

Lupei Zhang

List of Publications by Year in descending order

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67
papers

1,490
citations

361045

20
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377514

34
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68
all docs

68
docs citations

68
times ranked

1827
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Transcriptomic Analysis Reveals Diverse Expression Pattern Underlying Fatty Acid Composition among Different Beef Cuts. <i>Foods</i> , 2022, 11, 117.	1.9	6
2	Transcriptional atlas analysis from multiple tissues reveals the expression specificity patterns in beef cattle. <i>BMC Biology</i> , 2022, 20, 79.	1.7	12
3	Transcriptome Analysis of Bovine Rumen Tissue in Three Developmental Stages. <i>Frontiers in Genetics</i> , 2022, 13, 821406.	1.1	4
4	Transcriptional states and chromatin accessibility during bovine myoblasts proliferation and myogenic differentiation. <i>Cell Proliferation</i> , 2022, 55, e13219.	2.4	8
5	Identification of Candidate Genes Regulating Carcass Depth and Hind Leg Circumference in Simmental Beef Cattle Using Illumina Bovine Beadchip and Next-Generation Sequencing Analyses. <i>Animals</i> , 2022, 12, 1103.	1.0	12
6	Hereditary Basis of Coat Color and Excellent Feed Conversion Rate of Red Angus Cattle by Next-Generation Sequencing Data. <i>Animals</i> , 2022, 12, 1509.	1.0	1
7	Genomic sequencing analysis reveals copy number variations and their associations with economically important traits in beef cattle. <i>Genomics</i> , 2021, 113, 812-820.	1.3	10
8	Application of ensemble learning to genomic selection in chinese simmental beef cattle. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 291-299.	0.8	11
9	Genome-Wide Association Analysis of Growth Curve Parameters in Chinese Simmental Beef Cattle. <i>Animals</i> , 2021, 11, 192.	1.0	28
10	A Stacking Ensemble Learning Framework for Genomic Prediction. <i>Frontiers in Genetics</i> , 2021, 12, 600040.	1.1	31
11	KCRR: a nonlinear machine learning with a modified genomic similarity matrix improved the genomic prediction efficiency. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
12	Validation of the Prediction Accuracy for 13 Traits in Chinese Simmental Beef Cattle Using a Preselected Low-Density SNP Panel. <i>Animals</i> , 2021, 11, 1890.	1.0	4
13	Genomic Prediction Using LD-Based Haplotypes Inferred From High-Density Chip and Imputed Sequence Variants in Chinese Simmental Beef Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 665382.	1.1	13
14	Genome-Wide Association Study Based on Random Regression Model Reveals Candidate Genes Associated with Longitudinal Data in Chinese Simmental Beef Cattle. <i>Animals</i> , 2021, 11, 2524.	1.0	6
15	Integration of selection signatures and multi-trait GWAS reveals polygenic genetic architecture of carcass traits in beef cattle. <i>Genomics</i> , 2021, 113, 3325-3336.	1.3	19
16	Runs of homozygosity analysis reveals consensus homozygous regions affecting production traits in Chinese Simmental beef cattle. <i>BMC Genomics</i> , 2021, 22, 678.	1.2	8
17	Identification of Candidate Variants Associated With Bone Weight Using Whole Genome Sequence in Beef Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 750746.	1.1	7
18	Assessing the Genetic Background and Selection Signatures of Huaxi Cattle Using High-Density SNP Array. <i>Animals</i> , 2021, 11, 3469.	1.0	5

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19	Genome-wide association studies using binned genotypes. <i>Heredity</i> , 2020, 124, 288-298.	1.2	5
20	Identification and validation of a novel candidate gene regulating net meat weight in Simmental beef cattle based on imputed next-generation sequencing. <i>Cell Proliferation</i> , 2020, 53, e12870.	2.4	10
21	bta-miR-23a Regulates the Myogenic Differentiation of Fetal Bovine Skeletal Muscle-Derived Progenitor Cells by Targeting MDFIC Gene. <i>Genes</i> , 2020, 11, 1232.	1.0	3
22	Genome-Wide Assessment of Runs of Homozygosity in Chinese Wagyu Beef Cattle. <i>Animals</i> , 2020, 10, 1425.	1.0	22
23	A Novel Mechanism of bta-miR-210 in Bovine Early Intramuscular Adipogenesis. <i>Genes</i> , 2020, 11, 601.	1.0	5
24	Incorporating Genome Annotation Into Genomic Prediction for Carcass Traits in Chinese Simmental Beef Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 481.	1.1	22
25	Multiple association analysis of loci and candidate genes that regulate body size at three growth stages in Simmental beef cattle. <i>BMC Genetics</i> , 2020, 21, 32.	2.7	33
26	Weighted Single-Step Genome-Wide Association Study for Growth Traits in Chinese Simmental Beef Cattle. <i>Genes</i> , 2020, 11, 189.	1.0	18
27	NCAPG Dynamically Coordinates the Myogenesis of Fetal Bovine Tissue by Adjusting Chromatin Accessibility. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1248.	1.8	6
28	Genome-Wide Scan Identifies Selection Signatures in Chinese Wagyu Cattle Using a High-Density SNP Array. <i>Animals</i> , 2019, 9, 296.	1.0	14
29	A Fast and Powerful Empirical Bayes Method for Genome-Wide Association Studies. <i>Animals</i> , 2019, 9, 305.	1.0	3
30	Theoretical Evaluation of Multi-Breed Genomic Prediction in Chinese Indigenous Cattle. <i>Animals</i> , 2019, 9, 789.	1.0	4
31	Identification of muscle-specific candidate genes in Simmental beef cattle using imputed next generation sequencing. <i>PLoS ONE</i> , 2019, 14, e0223671.	1.1	11
32	Bta-miR-24-3p Controls the Myogenic Differentiation and Proliferation of Fetal, Bovine, Skeletal Muscle-Derived Progenitor Cells by Targeting ACVR1B. <i>Animals</i> , 2019, 9, 859.	1.0	11
33	Probe-based association analysis identifies several deletions associated with average daily gain in beef cattle. <i>BMC Genomics</i> , 2019, 20, 31.	1.2	22
34	Genome-wide scan reveals genetic divergence and diverse adaptive selection in Chinese local cattle. <i>BMC Genomics</i> , 2019, 20, 494.	1.2	34
35	Genome wide association study identifies SNPs associated with fatty acid composition in Chinese Wagyu cattle. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 27.	2.1	15
36	Evaluation of Linkage Disequilibrium, Effective Population Size and Haplotype Block Structure in Chinese Cattle. <i>Animals</i> , 2019, 9, 83.	1.0	21

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37	Evaluation of GBLUP, BayesB and elastic net for genomic prediction in Chinese Simmental beef cattle. PLoS ONE, 2019, 14, e0210442.	1.1	23
38	Genome-wide association study identifies the <i>PLAG1-OXR1</i> region on BTA14 for carcass meat yield in cattle. Physiological Genomics, 2019, 51, 137-144.	1.0	19
39	Genomic Patterns of Homozygosity in Chinese Local Cattle. Scientific Reports, 2019, 9, 16977.	1.6	40
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	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
42	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
43	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
44	PCA-Based Multiple-Trait GWAS Analysis: A Powerful Model for Exploring Pleiotropy. Animals, 2018, 8, 239.	1.0	23
45	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
46	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
47	Fast genomic prediction of breeding values using parallel Markov chain Monte Carlo with convergence diagnosis. BMC Bioinformatics, 2018, 19, 3.	1.2	10
48	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
49	bta-miR-23a involves in adipogenesis of progenitor cells derived from fetal bovine skeletal muscle. Scientific Reports, 2017, 7, 43716.	1.6	50
50	AMPK α 1 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
51	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
52	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
53	Constructing a comprehensive gene co-expression based interactome in <i>Bos taurus</i> . PeerJ, 2017, 5, e4107.	0.9	9
54	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

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55	Multi-strategy genome-wide association studies identify the DCAF16-NCAPG region as a susceptibility locus for average daily gain in cattle. <i>Scientific Reports</i> , 2016, 6, 38073.	1.6	33
56	Pathway-Based Genome-Wide Association Studies for Two Meat Production Traits in Simmental Cattle. <i>Scientific Reports</i> , 2016, 5, 18389.	1.6	28
57	Genome-wide association study identifies loci and candidate genes for meat quality traits in Simmental beef cattle. <i>Mammalian Genome</i> , 2016, 27, 246-255.	1.0	50
58	AMPK/ β -Ketoglutarate Axis Dynamically Mediates DNA Demethylation in the Prdm16 Promoter and Brown Adipogenesis. <i>Cell Metabolism</i> , 2016, 24, 542-554.	7.2	195
59	Maternal high-fat diet during lactation impairs thermogenic function of brown adipose tissue in offspring mice. <i>Scientific Reports</i> , 2016, 6, 34345.	1.6	69
60	Estimation of linkage disequilibrium levels and haplotype block structure in Chinese Simmental and Wagyu beef cattle using high-density genotypes. <i>Livestock Science</i> , 2016, 190, 1-9.	0.6	7
61	The Impact of Variable Degrees of Freedom and Scale Parameters in Bayesian Methods for Genomic Prediction in Chinese Simmental Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0154118.	1.1	14
62	A genome-wide scan for copy number variations using high-density single nucleotide polymorphism array in Simmental cattle. <i>Animal Genetics</i> , 2015, 46, 289-298.	0.6	39
63	Effect of thyroglobulin gene polymorphisms on growth, carcass composition and meat quality traits in Chinese beef cattle. <i>Molecular Biology Reports</i> , 2015, 42, 1403-1407.	1.0	7
64	Genome-wide detection of selective signatures in Simmental cattle. <i>Journal of Applied Genetics</i> , 2014, 55, 343-351.	1.0	30
65	Genome-Wide Association Studies Using Haplotypes and Individual SNPs in Simmental Cattle. <i>PLoS ONE</i> , 2014, 9, e109330.	1.1	42
66	Investigation on BRCA1 SNPs and its effects on mastitis in Chinese commercial cattle. <i>Gene</i> , 2012, 505, 190-194.	1.0	71
67	BRCA1: a new candidate gene for bovine mastitis and its association analysis between single nucleotide polymorphisms and milk somatic cell score. <i>Molecular Biology Reports</i> , 2012, 39, 6625-6631.	1.0	45