Zhi-Wu Zhang

List of Publications by Year
in descending order

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	Genome Assembly of Alfalfa Cultivar Zhongmu-4 and Identification of SNPs Associated with Agronomic Traits. Genomics, Proteomics and Bioinformatics, 2022, 20, 14-28.	6.9	26
2	Prospectus of Genomic Selection and Phenomics in Cereal, Legume and Oilseed Breeding Programs. Frontiers in Genetics, 2022, 12, .	2.3	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. Frontiers in Plant Science, 2022, 13, 823250.	3.6	5
4	As the number falls, alternatives to the Hagberg–Perten falling number method: A review. Comprehensive Reviews in Food Science and Food Safety, 2022, 21, 2105-2117.	11.7	6
5	VTag: a semi-supervised pipeline for tracking pig activity with a single top-view camera. Journal of Animal Science, 2022, 100, .	0.5	6
6	Performing Genome-Wide Association Studies with Multiple Models Using GAPIT. Methods in Molecular Biology, 2022, , 199-217.	0.9	1
7	Interpretation of Manhattan Plots and Other Outputs of Genome-Wide Association Studies. Methods in Molecular Biology, 2022, , 63-80.	0.9	2
8	Graph pangenome captures missing heritability and empowers tomato breeding. Nature, 2022, 606, 527-534.	27.8	131
9	MMAP: a cloud computing platform for mining the maximum accuracy of predicting phenotypes from genotypes. Bioinformatics, 2021, 37, 1324-1326.	4.1	3
10	Genomic mosaicism due to homoeologous exchange generates extensive phenotypic diversity in nascent allopolyploids. National Science Review, 2021, 8, nwaa277.	9.5	42
11	Validation of UAV-based alfalfa biomass predictability using photogrammetry with fully automatic plot segmentation. Scientific Reports, 2021, 11, 3336.	3.3	18
12	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. Genomics, Proteomics and Bioinformatics, 2021, 19, 619-628.	6.9	396
13	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	2.6	4
14	Chromosomal characteristics of salt stress heritable gene expression in the rice genome. BMC Genomic Data, 2021, 22, 17.	1.7	2
15	GridFree: a python package of imageanalysis for interactive grain counting and measuring. Plant Physiology, 2021, 186, 2239-2252.	4.8	7
16	GAPIT Version 3: Boosting Power and Accuracy for Genomic Association and Prediction. Genomics, Proteomics and Bioinformatics, 2021, 19, 629-640.	6.9	345
17	Status and prospects of genome-wide association studies in plants. Plant Genome, 2021, 14, e20077.	2.8	200
18	Human Breast Extracellular Matrix Microstructures and Protein Hydrogel 3D Cultures of Mammary Epithelial Cells. Cancers, 2021, 13, 5857.	3.7	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. Frontiers in Plant Science, 2021, 12, 772907.	3.6	10
20	Identification of loci controlling adaptation in Chinese soya bean landraces via a combination of conventional and bioclimatic GWAS. Plant Biotechnology Journal, 2020, 18, 389-401.	8.3	30
21	GWAS-Based Identification of New Loci for Milk Yield, Fat, and Protein in Holstein Cattle. Animals, 2020, 10, 2048.	2.3	26
22	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. G3: Genes, Genomes, Genetics, 2020, 10, 3741-3749.	1.8	16
23	Denser Markers and Advanced Statistical Method Identified More Genetic Loci Associated with Husk Traits in Maize. Scientific Reports, 2020, 10, 8165.	3.3	12
24	GRID: A Python Package for Field Plot Phenotyping Using Aerial Images. Remote Sensing, 2020, 12, 1697.	4.0	10
25	Identification of Stripe Rust Resistance Loci in U.S. Spring Wheat Cultivars and Breeding Lines Using Genome-Wide Association Mapping and Yr Gene Markers. Plant Disease, 2020, 104, 2181-2192.	1.4	34
26	Prospects for achieving durable disease resistance with elite fruit quality in apple breeding. Tree Genetics and Genomes, 2020, 16, 1.	1.6	22
27	Deep Learning for Predicting Complex Traits in Spring Wheat Breeding Program. Frontiers in Plant Science, 2020, 11, 613325.	3.6	64
28	Genomic Analyses Reveal Evidence of Independent Evolution, Demographic History, and Extreme Environment Adaptation of Tibetan Plateau Agaricus bisporus. Frontiers in Microbiology, 2019, 10, 1786.	3.5	14
29	Genome-wide association study of milk and reproductive traits in dual-purpose Xinjiang Brown cattle. BMC Genomics, 2019, 20, 827.	2.8	28
30	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of Auricularia Species. Frontiers in Microbiology, 2019, 10, 2255.	3.5	12
31	BLINK: a package for the next level of genome-wide association studies with both individuals and markers in the millions. GigaScience, 2019, 8, .	6.4	314
32	Aneuploidization under segmental allotetraploidy in rice and its phenotypic manifestation. Theoretical and Applied Genetics, 2018, 131, 1273-1285.	3.6	21
33	iPat: intelligent prediction and association tool for genomic research. Bioinformatics, 2018, 34, 1925-1927.	4.1	31
34	Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. Scientific Reports, 2018, 8, 6848.	3.3	16
35	Expanding the BLUP alphabet for genomic prediction adaptable to the genetic architectures of complex traits. Heredity, 2018, 121, 648-662.	2.6	53
36	Evaluation of the Potential for Genomic Selection to Improve Spring Wheat Resistance to Fusarium Head Blight in the Pacific Northwest. Frontiers in Plant Science, 2018, 9, 911.	3.6	50

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37	Genome-Wide Association Mapping for Tolerance to Preharvest Sprouting and Low Falling Numbers in Wheat. Frontiers in Plant Science, 2018, 9, 141.	3.6	62
38	Genetic Dissection of End-Use Quality Traits in Adapted Soft White Winter Wheat. Frontiers in Plant Science, 2018, 9, 271.	3.6	43
39	Genetic Diversity of Clinal Freezing Tolerance Variation in Winter Wheat Landraces. Agronomy, 2018, 8, 95.	3.0	5
40	Systematic bias of correlation coefficient may explain negative accuracy of genomic prediction. Briefings in Bioinformatics, 2017, 18, bbw064.	6.5	15
41	Genome-wide association study Identified multiple Genetic Loci on Chilling Resistance During Germination in Maize. Scientific Reports, 2017, 7, 10840.	3.3	49
42	Comparative Transcriptome Analysis Identified Candidate Genes Related to Bailinggu Mushroom Formation and Genetic Markers for Genetic Analyses and Breeding. Scientific Reports, 2017, 7, 9266.	3.3	50
43	TCF21 is related to testis growth and development in broiler chickens. Genetics Selection Evolution, 2017, 49, 25.	3.0	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. Plant Genome, 2017, 10, plantgenome2016.12.0124.	2.8	42
45	Genome-Wide Association Study Reveals Novel Genes Associated with Culm Cellulose Content in Bread Wheat (Triticum aestivum, L.). Frontiers in Plant Science, 2017, 8, 1913.	3.6	19
46	Genome-wide association studies dissect the genetic networks underlying agronomical traits in soybean. Genome Biology, 2017, 18, 161.	8.8	363
47	Genome-wide association studies identified multiple genetic loci for body size at four growth stages in Chinese Holstein cattle. PLoS ONE, 2017, 12, e0175971.	2.5	23
48	Identification of Resistance to Wet Bubble Disease and Genetic Diversity in Wild and Cultivated Strains of Agaricus bisporus. International Journal of Molecular Sciences, 2016, 17, 1568.	4.1	32
49	De Novo Sequencing and Transcriptome Analysis of Pleurotus eryngii subsp. tuoliensis (Bailinggu) Mycelia in Response to Cold Stimulation. Molecules, 2016, 21, 560.	3.8	48
50	Transcriptome Sequencing Identified Genes and Gene Ontologies Associated with Early Freezing Tolerance in Maize. Frontiers in Plant Science, 2016, 7, 1477.	3.6	43
51	Identification of genetic variants associated with maize flowering time using an extremely large multiâ€genetic background population. Plant Journal, 2016, 86, 391-402.	5.7	122
52	Domestication footprints anchor genomic regions of agronomic importance in soybeans. New Phytologist, 2016, 209, 871-884.	7.3	152
53	Analysis of recombination QTLs, segregation distortion, and epistasis for fitness in maize multiple populations using ultra-high-density markers. Theoretical and Applied Genetics, 2016, 129, 1775-1784.	3.6	9
54	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

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55	Numerous genetic loci identified for drought tolerance in the maize nested association mapping populations. BMC Genomics, 2016, 17, 894.	2.8	63
56	GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. Plant Genome, 2016, 9, plantgenome2015.11.0120.	2.8	421
57	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
58	Joint‐linkage mapping and <scp>GWAS</scp> reveal extensive genetic loci that regulate male inflorescence size in maize. Plant Biotechnology Journal, 2016, 14, 1551-1562.	8.3	121
59	Iterative Usage of Fixed and Random Effect Models for Powerful and Efficient Genome-Wide Association Studies. PLoS Genetics, 2016, 12, e1005767.	3.5	1,095
60	Construction of high-quality recombination maps with low-coverage genomic sequencing for joint linkage analysis in maize. BMC Biology, 2015, 13, 78.	3.8	40
61	Whole transcriptome analysis with sequencing: methods, challenges and potential solutions. Cellular and Molecular Life Sciences, 2015, 72, 3425-3439.	5.4	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. BMC Genomics, 2015, 16, 598.	2.8	104
63	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
64	A SUPER Powerful Method for Genome Wide Association Study. PLoS ONE, 2014, 9, e107684.	2.5	289
65	Enrichment of statistical power for genome-wide association studies. BMC Biology, 2014, 12, 73.	3.8	160
66	The Genetic Architecture Of Maize Height. Genetics, 2014, 196, 1337-1356.	2.9	329
67	Genomic analysis establishes correlation between growth and laryngeal neuropathy in Thoroughbreds. BMC Genomics, 2014, 15, 259.	2.8	40
68	Association Mapping Provides Insights into the Origin and the Fine Structure of the Sorghum Aluminum Tolerance Locus, AltSB. PLoS ONE, 2014, 9, e87438.	2.5	36
69	A New Genotype Imputation Method with Tolerance to High Missing Rate and Rare Variants. PLoS ONE, 2014, 9, e101025.	2.5	25
70	Genome-wide association study of the backfat thickness trait in two pig populations. Frontiers of Agricultural Science and Engineering, 2014, 1, 91.	1.4	6
71	Performance prediction of F1 hybrids between recombinant inbred lines derived from two elite maize inbred lines. Theoretical and Applied Genetics, 2013, 126, 189-201.	3.6	32
72	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

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73	Principal component analysis of canine hip dysplasia phenotypes and their statistical power for genome-wide association mapping. Journal of Applied Statistics, 2013, 40, 235-251.	1.3	4
74	Genotyping by Genome Reducing and Sequencing for Outbred Animals. PLoS ONE, 2013, 8, e67500.	2.5	86
75	Monitoring Hip and Elbow Dysplasia Achieved Modest Genetic Improvement of 74 Dog Breeds over 40 Years in USA. PLoS ONE, 2013, 8, e76390.	2.5	32
76	Identification of quantitative trait loci for canine hip dysplasia by two sequential multipoint linkage analyses. Journal of Applied Statistics, 2012, 39, 1719-1731.	1.3	5
77	GAPIT: genome association and prediction integrated tool. Bioinformatics, 2012, 28, 2397-2399.	4.1	2,016
78	Evaluation of Tibial Torsion in Yorkshire Terriers with and without Medial Patellar Luxation. Veterinary Surgery, 2012, 41, 966-972.	1.0	18
79	Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807.	21.4	577
80	Canine hip dysplasia is predictable by genotyping. Osteoarthritis and Cartilage, 2011, 19, 420-429.	1.3	46
81	Evaluation of a fibrillin 2 gene haplotype associated with hip dysplasia and incipient osteoarthritis in dogs. American Journal of Veterinary Research, 2011, 72, 530-540.	0.6	34
82	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
83	Mixed linear model approach adapted for genome-wide association studies. Nature Genetics, 2010, 42, 355-360.	21.4	2,022
84	Genome-wide association studies of 14 agronomic traits in rice landraces. Nature Genetics, 2010, 42, 961-967.	21.4	1,978
85	Fine Quantitative Trait Loci Mapping of Carbon and Nitrogen Metabolism Enzyme Activities and Seedling Biomass in the Maize IBM Mapping Population Â Â. Plant Physiology, 2010, 154, 1753-1765.	4.8	58
86	Retrospective Analysis for Genetic Improvement of Hip Joints of Cohort Labrador Retrievers in the United States: 1970â€"2007. PLoS ONE, 2010, 5, e9410.	2.5	42
87	Differential Genetic Regulation of Canine Hip Dysplasia and Osteoarthritis. PLoS ONE, 2010, 5, e13219.	2.5	52
88	Association Mapping: Critical Considerations Shift from Genotyping to Experimental Design. Plant Cell, 2009, 21, 2194-2202.	6.6	786
89	Software engineering the mixed model for genome-wide association studies on large samples. Briefings in Bioinformatics, 2009, 10, 664-675.	6.5	96
90	Estimation of heritabilities, genetic correlations, and breeding values of four traits that collectively define hip dysplasia in dogs. American Journal of Veterinary Research, 2009, 70, 483-492.	0.6	49

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91	The long (and winding) road to gene discovery for canine hip dysplasia. Veterinary Journal, 2009, 181, 97-110.	1.7	39
92	The Genetic Architecture of Maize Flowering Time. Science, 2009, 325, 714-718.	12.6	1,284
93	Simulation Appraisal of the Adequacy of Number of Background Markers for Relationship Estimation in Association Mapping. Plant Genome, 2009, 2, .	2.8	66
94	Single nucleotide polymorphisms refine QTL intervals for hip joint laxity in dogs. Animal Genetics, 2008, 39, 141-146.	1.7	19
95	Identification of quantitative trait loci for osteoarthritis of hip joints in dogs. American Journal of Veterinary Research, 2008, 69, 1294-1300.	0.6	22
96	Quantitative genetics of secondary hip joint osteoarthritis in a Labrador Retriever–Greyhound pedigree. American Journal of Veterinary Research, 2007, 68, 35-41.	0.6	14
97	TASSEL: software for association mapping of complex traits in diverse samples. Bioinformatics, 2007, 23, 2633-2635.	4.1	6,407
98	A random model for mapping imprinted quantitative trait loci in a structured pedigree: An implication for mapping canine hip dysplasia. Genomics, 2007, 90, 276-284.	2.9	20
99	Technical note: Use of marker-based relationships with multiple-trait derivative-free restricted maximal likelihood. Journal of Animal Science, 2007, 85, 881-885.	0.5	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. Animal Genetics, 2006, 37, 400-402.	1.7	133
101	Quantitative trait loci for hip dysplasia in a crossbreed canine pedigree. Mammalian Genome, 2005, 16, 720-730.	2.2	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 breeds1,2. Journal of Animal Science, 2005, 83, 2461-2467.	0.5	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. Journal of Heredity, 2005, 96, 847-853.	2.4	45