

Zhi-Wu Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

22,699
citations

53794

45
h-index

30087

103
g-index

125
all docs

125
docs citations

125
times ranked

14906
citing authors

#	ARTICLE	IF	CITATIONS
1	TASSEL: software for association mapping of complex traits in diverse samples. <i>Bioinformatics</i> , 2007, 23, 2633-2635.	4.1	6,407
2	Mixed linear model approach adapted for genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 355-360.	21.4	2,022
3	GAPIT: genome association and prediction integrated tool. <i>Bioinformatics</i> , 2012, 28, 2397-2399.	4.1	2,016
4	Genome-wide association studies of 14 agronomic traits in rice landraces. <i>Nature Genetics</i> , 2010, 42, 961-967.	21.4	1,978
5	The Genetic Architecture of Maize Flowering Time. <i>Science</i> , 2009, 325, 714-718.	12.6	1,284
6	Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2016, 12, e1005767.	3.5	1,095
7	Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. <i>Plant Cell</i> , 2009, 21, 2194-2202.	6.6	786
8	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	21.4	577
9	GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0120.	2.8	421
10	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.	6.9	396
11	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. <i>Genome Biology</i> , 2017, 18, 161.	8.8	363
12	GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 629-640.	6.9	345
13	The Genetic Architecture Of Maize Height. <i>Genetics</i> , 2014, 196, 1337-1356.	2.9	329
14	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, .	6.4	314
15	A SUPER Powerful Method for Genome Wide Association Study. <i>PLoS ONE</i> , 2014, 9, e107684.	2.5	289
16	Status and prospects of genome-wide association studies in plants. <i>Plant Genome</i> , 2021, 14, e20077.	2.8	200
17	Enrichment of statistical power for genome-wide association studies. <i>BMC Biology</i> , 2014, 12, 73.	3.8	160
18	Domestication footprints anchor genomic regions of agronomic importance in soybeans. <i>New Phytologist</i> , 2016, 209, 871-884.	7.3	152

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19	Whole transcriptome analysis with sequencing: methods, challenges and potential solutions. Cellular and Molecular Life Sciences, 2015, 72, 3425-3439.	5.4	141
20	The bovine fatty acid binding protein 4 gene is significantly associated with marbling and subcutaneous fat depth in Wagyu x Limousin F2 crosses. Animal Genetics, 2006, 37, 400-402.	1.7	133
21	Graph pangenome captures missing heritability and empowers tomato breeding. Nature, 2022, 606, 527-534.	27.8	131
22	Identification of genetic variants associated with maize flowering time using an extremely large multi-ethnic genetic background population. Plant Journal, 2016, 86, 391-402.	5.7	122
23	Joint-linkage mapping and GWAS reveal extensive genetic loci that regulate male inflorescence size in maize. Plant Biotechnology Journal, 2016, 14, 1551-1562.	8.3	121
24	Genetic association mapping identifies single nucleotide polymorphisms in genes that affect abscisic acid levels in maize floral tissues during drought. Journal of Experimental Botany, 2011, 62, 701-716.	4.8	110
25	Characterization of Biosynthetic Pathways for the Production of the Volatile Homoterpenes DMNT and TMTT in <i>Zea mays</i> . Plant Cell, 2016, 28, 2651-2665.	6.6	105
26	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. BMC Genomics, 2015, 16, 598.	2.8	104
27	Software engineering the mixed model for genome-wide association studies on large samples. Briefings in Bioinformatics, 2009, 10, 664-675.	6.5	96
28	Genotyping by Genome Reducing and Sequencing for Outbred Animals. PLoS ONE, 2013, 8, e67500.	2.5	86
29	Long Term Functional Outcome of Tibial Tuberosity Advancement vs. Tibial Plateau Leveling Osteotomy and Extracapsular Repair in a Heterogeneous Population of Dogs. Veterinary Surgery, 2016, 45, 261-268.	1.0	82
30	Long-Term Functional Outcome of Tibial Plateau Leveling Osteotomy Versus Extracapsular Repair in a Heterogeneous Population of Dogs. Veterinary Surgery, 2013, 42, 38-50.	1.0	80
31	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} . Journal of Animal Science, 2005, 83, 2461-2467.	0.5	69
32	Genetic Control of the Leaf Angle and Leaf Orientation Value as Revealed by Ultra-High Density Maps in Three Connected Maize Populations. PLoS ONE, 2015, 10, e0121624.	2.5	69
33	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. Plant Genome, 2009, 2, .	2.8	66
34	Quantitative trait loci for hip dysplasia in a crossbreed canine pedigree. Mammalian Genome, 2005, 16, 720-730.	2.2	64
35	Deep Learning for Predicting Complex Traits in Spring Wheat Breeding Program. Frontiers in Plant Science, 2020, 11, 613325.	3.6	64
36	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. BMC Genomics, 2016, 17, 894.	2.8	63

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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.	3.6	62
38	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.	0.5	58
39	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.	4.8	58
40	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. <i>Heredity</i> , 2018, 121, 648-662.	2.6	53
41	Differential Genetic Regulation of Canine Hip Dysplasia and Osteoarthritis. <i>PLoS ONE</i> , 2010, 5, e13219.	2.5	52
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.	3.3	50
43	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.	3.6	50
44	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.	0.6	49
45	Genome-wide association study Identified multiple Genetic Loci on Chilling Resistance During Germination in Maize. <i>Scientific Reports</i> , 2017, 7, 10840.	3.3	49
46	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.	3.8	48
47	Canine hip dysplasia is predictable by genotyping. <i>Osteoarthritis and Cartilage</i> , 2011, 19, 420-429.	1.3	46
48	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.	2.4	45
49	Transcriptome Sequencing Identified Genes and Gene Ontologies Associated with Early Freezing Tolerance in Maize. <i>Frontiers in Plant Science</i> , 2016, 7, 1477.	3.6	43
50	Genetic Dissection of End-Use Quality Traits in Adapted Soft White Winter Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 271.	3.6	43
51	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.	2.8	42
52	Genomic mosaicism due to homoeologous exchange generates extensive phenotypic diversity in nascent allopolyploids. <i>National Science Review</i> , 2021, 8, nwaa277.	9.5	42
53	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.	2.5	42
54	Genomic analysis establishes correlation between growth and laryngeal neuropathy in Thoroughbreds. <i>BMC Genomics</i> , 2014, 15, 259.	2.8	40

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55	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. <i>BMC Biology</i> , 2015, 13, 78.	3.8	40
56	The long (and winding) road to gene discovery for canine hip dysplasia. <i>Veterinary Journal</i> , 2009, 181, 97-110.	1.7	39
57	Association Mapping Provides Insights into the Origin and the Fine Structure of the Sorghum Aluminum Tolerance Locus, <i>AltSB</i> . <i>PLoS ONE</i> , 2014, 9, e87438.	2.5	36
58	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.	0.6	34
59	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.	1.4	34
60	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.	3.6	32
61	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.	2.5	32
62	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.	4.1	32
63	iPat: intelligent prediction and association tool for genomic research. <i>Bioinformatics</i> , 2018, 34, 1925-1927.	4.1	31
64	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.	8.3	30
65	Genome-wide association study of milk and reproductive traits in dual-purpose Xinjiang Brown cattle. <i>BMC Genomics</i> , 2019, 20, 827.	2.8	28
66	GWAS-Based Identification of New Loci for Milk Yield, Fat, and Protein in Holstein Cattle. <i>Animals</i> , 2020, 10, 2048.	2.3	26
67	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.	6.9	26
68	Prospectus of Genomic Selection and Phenomics in Cereal, Legume and Oilseed Breeding Programs. <i>Frontiers in Genetics</i> , 2022, 12, .	2.3	26
69	A New Genotype Imputation Method with Tolerance to High Missing Rate and Rare Variants. <i>PLoS ONE</i> , 2014, 9, e101025.	2.5	25
70	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.	2.5	23
71	Identification of quantitative trait loci for osteoarthritis of hip joints in dogs. <i>American Journal of Veterinary Research</i> , 2008, 69, 1294-1300.	0.6	22
72	Prospects for achieving durable disease resistance with elite fruit quality in apple breeding. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	22

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73	Aneuploidization under segmental allotetraploidy in rice and its phenotypic manifestation. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1273-1285.	3.6	21
74	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.	2.9	20
75	Single nucleotide polymorphisms refine QTL intervals for hip joint laxity in dogs. <i>Animal Genetics</i> , 2008, 39, 141-146.	1.7	19
76	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.	3.6	19
77	Evaluation of Tibial Torsion in Yorkshire Terriers with and without Medial Patellar Luxation. <i>Veterinary Surgery</i> , 2012, 41, 966-972.	1.0	18
78	Validation of UAV-based alfalfa biomass predictability using photogrammetry with fully automatic plot segmentation. <i>Scientific Reports</i> , 2021, 11, 3336.	3.3	18
79	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.	3.3	16
80	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3741-3749.	1.8	16
81	Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw064.	6.5	15
82	Quantitative genetics of secondary hip joint osteoarthritis in a Labrador Retriever and Greyhound pedigree. <i>American Journal of Veterinary Research</i> , 2007, 68, 35-41.	0.6	14
83	TCF21 is related to testis growth and development in broiler chickens. <i>Genetics Selection Evolution</i> , 2017, 49, 25.	3.0	14
84	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.	3.5	14
85	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of <i>Auricularia</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2255.	3.5	12
86	Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize. <i>Scientific Reports</i> , 2020, 10, 8165.	3.3	12
87	GRID: A Python Package for Field Plot Phenotyping Using Aerial Images. <i>Remote Sensing</i> , 2020, 12, 1697.	4.0	10
88	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.	3.6	10
89	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.	3.6	9
90	GridFree: a python package of imageanalysis for interactive grain counting and measuring. <i>Plant Physiology</i> , 2021, 186, 2239-2252.	4.8	7

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91	Genome-wide association study of the backfat thickness trait in two pig populations. <i>Frontiers of Agricultural Science and Engineering</i> , 2014, 1, 91.	1.4	6
92	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.	11.7	6
93	VTag: a semi-supervised pipeline for tracking pig activity with a single top-view camera. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	6
94	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.	1.3	5
95	Genetic Diversity of Clinal Freezing Tolerance Variation in Winter Wheat Landraces. <i>Agronomy</i> , 2018, 8, 95.	3.0	5
96	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.	3.6	5
97	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.	1.3	4
98	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	2.6	4
99	Human Breast Extracellular Matrix Microstructures and Protein Hydrogel 3D Cultures of Mammary Epithelial Cells. <i>Cancers</i> , 2021, 13, 5857.	3.7	4
100	MMAP: a cloud computing platform for mining the maximum accuracy of predicting phenotypes from genotypes. <i>Bioinformatics</i> , 2021, 37, 1324-1326.	4.1	3
101	Chromosomal characteristics of salt stress heritable gene expression in the rice genome. <i>BMC Genomic Data</i> , 2021, 22, 17.	1.7	2
102	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, , 63-80.	0.9	2
103	Performing Genome-Wide Association Studies with Multiple Models Using GAPIT. <i>Methods in Molecular Biology</i> , 2022, , 199-217.	0.9	1