

# Le Luo Guan

## List of Publications by Year in descending order

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Version: 2024-02-01

156  
papers

9,494  
citations

31902

53  
h-index

46693

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, , .	1.1	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.	1.6	3
3	Understanding the role of rumen epithelial host-microbe interactions in cattle feed efficiency. <i>Animal Nutrition</i> , 2022, 10, 41-53.	2.1	25
4	Expressions of resistome is linked to the key functions and stability of active rumen microbiome. <i>Animal Microbiome</i> , 2022, 4, .	1.5	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.	1.4	10
6	Strategies to improve the efficiency of beef cattle production. <i>Canadian Journal of Animal Science</i> , 2021, 101, 1-19.	0.7	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.	1.5	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.	1.8	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.	1.4	19
11	Ruminal resistome of dairy cattle is individualized and the resistotypes are associated with milking traits. <i>Animal Microbiome</i> , 2021, 3, 18.	1.5	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.	1.4	18
13	Whole-Blood Transcriptome Analysis of Feedlot Cattle With and Without Bovine Respiratory Disease. <i>Frontiers in Genetics</i> , 2021, 12, 627623.	1.1	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.	1.4	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.	1.8	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.	1.5	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.	1.3	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.	1.4	13

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19	An integrated gene catalog and over 10,000 metagenome-assembled genomes from the gastrointestinal microbiome of ruminants. <i>Microbiome</i> , 2021, 9, 137.	4.9	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.	1.4	10
21	Assessing Dietary Effects on the Rumen Microbiome: Different Sequencing Methods Tell Different Stories. <i>Veterinary Sciences</i> , 2021, 8, 138.	0.6	3
22	Noncoding RNAs: Regulatory Molecules of Host-Microbiome Crosstalk. <i>Trends in Microbiology</i> , 2021, 29, 713-724.	3.5	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, .	0.2	8
24	Rumen microbiota and its relation to fermentation in lactose-fed calves. <i>Journal of Dairy Science</i> , 2021, 104, 10744-10752.	1.4	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.	1.4	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.	2.1	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.	1.3	1
28	Microbial interaction-driven community differences as revealed by network analysis. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6000-6008.	1.9	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.	1.4	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.	4.9	10
31	A review of the resistome within the digestive tract of livestock. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 121.	2.1	17
32	Effects of seaweed extracts on in vitro rumen fermentation characteristics, methane production, and microbial abundance. <i>Scientific Reports</i> , 2021, 11, 24092.	1.6	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.	1.3	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, .	1.3	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.	1.8	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.	1.4	34

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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.	1.5	33
38	Rumen and Hindgut Bacteria Are Potential Indicators for Mastitis of Mid-Lactating Holstein Dairy Cows. <i>Microorganisms</i> , 2020, 8, 2042.	1.6	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.	4.9	165
40	The Bovine Metabolome. <i>Metabolites</i> , 2020, 10, 233.	1.3	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.	1.5	20
42	Comparative Microbiome Analysis Reveals the Ecological Relationships Between Rumen Methanogens, Acetogens, and Their Hosts. <i>Frontiers in Microbiology</i> , 2020, 11, 1311.	1.5	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.	1.4	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.	1.3	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.	3.6	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.	4.4	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.	1.4	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.	1.4	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.	1.4	12
50	Regulation of rumen development in neonatal ruminants through microbial metagenomes and host transcriptomes. <i>Genome Biology</i> , 2019, 20, 172.	3.8	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.	4.9	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.	1.0	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.	4.9	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, .	1.4	41

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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.	1.8	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, .	1.3	36
57	MicroRNA expression profiles across blood and different tissues in cattle. <i>Scientific Data</i> , 2019, 6, 190013.	2.4	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, .	1.3	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.	1.6	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.	1.4	24
61	Assessment of microbiome changes after rumen transfaunation: implications on improving feed efficiency in beef cattle. <i>Microbiome</i> , 2018, 6, 62.	4.9	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, .	1.3	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, .	1.4	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.	1.4	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.	1.6	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.	0.5	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.	1.2	7
68	Serum metabolome profiling revealed potential biomarkers for milk protein yield in dairy cows. <i>Journal of Proteomics</i> , 2018, 184, 54-61.	1.2	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, .	1.4	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.	1.5	41
71	Feedomics: Promises for food security with sustainable food animal production. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 107, 130-141.	5.8	14
72	Addressing Global Ruminant Agricultural Challenges Through Understanding the Rumen Microbiome: Past, Present, and Future. <i>Frontiers in Microbiology</i> , 2018, 9, 2161.	1.5	255

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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.	1.2	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.	2.1	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, .	1.4	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.	1.6	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.	1.4	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.	1.2	55
79	From pre- to postweaning: Transformation of the young calf's gastrointestinal tract. <i>Journal of Dairy Science</i> , 2017, 100, 5984-5995.	1.4	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.	1.4	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.	1.6	15
82	Gut microbiome and omics: a new definition to ruminant production and health. <i>Animal Frontiers</i> , 2016, 6, 8-12.	0.8	43
83	Transcriptome profiling of the rumen epithelium of beef cattle differing in residual feed intake. <i>BMC Genomics</i> , 2016, 17, 592.	1.2	93
84	Taxonomic Assessment of Rumen Microbiota Using Total RNA and Targeted Amplicon Sequencing Approaches. <i>Frontiers in Microbiology</i> , 2016, 7, 987.	1.5	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.	1.6	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.	1.6	54
87	Comparative miRNAome analysis revealed different miRNA expression profiles in bovine sera and exosomes. <i>BMC Genomics</i> , 2016, 17, 630.	1.2	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.	0.1	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.	1.2	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.	1.2	24

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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.	1.4	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.	1.1	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.	1.5	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.	1.6	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.	0.9	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.	1.2	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.	1.8	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.	1.6	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.	1.4	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.	0.8	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.	1.0	21
104	Potential Regulatory Role of MicroRNAs in the Development of Bovine Gastrointestinal Tract during Early Life. <i>PLoS ONE</i> , 2014, 9, e92592.	1.1	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.	1.1	39
106	Methanogen prevalence throughout the gastrointestinal tract of pre-weaned dairy calves. <i>Gut Microbes</i> , 2014, 5, 628-638.	4.3	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.	1.0	22
108	Increasing gene discovery and coverage using RNA-seq of globin RNA reduced porcine blood samples. <i>BMC Genomics</i> , 2014, 15, 954.	1.2	43

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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.	0.5	31
110	MicroRNAs in bovine adipogenesis: genomic context, expression and function. <i>BMC Genomics</i> , 2014, 15, 137.	1.2	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.	1.4	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.	1.2	65
113	MicroRNA Buffering and Altered Variance of Gene Expression in Response to <i>Salmonella</i> Infection. <i>PLoS ONE</i> , 2014, 9, e94352.	1.1	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.	1.2	19
115	Cellular and Molecular Implications of Mature Adipocyte Dedifferentiation. <i>Journal of Genomics</i> , 2013, 1, 5-12.	0.6	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.	1.1	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.	1.1	16
119	Gene expression alterations in Rocky Mountain elk infected with chronic wasting disease. <i>Prion</i> , 2012, 6, 282-301.	0.9	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.	1.4	166
121	Functional Genomics Approach for Identification of Molecular Processes Underlying Neurodegenerative Disorders in Prion Diseases. <i>Current Genomics</i> , 2012, 13, 369-378.	0.7	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.	0.8	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.	0.2	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.	0.5	86
125	Altered MicroRNA Expression in Bovine Subcutaneous and Visceral Adipose Tissues from Cattle under Different Diet. <i>PLoS ONE</i> , 2012, 7, e40605.	1.1	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.	1.3	59



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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.	0.8	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.	1.4	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.	1.1	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.	1.1	5
131	MicroRNA regulation in mammalian adipogenesis. <i>Experimental Biology and Medicine</i> , 2011, 236, 997-1004.	1.1	93
132	Mucosal dendritic cell subpopulations in the small intestine of newborn calves. <i>Developmental and Comparative Immunology</i> , 2011, 35, 1040-1051.	1.0	31
133	Antarctic Krill 454 Pyrosequencing Reveals Chaperone and Stress Transcriptome. <i>PLoS ONE</i> , 2011, 6, e15919.	1.1	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.	1.4	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.	4.3	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.	1.5	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.	2.6	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.	2.6	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.	1.4	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.	1.4	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.	0.4	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.	1.1	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.	0.9	119

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145	Characterization of bovine miRNAs by sequencing and bioinformatics analysis. <i>BMC Molecular Biology</i> , 2009, 10, 90.	3.0	73
146	Assessment of the Microbial Ecology of Ruminant Methanogens in Cattle with Different Feed Efficiencies. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6524-6533.	1.4	280
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