J Bennewitz

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/693705/publications.pdf

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20	362	12	19
papers	citations	h-index	g-index
20	20	20	362 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	Composition of the ileum microbiota is a mediator between the host genome and phosphorus utilization and other efficiency traits in Japanese quail (Coturnix japonica). Genetics Selection Evolution, 2022, 54, 20.	3.0	6
2	Mapping genes for phosphorus utilization and correlated traits using a 4k SNP linkage map in Japanese quail (<i>Coturnix japonica</i>). Animal Genetics, 2021, 52, 90-98.	1.7	10
3	Implementing a genomic rotational crossbreeding scheme to promote local dairy cattle breeds—A simulation study. Journal of Dairy Science, 2021, 104, 6873-6884.	3.4	7
4	A Novel Model to Explain Extreme Feather Pecking Behavior in Laying Hens. Behavior Genetics, 2020, 50, 41-50.	2.1	19
5	Selecting the hologenome to breed for an improved feed efficiency in pigs—A novel selection index. Journal of Animal Breeding and Genetics, 2020, 137, 14-22.	2.0	40
6	The Gut Microbial Architecture of Efficiency Traits in the Domestic Poultry Model Species Japanese Quail (Coturnix japonica) Assessed by Mixed Linear Models. G3: Genes, Genomes, Genetics, 2020, 10, 2553-2562.	1.8	23
7	lleal Transcriptome Profiles of Japanese Quail Divergent in Phosphorus Utilization. International Journal of Molecular Sciences, 2020, 21, 2762.	4.1	8
8	Identification of the Key Molecular Drivers of Phosphorus Utilization Based on Host miRNA-mRNA and Gut Microbiome Interactions. International Journal of Molecular Sciences, 2020, 21, 2818.	4.1	14
9	Genomic analysis of perinatal sucking reflex in German Brown Swiss calves. Journal of Dairy Science, 2019, 102, 6296-6305.	3.4	4
10	Linkage disequilibrium pattern and genomeâ€wide association mapping for meat traits in multiple porcine F ₂ crosses. Animal Genetics, 2018, 49, 403-412.	1.7	9
11	Application of a Bayesian dominance model improves power in quantitative trait genome-wide association analysis. Genetics Selection Evolution, 2017, 49, 7.	3.0	13
12	The presence of extreme feather peckers in groups of laying hens. Animal, 2017, 11, 500-506.	3.3	11
13	Inferring relationships between Phosphorus utilization, feed per gain, and bodyweight gain in an F2 cross of Japanese quail using recursive models. Poultry Science, 2016, 95, 764-773.	3.4	21
14	Short communication: Importance of introgression for milk traits in the German Vorderwald and Hinterwald cattle. Journal of Dairy Science, 2015, 98, 2033-2038.	3.4	17
15	The contribution of migrant breeds to the genetic gain of beef traits of German Vorderwald and Hinterwald cattle. Journal of Animal Breeding and Genetics, 2014, 131, 496-503.	2.0	24
16	Genetic parameters for feather pecking and aggressive behavior in a large F2-cross of laying hens using generalized linear mixed models. Poultry Science, 2014, 93, 810-817.	3.4	46
17	Genome-wide association analysis to identify genotype \tilde{A} — environment interaction for milk protein yield and level of somatic cell score as environmental descriptors in German Holsteins. Journal of Dairy Science, 2013, 96, 7318-7324.	3.4	17
18	Mapping quantitative trait loci for metabolic and cytological fatness traits of connected F2 crosses in pigs1. Journal of Animal Science, 2012, 90, 399-409.	0.5	7

#	Article	IF	CITATIONS
19	The distribution of QTL additive and dominance effects in porcine F2 crosses. Journal of Animal Breeding and Genetics, 2010, 127, 171-179.	2.0	38
20	Genetic and physiological factors influencing feather pecking in chickens. World's Poultry Science Journal, 2010, 66, 659-672.	3.0	28