

Mingxun Li

List of Publications by Year in descending order

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52
papers

935
citations

471509

17
h-index

477307

29
g-index

52
all docs

52
docs citations

52
times ranked

974
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide recombination map construction from single sperm sequencing in cattle. BMC Genomics, 2022, 23, 181.	2.8	4
2	Identification and Characterization of Circular RNAs in Mammary Tissue from Holstein Cows at Early Lactation and Non-Lactation. Biomolecules, 2022, 12, 478.	4.0	7
3	Effects of Seasonal Heat Stress during Late Gestation on Growth Performance, Metabolic and Immuno-Endocrine Parameters of Calves. Animals, 2022, 12, 716.	2.3	5
4	Epigenetic Regulation Mechanisms of the Cofilin-1 Gene in the Development and Differentiation of Bovine Primary Myoblasts. Genes, 2022, 13, 723.	2.4	4
5	Emerging functions of circular RNA in the regulation of adipocyte metabolism and obesity. Cell Death Discovery, 2022, 8, .	4.7	10
6	Abundance of solute carrier family 27 member 6 (<i>SLC27A6</i>) in the bovine mammary gland alters fatty acid metabolism. Food and Function, 2021, 12, 4909-4920.	4.6	6
7	Metformin Inhibits Lipoteichoic Acid-Induced Oxidative Stress and Inflammation Through AMPK/NRF2/NF- κ B Signaling Pathway in Bovine Mammary Epithelial Cells. Frontiers in Veterinary Science, 2021, 8, 661380.	2.2	18
8	Directed Expression of Tracheal Antimicrobial Peptide as a Treatment for Bovine-Associated Staphylococcus Aureus-Induced Mastitis in Mice. Frontiers in Veterinary Science, 2021, 8, 700930.	2.2	1
9	MIR221HG Is a Novel Long Noncoding RNA that Inhibits Bovine Adipocyte Differentiation. Genes, 2020, 11, 29.	2.4	9
10	Comparative analyses of copy number variations between Bos taurus and Bos indicus. BMC Genomics, 2020, 21, 682.	2.8	21
11	Copy number variation analysis reveals variants associated with milk production traits in dairy goats. Genomics, 2020, 112, 4934-4937.	2.9	11
12	Polymorphisms of the ACSL1 Gene Influence Milk Production Traits and Somatic Cell Score in Chinese Holstein Cows. Animals, 2020, 10, 2282.	2.3	8
13	<i>miR-497</i> regulates fatty acid synthesis via <i>LATS2</i> in bovine mammary epithelial cells. Food and Function, 2020, 11, 8625-8636.	4.6	18
14	Genome-Wide DNA Methylation Analysis of Mammary Gland Tissues From Chinese Holstein Cows With Staphylococcus aureus Induced Mastitis. Frontiers in Genetics, 2020, 11, 550515.	2.3	13
15	The polymorphism of bovine Cofilin-1 gene sequence variants and association analysis with growth traits in Qinchuan cattle. Animal Biotechnology, 2020, , 1-7.	1.5	3
16	<i>MicroRNA-212</i> targets <i>SIRT2</i> to influence lipogenesis in bovine mammary epithelial cell line. Journal of Dairy Research, 2020, 87, 232-238.	1.4	10
17	Polymorphisms in Fatty Acid Desaturase 2 Gene Are Associated with Milk Production Traits in Chinese Holstein Cows. Animals, 2020, 10, 671.	2.3	10
18	MicroRNA-141 participates in milk lipid metabolism by targeting SIRT1 in bovine mammary epithelial cells. Animal Production Science, 2020, 60, 1877.	1.3	4

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19	A novel lncRNA BADLNCR1 inhibits bovine adipogenesis by repressing <i>GLRX5</i> expression. Journal of Cellular and Molecular Medicine, 2020, 24, 7175-7186.	3.6	11
20	Analysis of longissimus muscle quality characteristics and associations with DNA methylation status in cattle. Genes and Genomics, 2019, 41, 1147-1163.	1.4	24
21	MicroRNA-106b Regulates Milk Fat Metabolism via ATP Binding Cassette Subfamily A Member 1 (<i>ABCA1</i>) in Bovine Mammary Epithelial Cells. Journal of Agricultural and Food Chemistry, 2019, 67, 3981-3990.	5.2	51
22	MicroRNA-145 regulates immune cytokines via targeting <i>FSCN1</i> in <i>Staphylococcus aureus</i> -induced mastitis in dairy cows. Reproduction in Domestic Animals, 2019, 54, 882-891.	1.4	36
23	Characterization of lncRNA-miRNA-mRNA Network to Reveal Potential Functional ceRNAs in Bovine Skeletal Muscle. Frontiers in Genetics, 2019, 10, 91.	2.3	39
24	A Functional 3' UTR Polymorphism of <i>FADS2</i> Affects Cow Milk Composition through Modifying Mir-744 Binding. Animals, 2019, 9, 1090.	2.3	9
25	In-depth characterization of the pituitary transcriptome in Simmental and Chinese native cattle. Domestic Animal Endocrinology, 2019, 66, 35-42.	1.6	6
26	Pathological Features of <i>Staphylococcus aureus</i> Induced Mastitis in Dairy Cows and Isobaric-Tags-for-Relative-and-Absolute-Quantitation Proteomic Analyses. Journal of Agricultural and Food Chemistry, 2018, 66, 3880-3890.	5.2	15
27	Genetic differentiation and phylogeny of 27 sheep populations based on structural gene loci. Molecular and Cellular Probes, 2018, 37, 55-59.	2.1	4
28	Global Transcriptome Analysis During Adipogenic Differentiation and Involvement of Transthyretin Gene in Adipogenesis in Cattle. Frontiers in Genetics, 2018, 9, 463.	2.3	25
29	Factors affecting the milk urea nitrogen concentration in Chinese Holstein cows. Animal Biology, 2018, 68, 193-211.	1.0	4
30	Transcriptomics and iTRAQ-Proteomics Analyses of Bovine Mammary Tissue with <i>Streptococcus agalactiae</i> -Induced Mastitis. Journal of Agricultural and Food Chemistry, 2018, 66, 11188-11196.	5.2	27
31	Characterization of candidate genes for bovine adipogenesis reveals differences of <i>TUSC5</i> isoforms caused by novel alternative splicing. Oncotarget, 2018, .	1.8	1
32	Association study and expression analysis of <i>CYP4A11</i> gene copy number variation in Chinese cattle. Scientific Reports, 2017, 7, 46599.	3.3	27
33	Long non-coding RNA <i>ADNCR</i> suppresses adipogenic differentiation by targeting miR-204. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 871-882.	1.9	148
34	The developmental transcriptome sequencing of bovine skeletal muscle reveals a long noncoding RNA, <i>lncMD</i> , promotes muscle differentiation by sponging miR-125b. Biochimica Et Biophysica Acta - Molecular Cell Research, 2016, 1863, 2835-2845.	4.1	120
35	Tetra-primer ARMS-PCR identified four pivotal genetic variations in bovine <i>PNPLA3</i> gene and its expression patterns. Gene, 2016, 575, 191-198.	2.2	1
36	Evaluation of the causality of the zinc finger BED-type containing gene (<i>ZBED6</i>) for six important growth traits in Nanyang beef cattle. Animal Genetics, 2015, 46, 225-226.	1.7	1

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37	The developmental transcriptome landscape of bovine skeletal muscle defined by Ribo-Zero ribonucleic acid sequencing ¹ . <i>Journal of Animal Science</i> , 2015, 93, 5648-5658.	0.5	31
38	Nicotinamide and resveratrol regulate bovine adipogenesis through a SIRT1-dependent mechanism. <i>Journal of Functional Foods</i> , 2015, 18, 492-500.	3.4	10
39	Two novel polymorphisms of bovine SIRT2 gene are associated with higher body weight in Nanyang cattle. <i>Molecular Biology Reports</i> , 2015, 42, 729-736.	2.3	9
40	Novel splice isoforms of dairy goat DBC1 and their diverse mRNA expression profiles. <i>Small Ruminant Research</i> , 2015, 130, 15-26.	1.2	5
41	Intragenic DNA methylation status down-regulates bovine IGF2 gene expression in different developmental stages. <i>Gene</i> , 2014, 534, 356-361.	2.2	29
42	Expression, SNP Identification, Linkage Disequilibrium, and Haplotype Association Analysis of the Growth Suppressor Gene <i>ZBED6</i> in Qinchuan Beef Cattle. <i>Animal Biotechnology</i> , 2014, 25, 35-54.	1.5	2
43	Identification of bovine NPC1 gene cSNPs and their effects on body size traits of Qinchuan cattle. <i>Gene</i> , 2014, 540, 153-160.	2.2	15
44	Tetra-primer ARMS-PCR is an efficient SNP genotyping method: An example from SIRT2. <i>Analytical Methods</i> , 2014, 6, 1835-1840.	2.7	24
45	Tetra-primer ARMS-PCR identifies the novel genetic variations of bovine HNF-4 β gene associating with growth traits. <i>Gene</i> , 2014, 546, 206-213.	2.2	14
46	An Asp7Gly Substitution in PPAR γ Is Associated with Decreased Transcriptional Activation Activity. <i>PLoS ONE</i> , 2014, 9, e86954.	2.5	1
47	Molecular characterization, alternative splicing and expression analysis of bovine DBC1. <i>Gene</i> , 2013, 527, 689-693.	2.2	12
48	SIRT1 gene polymorphisms are associated with growth traits in Nanyang cattle. <i>Molecular and Cellular Probes</i> , 2013, 27, 215-220.	2.1	29
49	Relationship of polymorphisms within ZBED6 gene and growth traits in beef cattle. <i>Gene</i> , 2013, 526, 107-111.	2.2	10
50	A novel c.274C>G polymorphism in bovine <i>SIRT1</i> gene contributes to diminished promoter activity and is associated with increased body size. <i>Animal Genetics</i> , 2013, 44, 584-587.	1.7	18
51	A 5' Regulatory Region and Two Coding Region Polymorphisms Modulate Promoter Activity and Gene Expression of the Growth Suppressor Gene ZBED6 in Cattle. <i>PLoS ONE</i> , 2013, 8, e79744.	2.5	15
52	A dual color fluorescent reporter system for the real time detection of promoter activity. <i>Biotechnology Letters</i> , 2012, 34, 823-830.	2.2	0