

Quratulain Hanif

List of Publications by Year in descending order

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36
papers

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38
all docs

38
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38
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302
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic variants identified from whole-genome resequencing of indicine cattle breeds from Pakistan. PLoS ONE, 2019, 14, e0215065.	1.1	28
2	An atlas of CNV maps in cattle, goat and sheep. Science China Life Sciences, 2021, 64, 1747-1764.	2.3	27
3	Expression and Purification of Hybrid LL-37T \pm 1 Peptide in <i>Pichia pastoris</i> and Evaluation of Its Immunomodulatory and Anti-inflammatory Activities by LPS Neutralization. Frontiers in Immunology, 2019, 10, 1365.	2.2	24
4	Whole Genome Scan and Selection Signatures for Climate Adaption in Yanbian Cattle. Frontiers in Genetics, 2020, 11, 94.	1.1	24
5	Four Novel SNPs of MYO1A Gene Associated with Heat-Tolerance in Chinese Cattle. Animals, 2019, 9, 964.	1.0	16
6	In silico identification of conserved miRNAs and their selective target gene prediction in indicine (Bos) Tj ETQq0 0 0,rgBT /Overlock 10 TF	1.1	15
7	Whole-genome resequencing reveals diversity, global and local ancestry proportions in Yunling cattle. Journal of Animal Breeding and Genetics, 2020, 137, 641-650.	0.8	15
8	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
9	Genome-wide association study identifies energy metabolism genes for resistance to ketosis in Chinese Holstein cattle. Animal Genetics, 2019, 50, 376-380.	0.6	13
10	Population structure, genetic diversity, and selective signature of Chaka sheep revealed by whole genome sequencing. BMC Genomics, 2020, 21, 520.	1.2	13
11	A SNP in PLAG1 is associated with body height trait in Chinese cattle. Animal Genetics, 2020, 51, 87-90.	0.6	12
12	Mitogenome Diversity and Maternal Origins of Guangxi Cattle Breeds. Animals, 2020, 10, 19.	1.0	12
13	Selection signatures of Fuzhong Buffalo based on whole-genome sequences. BMC Genomics, 2020, 21, 674.	1.2	12
14	Genome-Wide SNPs and InDels Characteristics of Three Chinese Cattle Breeds. Animals, 2019, 9, 596.	1.0	11
15	Mitogenome Diversity and Maternal Origins of Guangxi Buffalo Breeds. Animals, 2020, 10, 547.	1.0	10
16	Integrating Genome-Wide CNVs Into QTLs and High Confidence GWAScore Regions Identified Positional Candidates for Sheep Economic Traits. Frontiers in Genetics, 2020, 11, 569.	1.1	9
17	Whole-genome resequencing reveals diversity and selective signals in Longlin goat. Gene, 2021, 771, 145371.	1.0	8
18	Genome-wide association study identifies quantitative trait loci affecting cattle temperament. Zoological Research, 2022, 43, 14-25.	0.9	8

#	ARTICLE	IF	CITATIONS
19	Genome-wide association study identifies genomic loci associated with flight reaction in cattle. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 477-485.	0.8	6
20	Identification of Genomic Characteristics and Selective Signals in a Du'an Goat Flock. <i>Animals</i> , 2020, 10, 994.	1.0	6
21	<i>dgat1</i> K232A polymorphism is associated with milk production traits in Chinese cattle. <i>Animal Biotechnology</i> , 2021, 32, 427-431.	0.7	6
22	In vitro Impact of Yeast Expressed Hybrid Peptide CATH-2TP5 as a Prophylactic Measure Toward Sepsis and Inflammation. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 454.	2.0	5
23	Rich maternal and paternal genetic diversity and divergent lineage composition in wild yak (<i>Bos</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	0.7	5
24	Whole-Genome Analyses Reveal Genomic Characteristics and Selection Signatures of Lincang Humped Cattle at the China-Myanmar Border. <i>Frontiers in Genetics</i> , 2022, 13, 833503.	1.1	5
25	Copy Number Variations of Four Y-Linked Genes in Swamp Buffaloes. <i>Animals</i> , 2020, 10, 31.	1.0	4
26	Rich maternal and paternal genetic diversity and divergent lineage composition in wild yak (<i>Bos</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.7	4
27	Maternal genetic diversity, differentiation and phylogeny of three white yak breeds/populations in China. <i>Animal Biotechnology</i> , 2023, 34, 728-733.	0.7	4
28	Muscle transcriptome analysis reveal candidate genes and pathways related to fat and lipid metabolism in Yunling cattle. <i>Animal Biotechnology</i> , 2021, , 1-8.	0.7	4
29	MTOR Variation Related to Heat Resistance of Chinese Cattle. <i>Animals</i> , 2019, 9, 915.	1.0	3
30	A Hybrid Peptide DEFB-TP5 Expressed in Methylotrophic Yeast Neutralizes LPS With Potent Anti-inflammatory Activities. <i>Frontiers in Pharmacology</i> , 2020, 11, 461.	1.6	3
31	Whole-Genome Sequencing of Endangered Dengchuan Cattle Reveals Its Genomic Diversity and Selection Signatures. <i>Frontiers in Genetics</i> , 2022, 13, 833475.	1.1	2
32	Genetic diversity of mitochondrial cytochrome b gene in swamp buffalo. <i>Animal Genetics</i> , 2020, 51, 977-981.	0.6	1
33	A novel SNP of <i>TECPR2</i> gene associated with heat tolerance in Chinese cattle. <i>Animal Biotechnology</i> , 2023, 34, 1050-1057.	0.7	1
34	Distribution of the variant at AKIRIN2: c.*188G>A in Chinese cattle. <i>Animal Biotechnology</i> , 2020, , 1-5.	0.7	0
35	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.	0.6	0
36	Characterization of whole mitogenome sequence of the Tongde yak (<i>Bos grunniens</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2498-2500.	0.2	0