

Zhi-Wu Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

22,699
citations

53660

45
h-index

30010

103
g-index

125
all docs

125
docs citations

125
times ranked

14906
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Assembly of Alfalfa Cultivar Zhongmu-4 and Identification of SNPs Associated with Agronomic Traits. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 14-28.	3.0	26
2	Prospectus of Genomic Selection and Phenomics in Cereal, Legume and Oilseed Breeding Programs. <i>Frontiers in Genetics</i> , 2022, 12, .	1.1	26
3	Detection of Breeding-Relevant Fruit Cracking and Fruit Firmness Quantitative Trait Loci in Sweet Cherry via Pedigree-Based and Genome-Wide Association Approaches. <i>Frontiers in Plant Science</i> , 2022, 13, 823250.	1.7	5
4	As the number falls, alternatives to the Hagbergâ€Perten falling number method: A review. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2022, 21, 2105-2117.	5.9	6
5	VTag: a semi-supervised pipeline for tracking pig activity with a single top-view camera. <i>Journal of Animal Science</i> , 2022, 100, .	0.2	6
6	Performing Genome-Wide Association Studies with Multiple Models Using GAPIT. <i>Methods in Molecular Biology</i> , 2022, , 199-217.	0.4	1
7	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, , 63-80.	0.4	2
8	Graph pangenome captures missing heritability and empowers tomato breeding. <i>Nature</i> , 2022, 606, 527-534.	13.7	131
9	MMAP: a cloud computing platform for mining the maximum accuracy of predicting phenotypes from genotypes. <i>Bioinformatics</i> , 2021, 37, 1324-1326.	1.8	3
10	Genomic mosaicism due to homoeologous exchange generates extensive phenotypic diversity in nascent allopolyploids. <i>National Science Review</i> , 2021, 8, nwa277.	4.6	42
11	Validation of UAV-based alfalfa biomass predictability using photogrammetry with fully automatic plot segmentation. <i>Scientific Reports</i> , 2021, 11, 3336.	1.6	18
12	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 619-628.	3.0	396
13	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	1.2	4
14	Chromosomal characteristics of salt stress heritable gene expression in the rice genome. <i>BMC Genomic Data</i> , 2021, 22, 17.	0.7	2
15	GridFree: a python package of imageanalysis for interactive grain counting and measuring. <i>Plant Physiology</i> , 2021, 186, 2239-2252.	2.3	7
16	GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 629-640.	3.0	345
17	Status and prospects of genomeâ€wide association studies in plants. <i>Plant Genome</i> , 2021, 14, e20077.	1.6	200
18	Human Breast Extracellular Matrix Microstructures and Protein Hydrogel 3D Cultures of Mammary Epithelial Cells. <i>Cancers</i> , 2021, 13, 5857.	1.7	4

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19	Comparison of Single-Trait and Multi-Trait Genome-Wide Association Models and Inclusion of Correlated Traits in the Dissection of the Genetic Architecture of a Complex Trait in a Breeding Program. <i>Frontiers in Plant Science</i> , 2021, 12, 772907.	1.7	10
20	Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS. <i>Plant Biotechnology Journal</i> , 2020, 18, 389-401.	4.1	30
21	GWAS-Based Identification of New Loci for Milk Yield, Fat, and Protein in Holstein Cattle. <i>Animals</i> , 2020, 10, 2048.	1.0	26
22	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3741-3749.	0.8	16
23	Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize. <i>Scientific Reports</i> , 2020, 10, 8165.	1.6	12
24	GRID: A Python Package for Field Plot Phenotyping Using Aerial Images. <i>Remote Sensing</i> , 2020, 12, 1697.	1.8	10
25	Identification of Stripe Rust Resistance Loci in U.S. Spring Wheat Cultivars and Breeding Lines Using Genome-Wide Association Mapping and <i>Yr</i> Gene Markers. <i>Plant Disease</i> , 2020, 104, 2181-2192.	0.7	34
26	Prospects for achieving durable disease resistance with elite fruit quality in apple breeding. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	22
27	Deep Learning for Predicting Complex Traits in Spring Wheat Breeding Program. <i>Frontiers in Plant Science</i> , 2020, 11, 613325.	1.7	64
28	Genomic Analyses Reveal Evidence of Independent Evolution, Demographic History, and Extreme Environment Adaptation of Tibetan Plateau <i>Agaricus bisporus</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1786.	1.5	14
29	Genome-wide association study of milk and reproductive traits in dual-purpose Xinjiang Brown cattle. <i>BMC Genomics</i> , 2019, 20, 827.	1.2	28
30	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of <i>Auricularia</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2255.	1.5	12
31	BLINK: a package for the next level of genome-wide association studies with both individuals and markers in the millions. <i>GigaScience</i> , 2019, 8, .	3.3	314
32	Aneuploidization under segmental allotetraploidy in rice and its phenotypic manifestation. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1273-1285.	1.8	21
33	iPat: intelligent prediction and association tool for genomic research. <i>Bioinformatics</i> , 2018, 34, 1925-1927.	1.8	31
34	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. <i>Scientific Reports</i> , 2018, 8, 6848.	1.6	16
35	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , 2018, 121, 648-662.	1.2	53
36	Evaluation of the Potential for Genomic Selection to Improve Spring Wheat Resistance to Fusarium Head Blight in the Pacific Northwest. <i>Frontiers in Plant Science</i> , 2018, 9, 911.	1.7	50

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37	Genome-Wide Association Mapping for Tolerance to Preharvest Sprouting and Low Falling Numbers in Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 141.	1.7	62
38	Genetic Dissection of End-Use Quality Traits in Adapted Soft White Winter Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 271.	1.7	43
39	Genetic Diversity of Clinal Freezing Tolerance Variation in Winter Wheat Landraces. <i>Agronomy</i> , 2018, 8, 95.	1.3	5
40	Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw064.	3.2	15
41	Genome-wide association study Identified multiple Genetic Loci on Chilling Resistance During Germination in Maize. <i>Scientific Reports</i> , 2017, 7, 10840.	1.6	49
42	Comparative Transcriptome Analysis Identified Candidate Genes Related to Bailinggu Mushroom Formation and Genetic Markers for Genetic Analyses and Breeding. <i>Scientific Reports</i> , 2017, 7, 9266.	1.6	50
43	TCF21 is related to testis growth and development in broiler chickens. <i>Genetics Selection Evolution</i> , 2017, 49, 25.	1.2	14
44	Unlocking Diversity in Germplasm Collections via Genomic Selection: A Case Study Based on Quantitative Adult Plant Resistance to Stripe Rust in Spring Wheat. <i>Plant Genome</i> , 2017, 10, plantgenome2016.12.0124.	1.6	42
45	Genome-Wide Association Study Reveals Novel Genes Associated with Culm Cellulose Content in Bread Wheat (<i>Triticum aestivum</i> , L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1913.	1.7	19
46	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	3.8	363
47	Genome-wide association studies identified multiple genetic loci for body size at four growth stages in Chinese Holstein cattle. <i>PLoS ONE</i> , 2017, 12, e0175971.	1.1	23
48	Identification of Resistance to Wet Bubble Disease and Genetic Diversity in Wild and Cultivated Strains of <i>Agaricus bisporus</i> . <i>International Journal of Molecular Sciences</i> , 2016, 17, 1568.	1.8	32
49	De Novo Sequencing and Transcriptome Analysis of <i>Pleurotus eryngii</i> subsp. <i>tuoliensis</i> (Bailinggu) Mycelia in Response to Cold Stimulation. <i>Molecules</i> , 2016, 21, 560.	1.7	48
50	Transcriptome Sequencing Identified Genes and Gene Ontologies Associated with Early Freezing Tolerance in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 1477.	1.7	43
51	Identification of genetic variants associated with maize flowering time using an extremely large multi-genetic background population. <i>Plant Journal</i> , 2016, 86, 391-402.	2.8	122
52	Domestication footprints anchor genomic regions of agronomic importance in soybeans. <i>New Phytologist</i> , 2016, 209, 871-884.	3.5	152
53	Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1775-1784.	1.8	9
54	Long Term Functional Outcome of Tibial Tuberosity Advancement vs. Tibial Plateau Leveling Osteotomy and Extracapsular Repair in a Heterogeneous Population of Dogs. <i>Veterinary Surgery</i> , 2016, 45, 261-268.	0.5	82

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55	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. <i>BMC Genomics</i> , 2016, 17, 894.	1.2	63
56	GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0120.	1.6	421
57	Characterization of Biosynthetic Pathways for the Production of the Volatile Homoterpenes DMNT and TMTT in <i>Zea mays</i> . <i>Plant Cell</i> , 2016, 28, 2651-2665.	3.1	105
58	Joint linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. <i>Plant Biotechnology Journal</i> , 2016, 14, 1551-1562.	4.1	121
59	Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2016, 12, e1005767.	1.5	1,095
60	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , 2015, 13, 78.	1.7	40
61	Whole transcriptome analysis with sequencing: methods, challenges and potential solutions. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 3425-3439.	2.4	141
62	Genetic characteristics of soybean resistance to HG type 0 and HG type 1.2.3.5.7 of the cyst nematode analyzed by genome-wide association mapping. <i>BMC Genomics</i> , 2015, 16, 598.	1.2	104
63	Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. <i>PLoS ONE</i> , 2015, 10, e0121624.	1.1	69
64	A SUPER Powerful Method for Genome Wide Association Study. <i>PLoS ONE</i> , 2014, 9, e107684.	1.1	289
65	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014, 12, 73.	1.7	160
66	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	1.2	329
67	Genomic analysis establishes correlation between growth and laryngeal neuropathy in Thoroughbreds. <i>BMC Genomics</i> , 2014, 15, 259.	1.2	40
68	Association Mapping Provides Insights into the Origin and the Fine Structure of the Sorghum Aluminum Tolerance Locus, AltSB. <i>PLoS ONE</i> , 2014, 9, e87438.	1.1	36
69	A New Genotype Imputation Method with Tolerance to High Missing Rate and Rare Variants. <i>PLoS ONE</i> , 2014, 9, e101025.	1.1	25
70	Genome-wide association study of the backfat thickness trait in two pig populations. <i>Frontiers of Agricultural Science and Engineering</i> , 2014, 1, 91.	0.9	6
71	Performance prediction of F1 hybrids between recombinant inbred lines derived from two elite maize inbred lines. <i>Theoretical and Applied Genetics</i> , 2013, 126, 189-201.	1.8	32
72	Long-Term Functional Outcome of Tibial Plateau Leveling Osteotomy Versus Extracapsular Repair in a Heterogeneous Population of Dogs. <i>Veterinary Surgery</i> , 2013, 42, 38-50.	0.5	80

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73	Principal component analysis of canine hip dysplasia phenotypes and their statistical power for genome-wide association mapping. <i>Journal of Applied Statistics</i> , 2013, 40, 235-251.	0.6	4
74	Genotyping by Genome Reducing and Sequencing for Outbred Animals. <i>PLoS ONE</i> , 2013, 8, e67500.	1.1	86
75	Monitoring Hip and Elbow Dysplasia Achieved Modest Genetic Improvement of 74 Dog Breeds over 40 Years in USA. <i>PLoS ONE</i> , 2013, 8, e76390.	1.1	32
76	Identification of quantitative trait loci for canine hip dysplasia by two sequential multipoint linkage analyses. <i>Journal of Applied Statistics</i> , 2012, 39, 1719-1731.	0.6	5
77	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399.	1.8	2,016
78	Evaluation of Tibial Torsion in Yorkshire Terriers with and without Medial Patellar Luxation. <i>Veterinary Surgery</i> , 2012, 41, 966-972.	0.5	18
79	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
80	Canine hip dysplasia is predictable by genotyping. <i>Osteoarthritis and Cartilage</i> , 2011, 19, 420-429.	0.6	46
81	Evaluation of a fibrillin 2 gene haplotype associated with hip dysplasia and incipient osteoarthritis in dogs. <i>American Journal of Veterinary Research</i> , 2011, 72, 530-540.	0.3	34
82	Genetic association mapping identifies single nucleotide polymorphisms in genes that affect abscisic acid levels in maize floral tissues during drought. <i>Journal of Experimental Botany</i> , 2011, 62, 701-716.	2.4	110
83	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	9.4	2,022
84	Genome-wide association studies of 14 agronomic traits in rice landraces. <i>Nature Genetics</i> , 2010, 42, 961-967.	9.4	1,978
85	Fine Quantitative Trait Loci Mapping of Carbon and Nitrogen Metabolism Enzyme Activities and Seedling Biomass in the Maize IBM Mapping Population Å Å. <i>Plant Physiology</i> , 2010, 154, 1753-1765.	2.3	58
86	Retrospective Analysis for Genetic Improvement of Hip Joints of Cohort Labrador Retrievers in the United States: 1970â€“2007. <i>PLoS ONE</i> , 2010, 5, e9410.	1.1	42
87	Differential Genetic Regulation of Canine Hip Dysplasia and Osteoarthritis. <i>PLoS ONE</i> , 2010, 5, e13219.	1.1	52
88	Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. <i>Plant Cell</i> , 2009, 21, 2194-2202.	3.1	786
89	Software engineering the mixed model for genome-wide association studies on large samples. <i>Briefings in Bioinformatics</i> , 2009, 10, 664-675.	3.2	96
90	Estimation of heritabilities, genetic correlations, and breeding values of four traits that collectively define hip dysplasia in dogs. <i>American Journal of Veterinary Research</i> , 2009, 70, 483-492.	0.3	49

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91	The long (and winding) road to gene discovery for canine hip dysplasia. <i>Veterinary Journal</i> , 2009, 181, 97-110.	0.6	39
92	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	6.0	1,284
93	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. <i>Plant Genome</i> , 2009, 2, .	1.6	66
94	Single nucleotide polymorphisms refine QTL intervals for hip joint laxity in dogs. <i>Animal Genetics</i> , 2008, 39, 141-146.	0.6	19
95	Identification of quantitative trait loci for osteoarthritis of hip joints in dogs. <i>American Journal of Veterinary Research</i> , 2008, 69, 1294-1300.	0.3	22
96	Quantitative genetics of secondary hip joint osteoarthritis in a Labrador Retriever×Greyhound pedigree. <i>American Journal of Veterinary Research</i> , 2007, 68, 35-41.	0.3	14
97	TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , 2007, 23, 2633-2635.	1.8	6,407
98	A random model for mapping imprinted quantitative trait loci in a structured pedigree: An implication for mapping canine hip dysplasia. <i>Genomics</i> , 2007, 90, 276-284.	1.3	20
99	Technical note: Use of marker-based relationships with multiple-trait derivative-free restricted maximal likelihood. <i>Journal of Animal Science</i> , 2007, 85, 881-885.	0.2	58
100	The bovine fatty acid binding protein 4 gene is significantly associated with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses. <i>Animal Genetics</i> , 2006, 37, 400-402.	0.6	133
101	Quantitative trait loci for hip dysplasia in a crossbreed canine pedigree. <i>Mammalian Genome</i> , 2005, 16, 720-730.	1.0	64
102	Phenotypic ranges and relationships among carcass and meat palatability traits for fourteen cattle breeds, and heritabilities and expected progeny differences for Warner-Bratzler shear force in three beef cattle breeds ^{1,2} . <i>Journal of Animal Science</i> , 2005, 83, 2461-2467.	0.2	69
103	Analysis of Allele Fidelity, Polymorphic Information Content, and Density of Microsatellites in a Genome-Wide Screening for Hip Dysplasia in a Crossbreed Pedigree. <i>Journal of Heredity</i> , 2005, 96, 847-853.	1.0	45