

Stephen Moore

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,470
citations

567144

15
h-index

477173

29
g-index

30
all docs

30
docs citations

30
times ranked

2189
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide identification of copy number variation and association with fat deposition in thin and fat-tailed sheep breeds. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
2	Evolution of tissue and developmental specificity of transcription start sites in <i>Bos taurus indicus</i> . <i>Communications Biology</i> , 2021, 4, 829.	2.0	2
3	Unraveling genetic sensitivity of beef cattle to environmental variation under tropical conditions. <i>Genetics Selection Evolution</i> , 2019, 51, 29.	1.2	35
4	Shining a Light on <i>Haemonchus contortus</i> in Sheep. <i>Proceedings (mdpi)</i> , 2019, 36, 138.	0.2	0
5	In-depth characterization of the pituitary transcriptome in Simmental and Chinese native cattle. <i>Domestic Animal Endocrinology</i> , 2019, 66, 35-42.	0.8	6
6	Benchmarking Bayesian genome enabled-prediction models for age at first calving in Nellore cows. <i>Livestock Science</i> , 2018, 211, 75-79.	0.6	9
7	Accuracy of genomic selection predictions for hip height in Brahman cattle using different relationship matrices. <i>Pesquisa Agropecuaria Brasileira</i> , 2018, 53, 717-726.	0.9	3
8	Transcriptomics and iTRAQ-Proteomics Analyses of Bovine Mammary Tissue with <i>Streptococcus agalactiae</i> -Induced Mastitis. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 11188-11196.	2.4	27
9	Candidate Gene Expression in <i>Bos indicus</i> Ovarian Tissues: Prepubertal and Postpubertal Heifers in Diestrus. <i>Frontiers in Veterinary Science</i> , 2016, 3, 94.	0.9	7
10	History of the Hays Converter. <i>Canadian Journal of Animal Science</i> , 2016, 96, 471-477.	0.7	2
11	A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project. <i>GigaScience</i> , 2015, 4, 49.	3.3	38
12	Multi-Trait GWAS and New Candidate Genes Annotation for Growth Curve Parameters in Brahman Cattle. <i>PLoS ONE</i> , 2015, 10, e0139906.	1.1	66
13	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	3.8	331
14	Analysis of biological networks and biological pathways associated with residual feed intake in beef cattle. <i>Animal Science Journal</i> , 2014, 85, 374-387.	0.6	67
15	Single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. <i>BMC Genetics</i> , 2014, 15, 14.	2.7	47
16	Sequence, Structural and Expression Divergence of Duplicate Genes in the Bovine Genome. <i>PLoS ONE</i> , 2014, 9, e102868.	1.1	13
17	Genetic and Phenotypic Correlations between Performance Traits with Meat Quality and Carcass Characteristics in Commercial Crossbred Pigs. <i>PLoS ONE</i> , 2014, 9, e110105.	1.1	42
18	Complicated Relationships: A Review of Biological Interaction Networks and Pathways in Animal Science. <i>Springer Science Reviews</i> , 2013, 1, 73-83.	1.3	3

#	ARTICLE	IF	CITATIONS
19	Genome-wide association analyses for carcass quality in crossbred beef cattle. <i>BMC Genetics</i> , 2013, 14, 80.	2.7	32
20	Association analysis for feed efficiency traits in beef cattle using preserved haplotypes. <i>Genome</i> , 2013, 56, 586-591.	0.9	1
21	WHOLE GENOME IDENTITY-BY-DESCENT DETERMINATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350002.	0.3	10
22	The identification of candidate genes and SNP markers for classical bovine spongiform encephalopathy susceptibility. <i>Prion</i> , 2012, 6, 461-469.	0.9	3
23	Linkage disequilibrium in Angus, Charolais, and Crossbred beef cattle. <i>Frontiers in Genetics</i> , 2012, 3, 152.	1.1	93
24	Developing a genome-wide selection model for genetic improvement of residual feed intake and carcass merit in a beef cattle breeding program. <i>Science Bulletin</i> , 2012, 57, 2741-2746.	1.7	4
25	Antarctic Krill 454 Pyrosequencing Reveals Chaperone and Stress Transcriptome. <i>PLoS ONE</i> , 2011, 6, e15919.	1.1	73
26	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. <i>BMC Genomics</i> , 2011, 12, 318.	1.2	135
27	Whole genome fine mapping of quantitative trait loci for ultrasound and carcass merit traits in beef cattle. <i>Canadian Journal of Animal Science</i> , 2011, 91, 61-73.	0.7	7
28	A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. <i>BMC Genomics</i> , 2008, 9, 631.	1.2	78
29	Genetic mapping of the kuruma prawn <i>Penaeus japonicus</i> using AFLP markers. <i>Aquaculture</i> , 2003, 219, 143-156.	1.7	124
30	Genetic mapping of the black tiger shrimp <i>Penaeus monodon</i> with amplified fragment length polymorphism. <i>Aquaculture</i> , 2002, 204, 297-309.	1.7	205