>Microorganisms</i> , 2020, 8, 2042.	3.6	12
39	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
40	The Bovine Metabolome. <i>Metabolites</i> , 2020, 10, 233.	2.9	77
41	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
42	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
43	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
44	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
45	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
46	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
47	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
48	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
49	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
50	Regulation of rumen development in neonatal ruminants through microbial metagenomes and host transcriptomes. <i>Genome Biology</i> , 2019, 20, 172.	8.8	94
51	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
52	Days-in-Milk and Parity Affected Serum Biochemical Parameters and Hormone Profiles in Mid-Lactation Holstein Cows. <i>Animals</i> , 2019, 9, 230.	2.3	3
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	MicroRNA expression profiles across blood and different tissues in cattle. <i>Scientific Data</i> , 2019, 6, 190013.	5.3	26
58	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
59	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
60	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
61	Assessment of microbiome changes after rumen transfaunation: implications on improving feed efficiency in beef cattle. <i>Microbiome</i> , 2018, 6, 62.	11.1	70
62	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
63	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
64	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
65	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
66	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
67	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
68	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
69	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
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	Feedomics: Promises for food security with sustainable food animal production. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 107, 130-141.	11.4	14
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	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
76	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
77	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
78	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
79	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
80	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
81	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
82	Gut microbiome and omics: a new definition to ruminant production and health. <i>Animal Frontiers</i> , 2016, 6, 8-12.	1.7	43
83	Transcriptome profiling of the rumen epithelium of beef cattle differing in residual feed intake. <i>BMC Genomics</i> , 2016, 17, 592.	2.8	93
84	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 987.	3.5	61
85	Altered microRNA expression and pre-mRNA splicing events reveal new mechanisms associated with early stage <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> infection. <i>Scientific Reports</i> , 2016, 6, 24964.	3.3	47
86	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
87	Comparative miRNAome analysis revealed different miRNA expression profiles in bovine sera and exosomes. <i>BMC Genomics</i> , 2016, 17, 630.	2.8	45
88	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
89	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
90	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

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	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
94	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
95	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
96	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
97	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
98	Adipogenesis and Obesity. , 2015, , 539-565.		2
99	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
100	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
101	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
102	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
103	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
104	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
105	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
106	Methanogen prevalence throughout the gastrointestinal tract of pre-weaned dairy calves. <i>Gut Microbes</i> , 2014, 5, 628-638.	9.8	32
107	<i>In vitro</i> 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
108	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

#	ARTICLE	IF	CITATIONS
109	Gene expression profiling and putative biomarkers of calves 3 months after infection with <i>Mycobacterium avium</i> subspecies paratuberculosis. <i>Veterinary Immunology and Immunopathology</i> , 2014, 160, 107-117.	1.2	31
110	MicroRNAs in bovine adipogenesis: genomic context, expression and function. <i>BMC Genomics</i> , 2014, 15, 137.	2.8	77
111	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
112	Gene co-expression network analysis identifies porcine genes associated with variation in <i>Salmonella</i> shedding. <i>BMC Genomics</i> , 2014, 15, 452.	2.8	65
113	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
114	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
115	Cellular and Molecular Implications of Mature Adipocyte Dedifferentiation. <i>Journal of Genomics</i> , 2013, 1, 5-12.	0.9	27
116	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
117	Terrestrial Vertebrate Animal Metagenomics, Domesticated Bovinae. , 2013, , 1-12.		1
118	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
119	Gene expression alterations in Rocky Mountain elk infected with chronic wasting disease. <i>Prion</i> , 2012, 6, 282-301.	1.8	15
120	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
121	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
122	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
123	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
124	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
125	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
126	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

#	ARTICLE	IF	CITATIONS
127	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
128	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
129	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
130	Transcriptome Analysis of the Medulla Tissue from Cattle in Response to Bovine Spongiform Encephalopathy using Digital Gene Expression Tag Profiling. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , 2011, 74, 127-137.	2.3	5
131	MicroRNA regulation in mammalian adipogenesis. <i>Experimental Biology and Medicine</i> , 2011, 236, 997-1004.	2.4	93
132	Mucosal dendritic cell subpopulations in the small intestine of newborn calves. <i>Developmental and Comparative Immunology</i> , 2011, 35, 1040-1051.	2.3	31
133	Antarctic Krill 454 Pyrosequencing Reveals Chaperone and Stress Transcriptome. <i>PLoS ONE</i> , 2011, 6, e15919.	2.5	73
134	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
135	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
136	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
137	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
138	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
139	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
140	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
141	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
142	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
143	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
144	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

#	ARTICLE	IF	CITATIONS
145	Characterization of bovine miRNAs by sequencing and bioinformatics analysis. BMC Molecular Biology, 2009, 10, 90.	3.0	73
146	Assessment of the Microbial Ecology of Ruminant Methanogens in Cattle with Different Feed Efficiencies. Applied and Environmental Microbiology, 2009, 75, 6524-6533.	3.1	280
147	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
148	Selection of Aptamers against Live Bacterial Cells. Analytical Chemistry, 2008, 80, 7812-7819.	6.5	131
149	Linkage of microbial ecology to phenotype: correlation of rumen microbial ecology to cattle's feed efficiency. FEMS Microbiology Letters, 2008, 288, 85-91.	1.8	251
150	Adipogenesis of bovine perimuscular preadipocytes. Biochemical and Biophysical Research Communications, 2008, 366, 54-59.	2.1	67
151	Gene expression patterns of bovine perimuscular preadipocytes during adipogenesis. Biochemical and Biophysical Research Communications, 2008, 366, 346-351.	2.1	48
152	Comparative analysis on gene expression profiles in cattle subcutaneous fat tissues. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2008, 3, 251-256.	1.0	34
153	Detection, Characterization, and In Vitro and In Vivo Expression of Genes Encoding S-Proteins in Lactobacillus gallinarum Strains Isolated from Chicken Crops. Applied and Environmental Microbiology, 2005, 71, 6633-6643.	3.1	35
154	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. Applied and Environmental Microbiology, 2003, 69, 6750-6757.	3.1	117
155	Effect of Exogenous Siderophores on Iron Uptake Activity of Marine Bacteria under Iron-Limited Conditions. Applied and Environmental Microbiology, 2001, 67, 1710-1717.	3.1	84
156	Bacterial Growth Stimulation with Exogenous Siderophore and Synthetic N -Acyl Homoserine Lactone Autoinducers under Iron-Limited and Low-Nutrient Conditions. Applied and Environmental Microbiology, 2000, 66, 2797-2803.	3.1	57