

Chao Ning

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

449
citations

687220

13
h-index

794469

19
g-index

35
all docs

35
docs citations

35
times ranked

612
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide DNA methylation and transcriptome analyses reveal genes involved in immune responses of pig peripheral blood mononuclear cells to poly I:C. <i>Scientific Reports</i> , 2017, 7, 9709.	1.6	44
2	Genome-Wide Association Study of Piglet Uniformity and Farrowing Interval. <i>Frontiers in Genetics</i> , 2017, 8, 194.	1.1	37
3	Performance Gains in Genome-Wide Association Studies for Longitudinal Traits via Modeling Time-varied effects. <i>Scientific Reports</i> , 2017, 7, 590.	1.6	33
4	Eigen decomposition expedites longitudinal genome-wide association studies for milk production traits in Chinese Holstein. <i>Genetics Selection Evolution</i> , 2018, 50, 12.	1.2	28
5	A Novel lncRNA Regulates the Toll-Like Receptor Signaling Pathway and Related Immune Function by Stabilizing FOS mRNA as a Competitive Endogenous RNA. <i>Frontiers in Immunology</i> , 2019, 10, 838.	2.2	27
6	CNV analysis of Meishan pig by next-generation sequencing and effects of AHR gene CNV on pig reproductive traits. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 42.	2.1	27
7	Profiling long noncoding RNA of multi-tissue transcriptome enhances porcine noncoding genome annotation. <i>Epigenomics</i> , 2018, 10, 301-320.	1.0	22
8	Genome-wide association study for intramuscular fat content in Chinese Lulai black pigs. <i>Asian-Australasian Journal of Animal Sciences</i> , 2019, 32, 607-613.	2.4	22
9	Short communication: Replication of genome-wide association studies for milk production traits in Chinese Holstein by an efficient rotated linear mixed model. <i>Journal of Dairy Science</i> , 2019, 102, 2378-2383.	1.4	21
10	Characterization of genome-wide segmental duplications reveals a common genomic feature of association with immunity among domestic animals. <i>BMC Genomics</i> , 2017, 18, 293.	1.2	20
11	Efficient multivariate analysis algorithms for longitudinal genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 4879-4885.	1.8	19
12	A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values. <i>Bioinformatics</i> , 2018, 34, 1817-1825.	1.8	18
13	Quantitative proteome analysis of bovine mammary gland reveals protein dynamic changes involved in peak and late lactation stages. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 292-297.	1.0	16
14	Functional validation of GPIHBP1 and identification of a functional mutation in GPIHBP1 for milk fat traits in dairy cattle. <i>Scientific Reports</i> , 2017, 7, 8546.	1.6	14
15	Rapid epistatic mixed-model association studies by controlling multiple polygenic effects. <i>Bioinformatics</i> , 2020, 36, 4833-4837.	1.8	14
16	Transcriptome of Porcine PBMCs over Two Generations Reveals Key Genes and Pathways Associated with Variable Antibody Responses post PRRSV Vaccination. <i>Scientific Reports</i> , 2018, 8, 2460.	1.6	12
17	Polymorphism of mitochondrial tRNA genes associated with the number of pigs born alive. <i>Journal of Animal Science and Biotechnology</i> , 2018, 9, 86.	2.1	11
18	Assessment of the performance of different imputation methods for low-coverage sequencing in Holstein cattle. <i>Journal of Dairy Science</i> , 2022, 105, 3355-3366.	1.4	9

#	ARTICLE	IF	CITATIONS
19	Integrative analysis of genome-wide DNA methylation and gene expression profiles reveals important epigenetic genes related to milk production traits in dairy cattle. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 562-573.	0.8	8
20	Towards a Cost-Effective Implementation of Genomic Prediction Based on Low Coverage Whole Genome Sequencing in Dezhou Donkey. <i>Frontiers in Genetics</i> , 2021, 12, 728764.	1.1	7
21	Estimate of inbreeding depression on growth and reproductive traits in a Large White pig population. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
22	Integrated Metabolomics and Transcriptomics Analyses Reveal Metabolic Mechanisms in Porcine Intestinal Epithelial Cells under Zearalenone Stress. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 6561-6572.	2.4	6
23	Mitochondrial DNA enrichment reduced NUMT contamination in porcine NGS analyses. <i>Briefings in Bioinformatics</i> , 2020, 21, 1368-1377.	3.2	5
24	Cybrid Model Supports Mitochondrial Genetic Effect on Pig Litter Size. <i>Frontiers in Genetics</i> , 2020, 11, 579382.	1.1	5
25	A novel mutation in the promoter region of RPL8 regulates milk fat traits in dairy cattle by binding transcription factor Pax6. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 158528.	1.2	4
26	PIBLUP: High-Performance Software for Large-Scale Genetic Evaluation of Animals and Plants. <i>Frontiers in Genetics</i> , 2018, 9, 226.	1.1	3
27	RNA Expression Profile and Alternative Splicing Signatures of Genistein-Treated Breeder Hens Revealed by Hepatic Transcriptomic Analysis. <i>Oxidative Medicine and Cellular Longevity</i> , 2019, 2019, 1-19.	1.9	3
28	Mining Unknown Porcine Protein Isoforms by Tissue-based Map of Proteome Enhances Pig Genome Annotation. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 772-786.	3.0	2
29	Effects of Growth-Related Genes on Body Measurement Traits in Wenshang Barred Chickens. <i>Journal of Poultry Science</i> , 2022, 59, 323-327.	0.7	2
30	Breed-specific reference sequence optimized mapping accuracy of NGS analyses for pigs. <i>BMC Genomics</i> , 2021, 22, 736.	1.2	0
31	Transcriptional Regulation of the Chicken <i>ASMT</i> Gene- A Preliminary Analysis. <i>British Poultry Science</i> , 0, , .	0.8	0