Zhuqing Zheng

List of Publications by Year in descending order

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759190 1058452 14 772 12 14 citations h-index g-index papers 17 17 17 1122 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Ancient genomes reveal the genetic inheritance and recent introgression in Chinese indigenous pigs. Science China Life Sciences, 2022, 65, 842-845.	4.9	3
2	Enhancer-promoter interaction maps provide insights into skeletal muscle-related traits in pig genome. BMC Biology, 2022, 20, .	3.8	13
3	Geographical contrasts of Yâ€chromosomal haplogroups from wild and domestic goats reveal ancient migrations and recent introgressions. Molecular Ecology, 2022, 31, 4364-4380.	3.9	5
4	Modes of genetic adaptations underlying functional innovations in the rumen. Science China Life Sciences, 2021, 64, 1-21.	4.9	19
5	A near complete genome for goat genetic and genomic research. Genetics Selection Evolution, 2021, 53, 74.	3.0	16
6	An atlas of CNV maps in cattle, goat and sheep. Science China Life Sciences, 2021, 64, 1747-1764.	4.9	27
7	The origin of domestication genes in goats. Science Advances, 2020, 6, eaaz5216.	10.3	86
8	BGVD: An Integrated Database for Bovine Sequencing Variations and Selective Signatures. Genomics, Proteomics and Bioinformatics, 2020, 18, 186-193.	6.9	47
9	Genomic analyses reveal distinct genetic architectures and selective pressures in buffaloes. GigaScience, 2020, 9, .	6.4	18
10	Ancient Genomes Reveal the Evolutionary History and Origin of Cashmere-Producing Goats in China. Molecular Biology and Evolution, 2020, 37, 2099-2109.	8.9	29
11	Towards the Complete Goat Pan-Genome by Recovering Missing Genomic Segments From the Reference Genome. Frontiers in Genetics, 2019, 10, 1169.	2.3	29
12	Genetic basis of ruminant headgear and rapid antler regeneration. Science, 2019, 364, .	12.6	121
13	Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. Nature Communications, 2018, 9, 2337.	12.8	253
14	CNVcaller: highly efficient and widely applicable software for detecting copy number variations in large populations. GigaScience, 2017, 6, 1-12.	6.4	101