Stephen Moore

List of Publications by Year
in descending order

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	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	3.8	331
2	Genetic mapping of the black tiger shrimp Penaeus monodon with amplified fragment length polymorphism. Aquaculture, 2002, 204, 297-309.	1.7	205
3	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. BMC Genomics, 2011, 12, 318.	1.2	135
4	Genetic mapping of the kuruma prawn Penaeus japonicus using AFLP markers. Aquaculture, 2003, 219, 143-156.	1.7	124
5	Linkage disequilibrium in Angus, Charolais, and Crossbred beef cattle. Frontiers in Genetics, 2012, 3, 152.	1.1	93
6	A first generation whole genome RH map of the river buffalo with comparison to domestic cattle. BMC Genomics, 2008, 9, 631.	1.2	78
7	Antarctic Krill 454 Pyrosequencing Reveals Chaperone and Stress Transcriptome. PLoS ONE, 2011, 6, e15919.	1.1	73
8	Analysis of biological networks and biological pathways associated with residual feed intake in beef cattle. Animal Science Journal, 2014, 85, 374-387.	0.6	67
9	Multi-Trait GWAS and New Candidate Genes Annotation for Growth Curve Parameters in Brahman Cattle. PLoS ONE, 2015, 10, e0139906.	1.1	66
10	Single nucleotide polymorphisms for feed efficiency and performance in crossbred beef cattle. BMC Genetics, 2014, 15, 14.	2.7	47
11	Genetic and Phenotypic Correlations between Performance Traits with Meat Quality and Carcass Characteristics in Commercial Crossbred Pigs. PLoS ONE, 2014, 9, e110105.	1.1	42
12	A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project. GigaScience, 2015, 4, 49.	3.3	38
13	Unraveling genetic sensitivity of beef cattle to environmental variation under tropical conditions. Genetics Selection Evolution, 2019, 51, 29.	1.2	35
14	Genome-wide association analyses for carcass quality in crossbred beef cattle. BMC Genetics, 2013, 14, 80.	2.7	32
15	Transcriptomics and iTRAQ-Proteomics Analyses of Bovine Mammary Tissue with <i>Streptococcus agalactiae</i>-Induced Mastitis. Journal of Agricultural and Food Chemistry, 2018, 66, 11188-11196.	2.4	27
16	Sequence, Structural and Expression Divergence of Duplicate Genes in the Bovine Genome. PLoS ONE, 2014, 9, e102868.	1.1	13
17	WHOLE GENOME IDENTITY-BY-DESCENT DETERMINATION. Journal of Bioinformatics and Computational Biology, 2013, 11, 1350002.	0.3	10
18	Benchmarking Bayesian genome enabled-prediction models for age at first calving in Nellore cows. Livestock Science, 2018, 211, 75-79.	0.6	9

#	Article	IF	Citations
19	Whole genome fine mapping of quantitative trait loci for ultrasound and carcass merit traits in beef cattle. Canadian Journal of Animal Science, 2011, 91, 61-73.	0.7	7
20	Candidate Gene Expression in Bos indicus Ovarian Tissues: Prepubertal and Postpubertal Heifers in Diestrus. Frontiers in Veterinary Science, 2016, 3, 94.	0.9	7
21	Genome-wide identification of copy number variation and association with fat deposition in thin and fat-tailed sheep breeds. Scientific Reports, 2022, 12, .	1.6	7
22	In-depth characterization of the pituitary transcriptome in Simmental and Chinese native cattle. Domestic Animal Endocrinology, 2019, 66, 35-42.	0.8	6
23	Developing a genome-wide selection model for genetic improvement of residual feed intake and carcass merit in a beef cattle breeding program. Science Bulletin, 2012, 57, 2741-2746.	1.7	4
24	The identification of candidate genes and SNP markers for classical bovine spongiform encephalopathy susceptibility. Prion, 2012, 6, 461-469.	0.9	3
25	Complicated Relationships: A Review of Biological Interaction Networks and Pathways in Animal Science. Springer Science Reviews, 2013, 1, 73-83.	1.3	3
26	Accuracy of genomic selection predictions for hip height in Brahman cattle using different relationship matrices. Pesquisa Agropecuaria Brasileira, 2018, 53, 717-726.	0.9	3
27	History of the Hays Converter. Canadian Journal of Animal Science, 2016, 96, 471-477.	0.7	2
28	Evolution of tissue and developmental specificity of transcription start sites in Bos taurus indicus. Communications Biology, 2021, 4, 829.	2.0	2
29	Association analysis for feed efficiency traits in beef cattle using preserved haplotypes. Genome, 2013, 56, 586-591.	0.9	1
30	Shining a Light on Haemonchus contortus in Sheep. Proceedings (mdpi), 2019, 36, 138.	0.2	0