

Hong Chen

List of Publications by Year in descending order

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127
papers

4,632
citations

117625

34
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123424

61
g-index

128
all docs

128
docs citations

128
times ranked

4486
citing authors

#	ARTICLE	IF	CITATIONS
1	Population differentiation as a test for selective sweeps. <i>Genome Research</i> , 2010, 20, 393-402.	5.5	600
2	Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. <i>Nature Communications</i> , 2018, 9, 2337.	12.8	253
3	Circular RNA profiling reveals an abundant circLMO7 that regulates myoblasts differentiation and survival by sponging miR-378a-3p. <i>Cell Death and Disease</i> , 2017, 8, e3153-e3153.	6.3	190
4	Long non-coding RNA ADNCR suppresses adipogenic differentiation by targeting miR-204. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 871-882.	1.9	148
5	circFGFR4 Promotes Differentiation of Myoblasts via Binding miR-107 to Relieve Its Inhibition of Wnt3a. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 272-283.	5.1	142
6	CircFUT10 reduces proliferation and facilitates differentiation of myoblasts by sponging miR-133a. <i>Journal of Cellular Physiology</i> , 2018, 233, 4643-4651.	4.1	137
7	Exosome biogenesis, secretion and function of exosomal miRNAs in skeletal muscle myogenesis. <i>Cell Proliferation</i> , 2020, 53, e12857.	5.3	121
8	The developmental transcriptome sequencing of bovine skeletal muscle reveals a long noncoding RNA, lncMD, promotes muscle differentiation by sponging miR-125b. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 2835-2845.	4.1	120
9	Origin and phylogeographical structure of Chinese cattle. <i>Animal Genetics</i> , 2006, 37, 579-582.	1.7	109
10	Diethylhexyl phthalate and bisphenol A exposure impairs mouse primordial follicle assembly in vitro. <i>Environmental and Molecular Mutagenesis</i> , 2014, 55, 343-353.	2.2	99
11	miR-378a-3p promotes differentiation and inhibits proliferation of myoblasts by targeting HDAC4 in skeletal muscle development. <i>RNA Biology</i> , 2016, 13, 1300-1309.	3.1	79
12	A Zfp609 circular RNA regulates myoblast differentiation by sponging miR-194-5p. <i>International Journal of Biological Macromolecules</i> , 2019, 121, 1308-1313.	7.5	77
13	Two strongly linked single nucleotide polymorphisms (Q320P and V397I) in GDF9 gene are associated with litter size in cashmere goats. <i>Theriogenology</i> , 2019, 125, 115-121.	2.1	77
14	Detection of copy number variations and their effects in Chinese bulls. <i>BMC Genomics</i> , 2014, 15, 480.	2.8	76
15	Analysis of Long Non-Coding RNA and mRNA Expression Profiling in Immature and Mature Bovine (Bos) Tj ETQq1 10.784314.rgBT /Over	2.3	75
16	Circular RNA SNX29 Sponges miR-744 to Regulate Proliferation and Differentiation of Myoblasts by Activating the Wnt5a/Ca2+ Signaling Pathway. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 481-493.	5.1	74
17	Circular RNA TTN Acts As a miR-432 Sponge to Facilitate Proliferation and Differentiation of Myoblasts via the IGF2/PI3K/AKT Signaling Pathway. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 966-980.	5.1	69
18	Genetic variants and effects on milk traits of the caprine paired-like homeodomain transcription factor 2 (PITX2) gene in dairy goats. <i>Gene</i> , 2013, 532, 203-210.	2.2	68

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19	Identification and profiling of conserved and novel microRNAs from Chinese Qinchuan bovine longissimus thoracis. BMC Genomics, 2013, 14, 42.	2.8	61
20	InDels within caprine <i>IGF2BP1</i> intron 2 and the 3' untranslated regions are associated with goat growth traits. Animal Genetics, 2020, 51, 117-121.	1.7	57
21	circRNA Profiling Reveals an Abundant circFLUT10 that Promotes Adipocyte Proliferation and Inhibits Adipocyte Differentiation via Sponging let-7. Molecular Therapy - Nucleic Acids, 2020, 20, 491-501.	5.1	54
22	Genome-wide copy number variant analysis reveals variants associated with 10 diverse production traits in Holstein cattle. BMC Genomics, 2018, 19, 314.	2.8	52
23	miR-484p regulates proliferation and apoptosis of bovine muscle cells by targeting KLF6. Journal of Cellular Physiology, 2019, 234, 15742-15750.	4.1	48
24	BGVD: An Integrated Database for Bovine Sequencing Variations and Selective Signatures. Genomics, Proteomics and Bioinformatics, 2020, 18, 186-193.	6.9	47
25	Genetic Variation of Mitochondrial D-loop Region and Evolution Analysis in Some Chinese Cattle Breeds. Journal of Genetics and Genomics, 2007, 34, 510-518.	3.9	46
26	Paternal origins of Chinese cattle. Animal Genetics, 2013, 44, 446-449.	1.7	46
27	Goat DNMT3B: An indel mutation detection, association analysis with litter size and mRNA expression in gonads. Theriogenology, 2020, 147, 108-115.	2.1	46
28	The Circular RNA circHUWE1 Sponges the miR-29b-AKT3 Axis to Regulate Myoblast Development. Molecular Therapy - Nucleic Acids, 2020, 19, 1086-1097.	5.1	44
29	The role of germ cell loss during primordial follicle assembly: a review of current advances. International Journal of Biological Sciences, 2017, 13, 449-457.	6.4	42
30	Diversity of copy number variation in the worldwide goat population. Heredity, 2019, 122, 636-646.	2.6	42
31	Assessing genomic diversity and signatures of selection in Jiaxian Red cattle using whole-genome sequencing data. BMC Genomics, 2021, 22, 43.	2.8	42
32	Linc-smad7 promotes myoblast differentiation and muscle regeneration via sponging miR-125b. Epigenetics, 2018, 13, 591-604.	2.7	41
33	Characterization of lncRNA-miRNA-mRNA Network to Reveal Potential Functional ceRNAs in Bovine Skeletal Muscle. Frontiers in Genetics, 2019, 10, 91.	2.3	39
34	Long Non-coding RNA Profiling Reveals an Abundant MDNCR that Promotes Differentiation of Myoblasts by Sponging miR-133a. Molecular Therapy - Nucleic Acids, 2018, 12, 610-625.	5.1	38
35	The role of autophagy during murine primordial follicle assembly. Aging, 2018, 10, 197-211.	3.1	37
36	Copy number variations of MICAL-L2 shaping gene expression contribute to different phenotypes of cattle. Mammalian Genome, 2013, 24, 508-516.	2.2	36

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37	Comprehensive analysis of the mitochondrial DNA diversity in Chinese cattle. <i>Animal Genetics</i> , 2019, 50, 70-73.	1.7	35
38	Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. <i>BMC Genomics</i> , 2019, 20, 181.	2.8	34
39	A new insight into cattle's maternal origin in six Asian countries. <i>Journal of Genetics and Genomics</i> , 2010, 37, 173-180.	3.9	33
40	CircRILPL1 promotes muscle proliferation and differentiation via binding miR-145 to activate IGF1R/PI3K/AKT pathway. <i>Cell Death and Disease</i> , 2021, 12, 142.	6.3	33
41	Copy number variations at <i>LEPR</i> gene locus associated with gene expression and phenotypic traits in Chinese cattle. <i>Animal Science Journal</i> , 2016, 87, 336-343.	1.4	32
42	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
43	LncRNA MEG3 promotes bovine myoblast differentiation by sponging miR-135. <i>Journal of Cellular Physiology</i> , 2019, 234, 18361-18370.	4.1	31
44	MiR-208b regulates cell cycle and promotes skeletal muscle cell proliferation by targeting CDKN1A. <i>Journal of Cellular Physiology</i> , 2019, 234, 3720-3729.	4.1	31
45	miR-483 inhibits bovine myoblast cell proliferation and differentiation via IGF1/PI3K/AKT signal pathway. <i>Journal of Cellular Physiology</i> , 2019, 234, 9839-9848.	4.1	30
46	Novel Nucleotide Variations, Haplotypes Structure and Associations with Growth Related Traits of Goat AT Motif-Binding Factor (<i>ATBF1</i>) Gene. <i>Asian-Australasian Journal of Animal Sciences</i> , 2015, 28, 1394-1406.	2.4	30
47	Role of bta-miR-204 in the regulation of adipocyte proliferation, differentiation, and apoptosis. <i>Journal of Cellular Physiology</i> , 2019, 234, 11037-11046.	4.1	29
48	circINSR Promotes Proliferation and Reduces Apoptosis of Embryonic Myoblasts by Sponging miR-34a. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 986-999.	5.1	29
49	Polymorphisms of two Y chromosome microsatellites in Chinese cattle. <i>Genetics Selection Evolution</i> , 2006, 38, 525-34.	3.0	27
50	Association study and expression analysis of CYP4A11 gene copy number variation in Chinese cattle. <i>Scientific Reports</i> , 2017, 7, 46599.	3.3	27
51	Genetic diversity of Chinese cattle revealed by Y-SNP and Y-STR markers. <i>Animal Genetics</i> , 2019, 50, 64-69.	1.7	27
52	An atlas of CNV maps in cattle, goat and sheep. <i>Science China Life Sciences</i> , 2021, 64, 1747-1764.	4.9	27
53	Impact of Parental <i>Bos taurus</i> and <i>Bos indicus</i> Origins on Copy Number Variation in Traditional Chinese Cattle Breeds. <i>Genome Biology and Evolution</i> , 2015, 7, 2352-2361.	2.5	25
54	Developmental transcriptome profiling of bovine muscle tissue reveals an abundant <i>GosB</i> that regulates myoblast proliferation and apoptosis. <i>Oncotarget</i> , 2017, 8, 32083-32100.	1.8	25

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55	Global Transcriptome Analysis During Adipogenic Differentiation and Involvement of Transthyretin Gene in Adipogenesis in Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 463.	2.3	25
56	circFLT1 and lncCCPG1 Sponges miR-93 to Regulate the Proliferation and Differentiation of Adipocytes by Promoting lncSLC30A9 Expression. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 22, 484-499.	5.1	24
57	CircINSR Regulates Fetal Bovine Muscle and Fat Development. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 615638.	3.7	24
58	Abundant Genetic Diversity of Yunling Cattle Based on Mitochondrial Genome. <i>Animals</i> , 2019, 9, 641.	2.3	22
59	Copy number variation of bovine MAPK10 modulates the transcriptional activity and affects growth traits. <i>Livestock Science</i> , 2016, 194, 44-50.	1.6	21
60	<i>PRLH</i> and <i>SOD1</i> gene variations associated with heat tolerance in Chinese cattle. <i>Animal Genetics</i> , 2018, 49, 447-451.	1.7	21
61	Growth Performance and Meat Quality Evaluations in Three-Way Cross Cattle Developed for the Tibetan Plateau and their Molecular Understanding by Integrative Omics Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 541-550.	5.2	21
62	Integrating CNVs into meta-QTL identified GBP4 as positional candidate for adult cattle stature. <i>Functional and Integrative Genomics</i> , 2018, 18, 559-567.	3.5	19
63	MiR-204-5p promotes lipid synthesis in mammary epithelial cells by targeting SIRT1. <i>Biochemical and Biophysical Research Communications</i> , 2020, 533, 1490-1496.	2.1	19
64	Copy number variation (CNV) in the <i>IGF1R</i> gene across four cattle breeds and its association with economic traits. <i>Archives Animal Breeding</i> , 2019, 62, 171-179.	1.4	19
65	Association of HSF1 Genetic Variation with Heat Tolerance in Chinese Cattle. <i>Animals</i> , 2019, 9, 1027.	2.3	18
66	Genomic analyses reveal distinct genetic architectures and selective pressures in buffaloes. <i>GigaScience</i> , 2020, 9, .	6.4	18
67	Copy Number Variation of the PIGY Gene in Sheep and Its Association Analysis with Growth Traits. <i>Animals</i> , 2020, 10, 688.	2.3	18
68	Bta-miR-885 promotes proliferation and inhibits differentiation of myoblasts by targeting MyoD1. <i>Journal of Cellular Physiology</i> , 2020, 235, 6625-6636.	4.1	17
69	Copy Number Variation of the SHE Gene in Sheep and Its Association with Economic Traits. <i>Animals</i> , 2019, 9, 531.	2.3	16
70	Four Novel SNPs of MYO1A Gene Associated with Heat-Tolerance in Chinese Cattle. <i>Animals</i> , 2019, 9, 964.	2.3	16
71	Identification of a Novel Polymorphism in Bovine lncRNA ADNCR Gene and Its Association with Growth Traits. <i>Animal Biotechnology</i> , 2019, 30, 159-165.	1.5	16
72	Whole-genome resequencing reveals diversity, global and local ancestry proportions in Yunling cattle. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 641-650.	2.0	15

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73	Whole genome analyses revealed genomic difference between European taurine and East Asian taurine. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 56-68.	2.0	15
74	Circular RNA circMYL1 Inhibit Proliferation and Promote Differentiation of Myoblasts by Sponging miR-2400. <i>Cells</i> , 2021, 10, 176.	4.1	15
75	Novel lncRNA lncFAM200B: Molecular Characteristics and Effects of Genetic Variants on Promoter Activity and Cattle Body Measurement Traits. <i>Frontiers in Genetics</i> , 2019, 10, 968.	2.3	14
76	lncRNA IGF2 AS Regulates Bovine Myogenesis through Different Pathways. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 21, 874-884.	5.1	14
77	Biogenesis and ceRNA role of circular RNAs in skeletal muscle myogenesis. <i>International Journal of Biochemistry and Cell Biology</i> , 2019, 117, 105621.	2.8	13
78	A Novel SNP in EIF2AK4 Gene Is Associated with Thermal Tolerance Traits in Chinese Cattle. <i>Animals</i> , 2019, 9, 375.	2.3	13
79	Population structure, genetic diversity, and selective signature of Chaka sheep revealed by whole genome sequencing. <i>BMC Genomics</i> , 2020, 21, 520.	2.8	13
80	Detection of mRNA Expression and Copy Number Variations Within the Goat FecB Gene Associated With Litter Size. <i>Frontiers in Veterinary Science</i> , 2021, 8, 758705.	2.2	13
81	circMEF2D Negatively Regulated by HNRNPA1 Inhibits Proliferation and Differentiation of Myoblasts via miR-486-PI3K/AKT Axis. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 8145-8163.	5.2	13
82	Cold exposure induces the acquisition of brown adipocyte gene expression profiles in cattle inguinal fat normalized with a new set of reference genes for qRT-PCR. <i>Research in Veterinary Science</i> , 2017, 114, 1-5.	1.9	12
83	A SNP in PLAG1 is associated with body height trait in Chinese cattle. <i>Animal Genetics</i> , 2020, 51, 87-90.	1.7	12
84	Multiple morphological abnormalities of the sperm flagella (MMAF)-associated genes: The relationships between genetic variation and litter size in goats. <i>Gene</i> , 2020, 753, 144778.	2.2	12
85	Y chromosome diversity and paternal origin of Chinese cattle. <i>Molecular Biology Reports</i> , 2013, 40, 6633-6636.	2.3	11
86	Genome-Wide SNPs and InDels Characteristics of Three Chinese Cattle Breeds. <i>Animals</i> , 2019, 9, 596.	2.3	11
87	Identification of novel alternative splicing of bovine lncRNA lncFAM200B and its effects on preadipocyte proliferation. <i>Journal of Cellular Physiology</i> , 2021, 236, 601-611.	4.1	11
88	MicroRNA bta-miR-365-3p inhibits proliferation but promotes differentiation of primary bovine myoblasts by targeting the activin A receptor type I. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 16.	5.3	11
89	Mitochondrial genomes from modern and ancient Turano-Mongolian cattle reveal an ancient diversity of taurine maternal lineages in East Asia. <i>Heredity</i> , 2021, 126, 1000-1008.	2.6	11
90	CircARID1A regulates mouse skeletal muscle regeneration by functioning as a sponge of miR-6368. <i>FASEB Journal</i> , 2021, 35, e21324.	0.5	11

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91	A novel lncRNA BADLNCR1 inhibits bovine adipogenesis by repressing <i>GLRX5</i> expression. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 7175-7186.	3.6	11
92	Relationship of polymorphisms within ZBED6 gene and growth traits in beef cattle. <i>Gene</i> , 2013, 526, 107-111.	2.2	10
93	Nicotinamide and resveratrol regulate bovine adipogenesis through a SIRT1-dependent mechanism. <i>Journal of Functional Foods</i> , 2015, 18, 492-500.	3.4	10
94	Overexpression of DEC1 inhibits myogenic differentiation by modulating MyoG activity in bovine satellite cell. <i>Journal of Cellular Physiology</i> , 2018, 233, 9365-9374.	4.1	10
95	Multiple domestication of swamp buffalo in China and South East Asia. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 331-340.	2.0	10
96	Variants and haplotypes within MEF2C gene influence stature of chinese native cattle including body dimensions and weight. <i>Livestock Science</i> , 2016, 185, 106-109.	1.6	9
97	Characterization and Transcriptome Analysis of Exosomal and Nonexosomal RNAs in Bovine Adipocytes. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9313.	4.1	9
98	Integrating Genome-Wide CNVs Into QTLs and High Confidence GWAScore Regions Identified Positional Candidates for Sheep Economic Traits. <i>Frontiers in Genetics</i> , 2020, 11, 569.	2.3	9
99	The circular RNA circCPE regulates myoblast development by sponging miR-138. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 102.	5.3	9
100	SNPs of bovine HGF gene and their association with growth traits in Nanyang cattle. <i>Research in Veterinary Science</i> , 2013, 95, 483-488.	1.9	8
101	Association analysis of KMT2D copy number variation as a positional candidate for growth traits. <i>Gene</i> , 2020, 753, 144799.	2.2	8
102	Exploring genetic diversity and phylogenic relationships of Chinese cattle using gene mtDNA 16S rRNA. <i>Archives Animal Breeding</i> , 2019, 62, 325-333.	1.4	8
103	CircRNA Profiling Reveals CircPPAR β Modulates Adipogenic Differentiation via Sponging miR-92a-3p. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 6698-6708.	5.2	7
104	Effects of SNPs and alternative splicing within HGF gene on its expression patterns in Qinchuan cattle. <i>Journal of Animal Science and Biotechnology</i> , 2015, 6, 55.	5.3	6
105	Detection of Bovine TMEM95 p.Cys161X Mutation in 13 Chinese Indigenous Cattle Breeds. <i>Animals</i> , 2019, 9, 444.	2.3	6
106	Circular RNA ACTA1 Acts as a Sponge for miR-199a-5p and miR-433 to Regulate Bovine Myoblast Development through the MAP3K11/MAP2K7/JNK Pathway. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 3357-3373.	5.2	6
107	Genetic Variations and mRNA Expression of Goat DNAH1 and Their Associations with Litter Size. <i>Cells</i> , 2022, 11, 1371.	4.1	6
108	Novel transcripts and alternatively spliced genes are associated with early development in bovine embryos. <i>Animal</i> , 2012, 6, 1199-1205.	3.3	5

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109	Association analysis of SSTR2 copy number variation with cattle stature and its expression analysis in Chinese beef cattle. <i>Journal of Agricultural Science</i> , 2019, 157, 365-374.	1.3	5
110	Association Analysis to Copy Number Variation (CNV) of Opn4 Gene with Growth Traits of Goats. <i>Animals</i> , 2020, 10, 441.	2.3	5
111	Genetic Variations within the Bovine CRY2 Gene Are Significantly Associated with Carcass Traits. <i>Animals</i> , 2022, 12, 1616.	2.3	5
112	Determination of genetic effects of <i>SERPINA3</i> on important growth traits in beef cattle. <i>Animal Biotechnology</i> , 2020, 31, 164-173.	1.5	4
113	Two Different Copy Number Variations of the CLCN2 Gene in Chinese Cattle and Their Association with Growth Traits. <i>Animals</i> , 2022, 12, 41.	2.3	4
114	Circ <i>RIMKLB</i> promotes myoblast proliferation and inhibits differentiation by sponging <i>miR-29c</i> to release <i>KCNJ12</i> . <i>Epigenetics</i> , 2022, 17, 1686-1700.	2.7	3
115	Screening of Bovine Tissue-Specific Expressed Genes and Identification of Genetic Variation Within an Adipose Tissue-Specific lncRNA Gene. <i>Frontiers in Veterinary Science</i> , 2022, 9, .	2.2	3
116	lnc9141-a and -b Play a Different Role in Bovine Myoblast Proliferation, Apoptosis, and Differentiation. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 18, 554-566.	5.1	2
117	Distribution of Copy Number Variation in SYT11 Gene and Its Association with Growth Conformation Traits in Chinese Cattle. <i>Biology</i> , 2022, 11, 223.	2.8	2
118	Evaluation of the causality of the zinc finger BED-type containing 6 gene (ZBED6) for six important growth traits in Nanyang beef cattle. <i>Animal Genetics</i> , 2015, 46, 225-226.	1.7	1
119	<i>EGLN1</i> gene variation in Chinese native cattle and yaks. <i>Animal Genetics</i> , 2018, 49, 655-656.	1.7	1
120	Y-chromosomal haplogroup distributions in Chinese cattle. <i>Animal Genetics</i> , 2019, 50, 412-413.	1.7	1
121	Differential Expression of ACTL8 Gene and Association Study of Its Variations with Growth Traits in Chinese Cattle. <i>Animals</i> , 2019, 9, 1068.	2.3	1
122	A novel 28-bp indel in <i>IGF1R</i> gene associated with growth traits across four Chinese cattle breeds. <i>Journal of Agricultural Science</i> , 2021, 159, 762-768.	1.3	1
123	Are Copy Number Variations within the FecB Gene Significantly Associated with Morphometric Traits in Goats?. <i>Animals</i> , 2022, 12, 1547.	2.3	1
124	The three missense mutations of <i>EPAS1</i> , <i>IL37</i> and <i>EEF1D</i> genes associated with high-altitude adaptation in Chinese cattle. <i>Animal Genetics</i> , 2020, 51, 987-988.	1.7	0
125	Copy number variation of bovine <i>S100A7</i> as a positional candidate affected body measurements. <i>Animal Biotechnology</i> , 0, , 1-9.	1.5	0
126	Comparisons of Hematological and Biochemical Profiles in Brahman and Yunling Cattle. <i>Animals</i> , 2022, 12, 1813.	2.3	0

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127	Deletions in GSN gene associated with growth traits of four Chinese cattle breeds. Molecular Genetics and Genomics, 0, , .	2.1	0