

Fuki Kawaguchi

List of Publications by Year in descending order

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Version: 2024-02-01

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papers

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#	ARTICLE	IF	CITATIONS
1	<i>FGF5</i> and <i>EPAS1</i> gene polymorphisms are associated with high-altitude adaptation in Nepalese goat breeds. <i>Animal Science Journal</i> , 2021, 92, e13640.	0.6	4
2	Effect of Five Polymorphisms on Percentage of Oleic Acid in Beef and Investigation of Linkage Disequilibrium to Confirm the Locations of Quantitative Trait Loci on BTA19 in Japanese Black Cattle. <i>Life</i> , 2021, 11, 597.	1.1	5
3	Recent achievements of candidate polymorphism detection for fatty acid composition in Japanese Black cattle. <i>Journal of Animal Genetics</i> , 2021, 49, 67-75.	0.5	0
4	Indonesian native goats (<i>Capra hircus</i>) reveal highest genetic frequency of mitochondrial DNA haplogroup B in the world. <i>Animal Science Journal</i> , 2020, 91, e13485.	0.6	1
5	Cattle mitogenome variation reveals a post-glacial expansion of haplogroup P and an early incorporation into northeast Asian domestic herds. <i>Scientific Reports</i> , 2020, 10, 20842.	1.6	9
6	Detection of candidate polymorphisms around the QTL for fat area ratio to rib eye area on BTA7 using whole-genome resequencing in Japanese Black cattle. <i>Animal Science Journal</i> , 2020, 91, e13335.	0.6	8
7	Effect of DNA markers on the fertility traits of Japanese Black cattle for improving beef quantity and quality. <i>Archives Animal Breeding</i> , 2020, 63, 9-17.	0.5	5
8	Effect of <i>STARD3</i> gene polymorphism on carcass traits and fatty acid composition in Japanese Black cattle. <i>Journal of Animal Genetics</i> , 2019, 47, 37-45.	0.5	4
9	Whole-genome resequencing to identify candidate genes for the QTL for oleic acid percentage in Japanese Black cattle. <i>Animal Science Journal</i> , 2019, 90, 467-472.	0.6	17
10	The Eurasian Steppe is an important goat propagation route: A phylogeographic analysis using mitochondrial DNA and Y-chromosome sequences of Kazakhstani goats. <i>Animal Science Journal</i> , 2019, 90, 317-322.	0.6	18
11	Kazakhstani native cattle reveal highly divergent mtDNA from <i>Bos taurus</i> and <i>Bos indicus</i> lineages with an absence of <i>Bos indicus</i> Y chromosome. <i>Animal Science Journal</i> , 2019, 90, 29-34.	0.6	1
12	Phylogeographic Analysis of Madagascan Goats Using mtDNA Control Region and SRY Gene Sequences. <i>Zoological Science</i> , 2019, 36, 294.	0.3	5
13	A genome-wide association study for fat-related traits computed by image analysis in Japanese Black cattle. <i>Animal Science Journal</i> , 2018, 89, 743-751.	0.6	13
14	Application of DNA markers for discrimination between Japanese and Australian Wagyu beef. <i>Animal Science Journal</i> , 2018, 89, 257-258.	0.6	4
15	The rare mtDNA haplogroup P observed in Japanese Holstein cattle. <i>Journal of Animal Genetics</i> , 2018, 46, 49-55.	0.5	0
16	Pool-based genome-wide association study identified novel candidate regions on <sc>BTA</sc>9 and 14 for oleic acid percentage in Japanese Black cattle. <i>Animal Science Journal</i> , 2018, 89, 1060-1066.	0.6	7
17	Identification of leptin gene polymorphisms associated with carcass traits and fatty acid composition in Japanese Black cattle. <i>Animal Science Journal</i> , 2017, 88, 433-438.	0.6	18