

Guosheng Su

List of Publications by Year in descending order

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76
papers

2,553
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186254

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docs citations

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2263
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#	ARTICLE	IF	CITATIONS
1	Estimating Additive and Non-Additive Genetic Variances and Predicting Genetic Merits Using Genome-Wide Dense Single Nucleotide Polymorphism Markers. <i>PLoS ONE</i> , 2012, 7, e45293.	2.5	261
2	A common reference population from four European Holstein populations increases reliability of genomic predictions. <i>Genetics Selection Evolution</i> , 2011, 43, 43.	3.0	179
3	Comparison of single-trait and multiple-trait genomic prediction models. <i>BMC Genetics</i> , 2014, 15, 30.	2.7	152
4	Comparison on genomic predictions using three GBLUP methods and two single-step blending methods in the Nordic Holstein population. <i>Genetics Selection Evolution</i> , 2012, 44, 8.	3.0	114
5	Strategies for imputation to whole genome sequence using a single or multi-breed reference population in cattle. <i>BMC Genomics</i> , 2014, 15, 728.	2.8	96
6	Genome-wide association study in Chinese Holstein cows reveal two candidate genes for somatic cell score as an indicator for mastitis susceptibility. <i>BMC Genetics</i> , 2015, 16, 111.	2.7	94
7	Deregressed EBV as the response variable yield more reliable genomic predictions than traditional EBV in pure-bred pigs. <i>Genetics Selection Evolution</i> , 2011, 43, 38.	3.0	90
8	Genomic prediction of genetic merit using LD-based haplotypes in the Nordic Holstein population. <i>BMC Genomics</i> , 2014, 15, 1171.	2.8	90
9	Genomic evaluation of cattle in a multi-breed context. <i>Livestock Science</i> , 2014, 166, 101-110.	1.6	84
10	Integrating Sequence-based GWAS and RNA-Seq Provides Novel Insights into the Genetic Basis of Mastitis and Milk Production in Dairy Cattle. <i>Scientific Reports</i> , 2017, 7, 45560.	3.3	81
11	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. <i>Nature Communications</i> , 2021, 12, 5848.	12.8	70
12	Genomic evaluation of both purebred and crossbred performances. <i>Genetics Selection Evolution</i> , 2014, 46, 23.	3.0	67
13	Association analysis for udder health based on SNP-panel and sequence data in Danish Holsteins. <i>Genetics Selection Evolution</i> , 2015, 47, 50.	3.0	59
14	Identification of selective sweeps reveals divergent selection between Chinese Holstein and Simmental cattle populations. <i>Genetics Selection Evolution</i> , 2016, 48, 76.	3.0	59
15	Partitioning additive genetic variance into genomic and remaining polygenic components for complex traits in dairy cattle. <i>BMC Genetics</i> , 2012, 13, 44.	2.7	56
16	Exploring the genetic architecture and improving genomic prediction accuracy for mastitis and milk production traits in dairy cattle by mapping variants to hepatic transcriptomic regions responsive to intra-mammary infection. <i>Genetics Selection Evolution</i> , 2017, 49, 44.	3.0	53
17	Genome-wide Association Studies for Female Fertility Traits in Chinese and Nordic Holsteins. <i>Scientific Reports</i> , 2017, 7, 8487.	3.3	45
18	Consistency of linkage disequilibrium between Chinese and Nordic Holsteins and genomic prediction for Chinese Holsteins using a joint reference population. <i>Genetics Selection Evolution</i> , 2013, 45, 7.	3.0	44

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19	Selection of haplotype variables from a high-density marker map for genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 61.	3.0	44
20	Use of biological priors enhances understanding of genetic architecture and genomic prediction of complex traits within and between dairy cattle breeds. <i>BMC Genomics</i> , 2017, 18, 604.	2.8	43
21	Genome position specific priors for genomic prediction. <i>BMC Genomics</i> , 2012, 13, 543.	2.8	38
22	Joint genome-wide association study for milk fatty acid traits in Chinese and Danish Holstein populations. <i>Journal of Dairy Science</i> , 2015, 98, 8152-8163.	3.4	34
23	Improvement of genomic prediction by integrating additional single nucleotide polymorphisms selected from imputed whole genome sequencing data. <i>Heredity</i> , 2020, 124, 37-49.	2.6	33
24	Genetic evaluation for three-way crossbreeding. <i>Genetics Selection Evolution</i> , 2015, 47, 98.	3.0	32
25	Genome-wide association analyses using a Bayesian approach for litter size and piglet mortality in Danish Landrace and Yorkshire pigs. <i>BMC Genomics</i> , 2016, 17, 468.	2.8	32
26	An efficient unified model for genome-wide association studies and genomic selection. <i>Genetics Selection Evolution</i> , 2017, 49, 64.	3.0	30
27	Genomic Prediction Using Multi-trait Weighted GBLUP Accounting for Heterogeneous Variances and Covariances Across the Genome. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3549-3558.	1.8	30
28	Genotype-by-environment interaction of fertility traits in Danish Holstein cattle using a single-step genomic reaction norm model. <i>Heredity</i> , 2019, 123, 202-214.	2.6	30
29	MicroRNA-guided prioritization of genome-wide association signals reveals the importance of microRNA-target gene networks for complex traits in cattle. <i>Scientific Reports</i> , 2018, 8, 9345.	3.3	27
30	Variance components and correlations of female fertility traits in Chinese Holstein population. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 56.	5.3	24
31	Genetic parameters for rectal temperature, respiration rate, and drooling score in Holstein cattle and their relationships with various fertility, production, body conformation, and health traits. <i>Journal of Dairy Science</i> , 2021, 104, 4390-4403.	3.4	24
32	Genomic prediction using a reference population of multiple pure breeds and admixed individuals. <i>Genetics Selection Evolution</i> , 2021, 53, 46.	3.0	24
33	Pedigree relationships to control inbreeding in optimum-contribution selection realise more genetic gain than genomic relationships. <i>Genetics Selection Evolution</i> , 2019, 51, 39.	3.0	23
34	Genomic prediction using models with dominance and imprinting effects for backfat thickness and average daily gain in Danish Duroc pigs. <i>Genetics Selection Evolution</i> , 2016, 48, 67.	3.0	21
35	Genetic parameters of semen quality traits and genetic correlations with service sire nonreturn rate in Nordic Holstein bulls. <i>Journal of Dairy Science</i> , 2021, 104, 10010-10019.	3.4	21
36	Multi-trait single-step genomic prediction accounting for heterogeneous (co)variances over the genome. <i>Heredity</i> , 2020, 124, 274-287.	2.6	20

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37	MiR-696 Regulates C2C12 Cell Proliferation and Differentiation by Targeting CNTFR β . <i>International Journal of Biological Sciences</i> , 2017, 13, 413-425.	6.4	19
38	A bivariate genomic model with additive, dominance and inbreeding depression effects for sire line and three-way crossbred pigs. <i>Genetics Selection Evolution</i> , 2019, 51, 45.	3.0	18
39	Genomic Selection for the Improvement of Antibody Response to Newcastle Disease and Avian Influenza Virus in Chickens. <i>PLoS ONE</i> , 2014, 9, e112685.	2.5	16
40	Impact of the Order of Legendre Polynomials in Random Regression Model on Genetic Evaluation for Milk Yield in Dairy Cattle Population. <i>Frontiers in Genetics</i> , 2020, 11, 586155.	2.3	16
41	Short communication: Improving accuracy of predicting breeding values in Brazilian Holstein population by adding data from Nordic and French Holstein populations. <i>Journal of Dairy Science</i> , 2016, 99, 4574-4579.	3.4	15
42	Genomic relationships based on X chromosome markers and accuracy of genomic predictions with and without X chromosome markers. <i>Genetics Selection Evolution</i> , 2014, 46, 47.	3.0	14
43	Assessment of the genomic prediction accuracy for feed efficiency traits in meat-type chickens. <i>PLoS ONE</i> , 2017, 12, e0173620.	2.5	13
44	Use of a Bayesian model including QTL markers increases prediction reliability when test animals are distant from the reference population. <i>Journal of Dairy Science</i> , 2019, 102, 7237-7247.	3.4	13
45	Improving genetic evaluation using a multitrait single-step genomic model for ability to resume cycling after calving, measured by activity tags in Holstein cows. <i>Journal of Dairy Science</i> , 2017, 100, 8188-8196.	3.4	12
46	Impact of rare and low-frequency sequence variants on reliability of genomic prediction in dairy cattle. <i>Genetics Selection Evolution</i> , 2018, 50, 62.	3.0	12
47	Genetic Parameters and Genome-Wide Association Studies of Eight Longevity Traits Representing Either Full or Partial Lifespan in Chinese Holsteins. <i>Frontiers in Genetics</i> , 2021, 12, 634986.	2.3	12
48	Estimation of variance components and prediction of breeding values based on group records from varying group sizes. <i>Genetics Selection Evolution</i> , 2018, 50, 42.	3.0	11
49	Weighted single-step genomic best linear unbiased prediction integrating variants selected from sequencing data by association and bioinformatics analyses. <i>Genetics Selection Evolution</i> , 2020, 52, 48.	3.0	11
50	Comparisons of improved genomic predictions generated by different imputation methods for genotyping by sequencing data in livestock populations. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 3.	5.3	11
51	Phenotypically Selective Genotyping Realizes More Genetic Gains in a Rainbow Trout Breeding Program in the Presence of Genotype-by-Environment Interactions. <i>Frontiers in Genetics</i> , 2020, 11, 866.	2.3	10
52	Breed of origin of alleles and genomic predictions for crossbred dairy cows. <i>Genetics Selection Evolution</i> , 2021, 53, 84.	3.0	10
53	Genome-wide association studies for the concentrations of insulin, triiodothyronine, and thyroxine in Chinese Holstein cattle. <i>Tropical Animal Health and Production</i> , 2020, 52, 1655-1660.	1.4	9
54	Genetic Parameter Estimation and Genome-Wide Association Study-Based Loci Identification of Milk-Related Traits in Chinese Holstein. <i>Frontiers in Genetics</i> , 2021, 12, 799664.	2.3	9

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55	The patterns of genomic variances and covariances across genome for milk production traits between Chinese and Nordic Holstein populations. <i>BMC Genetics</i> , 2017, 18, 26.	2.7	8
56	Improving genomic predictions by correction of genotypes from genotyping by sequencing in livestock populations. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 8.	5.3	8
57	Bayesian methods for jointly estimating genomic breeding values of one continuous and one threshold trait. <i>PLoS ONE</i> , 2017, 12, e0175448.	2.5	8
58	Overview of Metabolomic Analysis and the Integration with Multi-Omics for Economic Traits in Cattle. <i>Metabolites</i> , 2021, 11, 753.	2.9	7
59	Genomic prediction in Nordic Red dairy cattle considering breed origin of alleles. <i>Journal of Dairy Science</i> , 2022, 105, 2426-2438.	3.4	7
60	Prediction of breeding values for group-recorded traits including genomic information and an individually recorded correlated trait. <i>Heredity</i> , 2021, 126, 206-217.	2.6	6
61	Genomic Prediction Using Bayesian Regression Models With Global and Local Prior. <i>Frontiers in Genetics</i> , 2021, 12, 628205.	2.3	6
62	Population admixture in Chinese and European <i>Sus scrofa</i> . <i>Scientific Reports</i> , 2017, 7, 13178.	3.3	5
63	Introgression of Chinese haplotypes contributed to the improvement of Danish Duroc pigs. <i>Evolutionary Applications</i> , 2019, 12, 292-300.	3.1	5
64	Reliabilities of Genomic Prediction for Young Stock Survival Traits Using 54K SNP Chip Augmented With Additional Single-Nucleotide Polymorphisms Selected From Imputed Whole-Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2021, 12, 667300.	2.3	5
65	Long-term impact of conventional and optimal contribution conservation methods on genetic diversity and genetic gain in local pig breeds. <i>Heredity</i> , 2021, 127, 546-553.	2.6	4
66	Genomic predictions for crossbred dairy cows by combining solutions from purebred evaluation based on breed origin of alleles. <i>Journal of Dairy Science</i> , 2022, 105, 5178-5191.	3.4	4
67	Use of Repeated Group Measurements with Drop Out Animals for Variance Component Estimation and Genetic Evaluation: A Simulation Study. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2935-2940.	1.8	3
68	Novel approach to incorporate information about recessive lethal genes increases the accuracy of genomic prediction for mortality traits. <i>Heredity</i> , 2020, 125, 155-166.	2.6	3
69	High-Throughput Sequencing With the Preselection of Markers Is a Good Alternative to SNP Chips for Genomic Prediction in Broilers. <i>Frontiers in Genetics</i> , 2020, 11, 108.	2.3	3
70	Impact of phenotypic information and composition of reference population on genomic prediction in fish under the presence of genotype by environment interaction. <i>Aquaculture</i> , 2020, 526, 735358.	3.5	3
71	Genetic parameters and genomic prediction for feed intake recorded at the group and individual level in different production systems for growing pigs. <i>Genetics Selection Evolution</i> , 2021, 53, 33.	3.0	3
72	Including dominance effects in the prediction model through locus-specific weights on heterozygous genotypes can greatly improve genomic predictive abilities. <i>Heredity</i> , 2022, , .	2.6	3

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73	Imputation for sequencing variants preselected to a customized low-density chip. Scientific Reports, 2020, 10, 9524.	3.3	2
74	Comparison of models for genetic evaluation of number of inseminations to conception in Danish Holstein cows. Animal Science Journal, 2017, 88, 567-574.	1.4	1
75	Genomic selection in American mink (Neovison vison) using a single-step genomic best linear unbiased prediction model for size and quality traits graded on live mink. Journal of Animal Science, 2021, 99, .	0.5	1
76	Short communication: investigation of the feasibility of genomic selection in Icelandic Cattle. Journal of Animal Science, 2021, 99, .	0.5	1