

Magdalena Fräschczak

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

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1478505

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16
all docs

16
docs citations

16
times ranked

203
citing authors

#	ARTICLE	IF	CITATIONS
1	The Unique hmuY Gene Sequence as a Specific Marker of Porphyromonas gingivalis. PLoS ONE, 2013, 8, e67719.	2.5	17
2	The assessment of inter-individual variation of whole-genome DNA sequence in 32 cows. Mammalian Genome, 2015, 26, 658-665.	2.2	12
3	Analysis of copy number variations in Holstein-Friesian cow genomes based on whole-genome sequence data. Journal of Dairy Science, 2017, 100, 5515-5525.	3.4	11
4	Population Structure Analysis of Bull Genomes of European and Western Ancestry. Scientific Reports, 2017, 7, 40688.	3.3	9
5	Comparison of significant single nucleotide polymorphisms selections in GWAS for complex traits. Journal of Applied Genetics, 2016, 57, 207-213.	1.9	8
6	Identification and annotation of breed-specific single nucleotide polymorphisms in Bos taurus genomes. PLoS ONE, 2018, 13, e0198419.	2.5	8
7	Identification of candidate genes and mutations in QTL regions for immune responses in chicken. Animal Genetics, 2015, 46, 247-254.	1.7	7
8	Single nucleotide polymorphisms associated with osteochondrosis dissecans in Warmblood horses at different stages of training. Animal Production Science, 2017, 57, 608.	1.3	6
9	Exploring the Potential Genetic Heterogeneity in the Incidence of Hoof Disorders in Austrian Fleckvieh and Braunvieh Cattle. Frontiers in Genetics, 2020, 11, 577116.	2.3	3
10	Utilization of information from gene networks towards a better understanding of functional similarities between complex traits: a dairy cattle model. Journal of Applied Genetics, 2016, 57, 129-133.	1.9	2
11	Differences between horse selection based on two forms of osteochondrosis in fetlock. Journal of Applied Genetics, 2018, 59, 225-230.	1.9	1
12	DNA sequence features underlying copy number variants. Acta Scientiarum Polonorum Zootechnica, 2019, 18, 25-30.	0.2	1
13	Invariance of relative inverse function orderings under compositions of distributions. Applicationes Mathematicae, 2012, 39, 283-292.	0.1	0
14	DNA sequence features underlying large-scale duplications and deletions in human. Journal of Applied Genetics, 2022, , .	1.9	0