Ruihua Dang

List of Publications by Year
in descending order

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44	766	840585 11	580701 25
papers	citations	h-index	g-index

45	45	45	828
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A novel 31bp deletion within the CDKL5 gene is significantly associated with growth traits in Dezhou donkey. Animal Biotechnology, 2023, 34, 503-507.	0.7	2
2	Association analysis of IGF2 gene polymorphisms with growth traits of Dezhou donkey. Animal Biotechnology, 2023, 34, 1143-1153.	0.7	4
3	Metabolomic profiling of Dezhou donkey sperm associated with freezability. Theriogenology, 2022, 181, 131-139.	0.9	11
4	MiR-24-3p Conservatively Regulates Muscle Cell Proliferation and Apoptosis by Targeting Common Gene CAMK2B in Rat and Cattle. Animals, 2022, 12, 505.	1.0	4
5	Whole genome analyses revealed genomic difference between European taurine and East Asian taurine. Journal of Animal Breeding and Genetics, 2021, 138, 56-68.	0.8	15
6	Tissue expression profile, polymorphism of IGF1 gene and its effect on body size traits of Dezhou donkey. Gene, 2021, 766, 145118.	1.0	9
7	A novel AÂ>ÂG polymorphism in the intron 2 of TBX3 gene is significantly associated with body size in donkeys. Gene, 2021, 785, 145602.	1.0	10
8	Genomic analyses reveal distinct genetic architectures and selective pressures in Chinese donkeys. Journal of Genetics and Genomics, 2021, 48, 737-745.	1.7	16
9	Comparative proteomic analysis of seminal plasma proteins in relation to freezability of Dezhou donkey semen. Animal Reproduction Science, 2021, 231, 106794.	0.5	8
10	Multiple domestication of swamp buffalo in China and South East Asia. Journal of Animal Breeding and Genetics, 2020, 137, 331-340.	0.8	10
11	Copy Number Variations of Four Y-Linked Genes in Swamp Buffaloes. Animals, 2020, 10, 31.	1.0	4
12	Detection of Selection Signatures Underlying Production and Adaptive Traits Based on Whole-Genome Sequencing of Six Donkey Populations. Animals, 2020, 10, 1823.	1.0	7
13	MiRNAs Expression Profiling of Bovine (Bos taurus) Testes and Effect of bta-miR-146b on Proliferation and Apoptosis in Bovine Male Germline Stem Cells. International Journal of Molecular Sciences, 2020, 21, 3846.	1.8	22
14	Comparative Transcriptomics Analysis of Testicular miRNA from Cryptorchid and Normal Horses. Animals, 2020, 10, 338.	1.0	5
15	Genomic analyses reveal distinct genetic architectures and selective pressures in buffaloes. GigaScience, 2020, 9, .	3.3	18
16	Genotypes and haplotype combination of ACSL3 gene sequence variants is associated with growth traits in Dezhou donkey. Gene, 2020, 743, 144600.	1.0	8
17	A missense mutation in ASIP is associated with light point variation in donkeys. Animal Genetics, 2020, 51, 629-629.	0.6	2
18	Expression profiles and polymorphic identification of the <i>ACSL1</i> gene and their association with body size traits in Dezhou donkeys. Archives Animal Breeding, 2020, 63, 377-386.	0.5	7

#	Article	IF	Citations
19	Two Novel SNPs in RET Gene Are Associated with Cattle Body Measurement Traits. Animals, 2019, 9, 836.	1.0	7
20	Genome-Wide SNPs and InDels Characteristics of Three Chinese Cattle Breeds. Animals, 2019, 9, 596.	1.0	11
21	Null mutation of the endothelin receptor type B gene causes embryonic death in the GK rat. PLoS ONE, 2019, 14, e0217132.	1.1	6
22	Analysis of Long Non-Coding RNA and mRNA Expression Profiling in Immature and Mature Bovine (Bos) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.1	75
23	Yâ€chromosomal haplogroup distributions in Chinese cattle. Animal Genetics, 2019, 50, 412-413.	0.6	1
24	A Novel SNP in EIF2AK4 Gene Is Associated with Thermal Tolerance Traits in Chinese Cattle. Animals, 2019, 9, 375.	1.0	13
25	The Distribution Characteristics of a 19-bp Indel of the PLAG1 Gene in Chinese Cattle. Animals, 2019, 9, 1082.	1.0	7
26	A Novel 13 bp Deletion within the NR6A1 Gene Is Significantly Associated with Growth Traits in Donkeys. Animals, 2019, 9, 681.	1.0	10
27	Identification of a Novel Polymorphism in Bovine lncRNA ADNCR Gene and Its Association with Growth Traits. Animal Biotechnology, 2019, 30, 159-165.	0.7	16
28	Exploring insertions and deletions (indels) of <i>MSRB3</i> gene and their association with growth traits in four Chinese indigenous cattle breeds. Archives Animal Breeding, 2019, 62, 465-475.	0.5	8
29	Polymorphisms in MX2 Gene Are Related with SCS in Chinese Dairy Cows. Animal Biotechnology, 2018, 29, 81-89.	0.7	3
30	Yâ€chromosome haplotype analysis revealing multiple paternal origins in swamp buffaloes of China and Southeast Asia. Journal of Animal Breeding and Genetics, 2018, 135, 442-449.	0.8	3
31	Bovine pituitary homeobox 2 (PITX2): mRNA expression profiles of different alternatively spliced variants and association analyses with growth traits. Gene, 2018, 669, 1-7.	1.0	10
32	Goat Boule: Isoforms identification, mRNA expression in testis and functional study and promoter methylation profiles. Theriogenology, 2018, 116, 53-63.	0.9	5
33	Identification and characterization of circular RNAs in Qinchuan cattle testis. Royal Society Open Science, 2018, 5, 180413.	1.1	59
34	Detection of Insertions/Deletions Within SIRT1, SIRT2 and SIRT3 Genes and Their Associations with Body Measurement Traits in Cattle. Biochemical Genetics, 2018, 56, 663-676.	0.8	14
35	Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. Nature Communications, 2018, 9, 2337.	5.8	253
36	<scp>ASIP</scp> gene variation in <scp>C</scp>hinese donkeys. Animal Genetics, 2017, 48, 372-373.	0.6	3

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37	Genetic variation in the GDNF promoter affects its expression and modifies the severity of Hirschsprung's disease (HSCR) in rats carrying Ednrbsl mutations. Gene, 2016, 575, 144-148.	1.0	12
38	Identification of novel isoforms of dairy goat EEF1D and their mRNA expression characterization. Gene, 2016, 581, 14-20.	1.0	5
39	Identification of novel alternative splicing transcript and expression analysis of bovine TMEM95 gene. Gene, 2016, 575, 531-536.	1.0	16
40	Novel alternative splice variants of NFIX and their diverse mRNA expression patterns in dairy goat. Gene, 2015, 569, 250-258.	1.0	11
41	Anatomic Modifications in the Enteric Nervous System of JF1 Mice with the Classic Piebald Mutation. Journal of Veterinary Medical Science, 2012, 74, 391-394.	0.3	6
42	Lymphopenia in Ednrb-deficient rat was strongly modified by genetic background. Biomedical Research, 2012, 33, 249-253.	0.3	8
43	Genetic Background Strongly Modifies the Severity of Symptoms of Hirschsprung Disease, but Not Hearing Loss in Rats Carrying Ednrbsl Mutations. PLoS ONE, 2011, 6, e24086.	1.1	31
44	QTL Analysis Identifies a Modifier Locus of Aganglionosis in the Rat Model of Hirschsprung Disease Carrying Ednrbsl Mutations. PLoS ONE, 2011, 6, e27902.	1.1	10