Lupei Zhang

List of Publications by Year
in descending order

67 papers	1,490 citations
361045 20 h-index	377514 34 g-index
68 all docs	68 docs citations
68 times ranked	1827 citing authors

#	Article	IF	Citations
1	AMPK/Î±-Ketoglutarate Axis Dynamically Mediates DNA Demethylation in the Prdm16 Promoter and Brown Adipogenesis. Cell Metabolism, 2016, 24, 542-554.	7.2	195
2	Investigation on BRCA1 SNPs and its effects on mastitis in Chinese commercial cattle. Gene, 2012, 505, 190-194.	1.0	71
3	Maternal high-fat diet during lactation impairs thermogenic function of brown adipose tissue in offspring mice. Scientific Reports, 2016, 6, 34345.	1.6	69
4	Searching for new loci and candidate genes for economically important traits through gene-based association analysis of Simmental cattle. Scientific Reports, 2017, 7, 42048.	1.6	52
5	Genome wide association study and genomic prediction for fatty acid composition in Chinese Simmental beef cattle using high density SNP array. BMC Genomics, 2017, 18, 464.	1.2	52
6	Genome-wide association study identifies loci and candidate genes for meat quality traits in Simmental beef cattle. Mammalian Genome, 2016, 27, 246-255.	1.0	50
7	bta-miR-23a involves in adipogenesis of progenitor cells derived from fetal bovine skeletal muscle. Scientific Reports, 2017, 7, 43716.	1.6	50
8	BRCA1: a new candidate gene for bovine mastitis and its association analysis between single nucleotide polymorphisms and milk somatic cell score. Molecular Biology Reports, 2012, 39, 6625-6631.	1.0	45
9	Genome-Wide Association Studies Using Haplotypes and Individual SNPs in Simmental Cattle. PLoS ONE, 2014, 9, e109330.	1.1	42
10	Genomic Patterns of Homozygosity in Chinese Local Cattle. Scientific Reports, 2019, 9, 16977.	1.6	40
11	A genome-wide scan for copy number variations using high-density single nucleotide polymorphism array in Simmental cattle. Animal Genetics, 2015, 46, 289-298.	0.6	39
12	Genome-wide scan reveals genetic divergence and diverse adaptive selection in ChineseÂlocal cattle. BMC Genomics, 2019, 20, 494.	1.2	34
13	Multi-strategy genome-wide association studies identify the DCAF16-NCAPG region as a susceptibility locus for average daily gain in cattle. Scientific Reports, 2016, 6, 38073.	1.6	33
14	Multiple association analysis of loci and candidate genes that regulate body size at three growth stages in Simmental beef cattle. BMC Genetics, 2020, 21, 32.	2.7	33
15	A Stacking Ensemble Learning Framework for Genomic Prediction. Frontiers in Genetics, 2021, 12, 600040.	1.1	31
16	Genome-wide detection of selective signatures in Simmental cattle. Journal of Applied Genetics, 2014, 55, 343-351.	1.0	30
17	Genome-Wide Association Study Reveals the PLAG1 Gene for Knuckle, Biceps and Shank Weight in Simmental Beef Cattle. PLoS ONE, 2016, 11, e0168316.	1.1	29
18	Pathway-Based Genome-Wide Association Studies for Two Meat Production Traits in Simmental Cattle. Scientific Reports, 2016, 5, 18389.	1.6	28

#	Article	IF	Citations
19	Genome-Wide Association Analysis of Growth Curve Parameters in Chinese Simmental Beef Cattle. Animals, 2021, 11, 192.	1.0	28
20	Genome-wide association study identifies loci and candidate genes for internal organ weights in Simmental beef cattle. Physiological Genomics, 2018, 50, 523-531.	1.0	27
21	PCA-Based Multiple-Trait GWAS Analysis: A Powerful Model for Exploring Pleiotropy. Animals, 2018, 8, 239.	1.0	23
22	Evaluation of GBLUP, BayesB and elastic net for genomic prediction in Chinese Simmental beef cattle. PLoS ONE, 2019, 14, e0210442.	1.1	23
23	Detection of candidate genes for growth and carcass traits using genome-wide association strategy in Chinese Simmental beef cattle. Animal Production Science, 2018, 58, 224.	0.6	22
24	Probe-based association analysis identifies several deletions associated with average daily gain in beef cattle. BMC Genomics, 2019, 20, 31.	1.2	22
25	Genome-Wide Assessment of Runs of Homozygosity in Chinese Wagyu Beef Cattle. Animals, 2020, 10, 1425.	1.0	22
26	Incorporating Genome Annotation Into Genomic Prediction for Carcass Traits in Chinese Simmental Beef Cattle. Frontiers in Genetics, 2020, 11, 481.	1.1	22
27	Evaluation of Linkage Disequilibrium, Effective Population Size and Haplotype Block Structure in Chinese Cattle. Animals, 2019, 9, 83.	1.0	21
28	Genome-wide association study identifies the *PLAG1-OXR1* region on BTA14 for carcass meat yield in cattle. Physiological Genomics, 2019, 51, 137-144.	1.0	19
29	Integration of selection signatures and multi-trait GWAS reveals polygenic genetic architecture of carcass traits in beef cattle. Genomics, 2021, 113, 3325-3336.	1.3	19
30	AMPKα1 deficiency suppresses brown adipogenesis in favor of fibrogenesis during brown adipose tissue development. Biochemical and Biophysical Research Communications, 2017, 491, 508-514.	1.0	18
31	Weighted Single-Step Genome-Wide Association Study for Growth Traits in Chinese Simmental Beef Cattle. Genes, 2020, 11, 189.	1.0	18
32	Genome wide association study identifies SNPs associated with fatty acid composition in Chinese Wagyu cattle. Journal of Animal Science and Biotechnology, 2019, 10, 27.	2.1	15
33	Genome-Wide Scan Identifies Selection Signatures in Chinese Wagyu Cattle Using a High-Density SNP Array. Animals, 2019, 9, 296.	1.0	14
34	The Impact of Variable Degrees of Freedom and Scale Parameters in Bayesian Methods for Genomic Prediction in Chinese Simmental Beef Cattle. PLoS ONE, 2016, 11, e0154118.	1.1	14
35	Genomic Prediction Using LD-Based Haplotypes Inferred From High-Density Chip and Imputed Sequence Variants in Chinese Simmental Beef Cattle. Frontiers in Genetics, 2021, 12, 665382.	1.1	13
36	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. BMC Biology, 2022, 20, 79.	1.7	12

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37	Identification of Candidate Genes Regulating Carcass Depth and Hind Leg Circumference in Simmental Beef Cattle Using Illumina Bovine Beadchip and Next-Generation Sequencing Analyses. Animals, 2022, 12, 1103.	1.0	12
38	Identification of muscle-specific candidate genes in Simmental beef cattle using imputed next generation sequencing. PLoS ONE, 2019, 14, e0223671.	1.1	11
39	Bta-miR-24-3p Controls the Myogenic Differentiation and Proliferation of Fetal, Bovine, Skeletal Muscle-Derived Progenitor Cells by Targeting ACVR1B. Animals, 2019, 9, 859.	1.0	11
40	Genomic Prediction and Association Analysis with Models Including Dominance Effects for Important Traits in Chinese Simmental Beef Cattle. Animals, 2019, 9, 1055.	1.0	11
41	Application of ensemble learning to genomic selection in chinese simmental beef cattle. Journal of Animal Breeding and Genetics, 2021, 138, 291-299.	0.8	11
42	Selection and effectiveness of informative SNPs for paternity in Chinese Simmental cattle based on a high-density SNP array. Gene, 2018, 673, 211-216.	1.0	10
43	Fast genomic prediction of breeding values using parallel Markov chain Monte Carlo with convergence diagnosis. BMC Bioinformatics, 2018, 19, 3.	1.2	10
44	Identification and validation of a novel candidate gene regulating net meat weight in Simmental beef cattle based on imputed next‐generation sequencing. Cell Proliferation, 2020, 53, e12870.	2.4	10
45	Genomic sequencing analysis reveals copy number variations and their associations with economically important traits in beef cattle. Genomics, 2021, 113, 812-820.	1.3	10
46	Constructing a comprehensive gene co-expression based interactome in <i>Bos taurus</i>. PeerJ, 2017, 5, e4107.	0.9	9
47	Runs of homozygosity analysis reveals consensus homozygous regions affecting production traits in Chinese Simmental beef cattle. BMC Genomics, 2021, 22, 678.	1.2	8
48	Transcriptional states and chromatin accessibility during bovine myoblasts proliferation and myogenic differentiation. Cell Proliferation, 2022, 55, e13219.	2.4	8
49	Effect of thyroglobulin gene polymorphisms on growth, carcass composition and meat quality traits in Chinese beef cattle. Molecular Biology Reports, 2015, 42, 1403-1407.	1.0	7
50	Estimation of linkage disequilibrium levels and haplotype block structure in Chinese Simmental and Wagyu beef cattle using high-density genotypes. Livestock Science, 2016, 190, 1-9.	0.6	7
51	Identifying novel genes for carcass traits by testing G×E interaction through genome-wide meta-analysis in Chinese Simmental beef cattle. Livestock Science, 2018, 212, 75-82.	0.6	7
52	KCRR: a nonlinear machine learning with a modified genomic similarity matrix improved the genomic prediction efficiency. Briefings in Bioinformatics, 2021, 22, .	3.2	7
53	Identification of Candidate Variants Associated With Bone Weight Using Whole Genome Sequence in Beef Cattle. Frontiers in Genetics, 2021, 12, 750746.	1.1	7
54	Genome-Wide Association Study Based on Random Regression Model Reveals Candidate Genes Associated with Longitudinal Data in Chinese Simmental Beef Cattle. Animals, 2021, 11, 2524.	1.0	6

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55	NCAPG Dynamically Coordinates the Myogenesis of Fetal Bovine Tissue by Adjusting Chromatin Accessibility. International Journal of Molecular Sciences, 2020, 21, 1248.	1.8	6
56	Comparative Transcriptomic Analysis Reveals Diverse Expression Pattern Underlying Fatty Acid Composition among Different Beef Cuts. Foods, 2022, 11, 117.	1.9	6
57	Genome-wide association studies using binned genotypes. Heredity, 2020, 124, 288-298.	1.2	5
58	A Novel Mechanism of bta-miR-210 in Bovine Early Intramuscular Adipogenesis. Genes, 2020, 11, 601.	1.0	5
59	Assessing the Genetic Background and Selection Signatures of Huaxi Cattle Using High-Density SNP Array. Animals, 2021, 11, 3469.	1.0	5
60	Theoretical Evaluation of Multi-Breed Genomic Prediction in Chinese Indigenous Cattle. Animals, 2019, 9, 789.	1.0	4
61	A rapid and efficient linear mixed model approach using the score test and its application to GWAS. Livestock Science, 2019, 220, 37-45.	0.6	4
62	Validation of the Prediction Accuracy for 13 Traits in Chinese Simmental Beef Cattle Using a Preselected Low-Density SNP Panel. Animals, 2021, 11, 1890.	1.0	4
63	Transcriptome Analysis of Bovine Rumen Tissue in Three Developmental Stages. Frontiers in Genetics, 2022, 13, 821406.	1.1	4
64	A Fast and Powerful Empirical Bayes Method for Genome-Wide Association Studies. Animals, 2019, 9, 305.	1.0	3
65	bta-miR-23a Regulates the Myogenic Differentiation of Fetal Bovine Skeletal Muscle-Derived Progenitor Cells by Targeting MDFIC Gene. Genes, 2020, 11, 1232.	1.0	3
66	Genomic prediction with parallel computing for slaughter traits in Chinese Simmental beef cattle using high-density genotypes. PLoS ONE, 2017, 12, e0179885.	1.1	3
67	Hereditary Basis of Coat Color and Excellent Feed Conversion Rate of Red Angus Cattle by Next-Generation Sequencing Data. Animals, 2022, 12, 1509.	1.0	1