

Jun Zhu

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

78
papers

3,493
citations

25
h-index

58
g-index

79
ext. papers

3,928
ext. citations

4.4
avg, IF

4.83
L-index

#	Paper	IF	Citations
78	An integrative genomics approach to infer causal associations between gene expression and disease. <i>Nature Genetics</i> , 2005 , 37, 710-7	36.3	820
77	A generalized combinatorial approach for detecting gene-by-gene and gene-by-environment interactions with application to nicotine dependence. <i>American Journal of Human Genetics</i> , 2007 , 80, 1125-37	11	470
76	QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations. <i>Bioinformatics</i> , 2008 , 24, 721-3	7.2	339
75	Mapping the genetic architecture of complex traits in experimental populations. <i>Bioinformatics</i> , 2007 , 23, 1527-36	7.2	253
74	Molecular dissection of developmental behavior of plant height in rice (<i>Oryza sativa</i> L.). <i>Genetics</i> , 1998 , 150, 1257-65	4	127
73	Developmental quantitative genetics, conditional epigenetic variability and growth in mice. <i>Genetics</i> , 1997 , 147, 765-76	4	126
72	Methods for predicting superior genotypes under multiple environments based on QTL effects. <i>Theoretical and Applied Genetics</i> , 2005 , 110, 1268-74	6	114
71	THE GENETIC BASIS OF LIFE-HISTORY CHARACTERS IN A POLYCHAETE EXHIBITING PLANKTOTROPHY AND LECITHOTROPHY. <i>Evolution; International Journal of Organic Evolution</i> , 1991 , 45, 380-397	3.8	94
70	A combinatorial approach to detecting gene-gene and gene-environment interactions in family studies. <i>American Journal of Human Genetics</i> , 2008 , 83, 457-67	11	77
69	Molecular Marker-Assisted Dissection of Genotype × Environment Interaction for Plant Type Traits in Rice (<i>Oryza sativa</i> L.). <i>Crop Science</i> , 1999 , 39, 538-544	2.4	77
68	Quantitative analysis and QTL mapping for agronomic and fiber traits in an RI population of upland cotton. <i>Euphytica</i> , 2009 , 165, 231-245	2.1	72
67	A functional-structural model of rice linking quantitative genetic information with morphological development and physiological processes. <i>Annals of Botany</i> , 2011 , 107, 817-28	4.1	63
66	Genetic analysis for developmental behavior of some seed quality traits in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Euphytica</i> , 2003 , 129, 183-191	2.1	45
65	Development of GMDR-GPU for gene-gene interaction analysis and its application to WTCCC GWAS data for type 2 diabetes. <i>PLoS ONE</i> , 2013 , 8, e61943	3.7	43
64	Practical and theoretical considerations in study design for detecting gene-gene interactions using MDR and GMDR approaches. <i>PLoS ONE</i> , 2011 , 6, e16981	3.7	43
63	Functional mapping for genetic control of programmed cell death. <i>Physiological Genomics</i> , 2006 , 25, 458-69	3.69	34
62	Mixed model approaches for diallel analysis based on a bio-model. <i>Genetical Research</i> , 1996 , 68, 233-40	1.1	34

61	Analysis of gene expression profiles of two near-isogenic lines differing at a QTL region affecting oil content at high temperatures during seed maturation in oilseed rape (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2012 , 124, 515-31	6	31
60	Association mapping for epistasis and environmental interaction of yield traits in 323 cotton cultivars under 9 different environments. <i>PLoS ONE</i> , 2014 , 9, e95882	3.7	30
59	Mixed Linear Model Approaches of Association Mapping for Complex Traits Based on Omics Variants. <i>Scientific Reports</i> , 2015 , 5, 10298	4.9	28
58	Marker-assisted selection in segregating generations of self-fertilizing crops. <i>Theoretical and Applied Genetics</i> , 2004 , 109, 370-6	6	28
57	An approach for predicting heterosis based on an additive, dominance and additive x additive model with environment interaction. <i>Heredity</i> , 1999 , 82 (Pt 5), 510-7	3.6	27
56	Sampling a Core Collection of Island Cotton (<i>Gossypium barbadense</i> L.) Based on the Genotypic Values of Fiber Traits. <i>Genetic Resources and Crop Evolution</i> , 2006 , 53, 515-521	2	25
55	A unified statistical model for functional mapping of environment-dependent genetic expression and genotype x environment interactions for ontogenetic development. <i>Genetics</i> , 2004 , 168, 1751-62	4	25
54	Identification of candidate genes for drought stress tolerance in rice by the integration of a genetic (QTL) map with the rice genome physical map. <i>Journal of Zhejiang University Science B</i> , 2005 , 6, 382-8		25
53	Mapping QTLs with digenic epistasis under multiple environments and predicting heterosis based on QTL effects. <i>Theoretical and Applied Genetics</i> , 2007 , 115, 325-33	6	24
52	Genetic association of yield with its component traits in a recombinant inbred line population of cotton. <i>Euphytica</i> , 2004 , 140, 171-179	2.1	24
51	A method for marker-assisted selection based on QTLs with epistatic effects. <i>Genetica</i> , 2003 , 119, 75-86	1.5	23
50	Genetic analysis for protein content in indica rice. <i>Euphytica</i> , 1999 , 107, 135-140	2.1	23
49	Mapping epigenetic quantitative trait loci (QTL) altering a developmental trajectory. <i>Genome</i> , 2002 , 45, 28-33	2.4	20
48	Using matrix of thresholding partial correlation coefficients to infer regulatory network. <i>BioSystems</i> , 2008 , 91, 158-65	1.9	19
47	Genetic studies of anther culture ability in rice (<i>Oryza sativa</i>). <i>Plant Cell, Tissue and Organ Culture</i> , 1996 , 45, 253-258	2.7	18
46	Genetic and genotype x environment interaction effects from embryo, endosperm, cytoplasm and maternal plant for rice grain shape traits of indica rice. <i>Field Crops Research</i> , 2000 , 68, 191-198	5.5	17
45	Dominance and Epistasis Interactions Revealed as Important Variants for Leaf Traits of Maize NAM Population. <i>Frontiers in Plant Science</i> , 2018 , 9, 627	6.2	16
44	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , 2018 , 19, 451	4.5	16

43	Mapping QTL for biomass yield and its components in rice (<i>Oryza sativa</i> L.). <i>Journal of Genetics and Genomics</i> , 2006 , 33, 607-16		15
42	Genomic Prediction of Genotypic Effects with Epistasis and Environment Interactions for Yield-Related Traits of Rapeseed (<i>L.</i>). <i>Frontiers in Genetics</i> , 2017 , 8, 15	4.5	14
41	Gene Polymorphism Association with Type 2 Diabetes and Related Gene-Gene and Gene-Environment Interactions in a Uyghur Population. <i>Medical Science Monitor</i> , 2016 , 22, 474-87	3.2	13
40	Comparing GWAS Results of Complex Traits Using Full Genetic Model and Additive Models for Revealing Genetic Architecture. <i>Scientific Reports</i> , 2017 , 7, 38600	4.9	12
39	A two-step strategy for detecting differential gene expression in cDNA microarray data. <i>Current Genetics</i> , 2005 , 47, 121-31	2.9	12
38	Genetic effects and genotype × environment interactions for cooking quality traits in Indica-japonica crosses of rice (<i>Oryza sativa</i> L.). <i>Euphytica</i> , 1999 , 109, 9-15	2.1	12
37	A robust statistical procedure to discover expression biomarkers using microarray genomic expression data. <i>Journal of Zhejiang University: Science B</i> , 2006 , 7, 603-7	4.5	10
36	Analysis of genetic effects of major genes and polygenes on quantitative traits. II. Genetic models for seed traits of crops. <i>Theoretical and Applied Genetics</i> , 2002 , 105, 964-971	6	10
35	An association study revealed substantial effects of dominance, epistasis and substance dependence co-morbidity on alcohol dependence symptom count. <i>Addiction Biology</i> , 2017 , 22, 1475-1485	4.6	9
34	Impacts of QTL × environment interactions on genetic response to marker-assisted selection. <i>Journal of Genetics and Genomics</i> , 2006 , 33, 63-71		9
33	A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. <i>Statistics and Its Interface</i> , 2011 , 4, 295-304	0.4	9
32	Statistical approaches in QTL mapping and molecular breeding for complex traits. <i>Science Bulletin</i> , 2012 , 57, 2637-2644		8
31	Nonparametric functional mapping of quantitative trait loci underlying programmed cell death. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008 , 7, Article4	1.2	8
30	Genome-wide association study of maize plant architecture using F populations. <i>Plant Molecular Biology</i> , 2019 , 99, 1-15	4.6	8
29	Quantitative genetic analysis station for the genetic analysis of complex traits. <i>Science Bulletin</i> , 2012 , 57, 2721-2726		7
28	Genetic control of the opaque-2 gene and background polygenes over some kernel traits in maize (<i>Zea mays</i> L.). <i>Genetica</i> , 2005 , 124, 291-300	1.5	7
27	Genetic effects of embryo and endosperm for four malting quality traits of barley. <i>Euphytica</i> , 1999 , 106, 27-34	2.1	7
26	Mapping epistasis and environment × QTX interaction based on four -omics genotypes for the detected QTX loci controlling complex traits in tobacco. <i>Crop Journal</i> , 2013 , 1, 151-159	4.6	6

25	Mapping interspecific genetic architecture in a host-parasite interaction system. <i>Genetics</i> , 2008 , 178, 1737-43	4	6
24	Influence of outliers on QTL mapping for complex traits. <i>Journal of Zhejiang University: Science B</i> , 2008 , 9, 931-7	4.5	6
23	Improvement of mapping accuracy by unifying linkage and association analysis. <i>Genetics</i> , 2006 , 172, 647-61	4	6
22	Dissecting Genetic Network of Fruit Branch Traits in Upland Cotton by Association Mapping Using SSR Markers. <i>PLoS ONE</i> , 2017 , 12, e0162815	3.7	6
21	Full genetic analysis for genome-wide association study of Fangji: a powerful approach for effectively dissecting the molecular architecture of personalized traditional Chinese medicine. <i>Acta Pharmacologica Sinica</i> , 2018 , 39, 906-911	8	5
20	Functional mapping of dynamic traits with robust t-distribution. <i>PLoS ONE</i> , 2011 , 6, e24902	3.7	4
19	Analysis of the 3' ends of tRNA as the cause of insertion sites of foreign DNA in <i>Prochlorococcus</i> . <i>Journal of Zhejiang University: Science B</i> , 2010 , 11, 708-18	4.5	4
18	MIXED LINEAR MODEL APPROACHES FOR ANALYZING GENETIC MODELS OF COMPLEX QUANTITATIVE TRAITS. <i>Journal of Zhejiang University Science B</i> , 2000 , 1, 78		4
17	Large Population with Low Marker Density Versus Small Population with High Marker Density for QTL Mapping: A Case Study for Mapping QTL Controlling Barley Net Blotch Resistance 2013 , 301-315		4
16	Dissecting genetic architecture of startle response in <i>Drosophila melanogaster</i> using multi-omics information. <i>Scientific Reports</i> , 2017 , 7, 12367	4.9	3
15	Combined analysis with copy number variation identifies risk loci in lung cancer. <i>BioMed Research International</i> , 2014 , 2014, 469103	3	3
14	A new approach to dissecting complex traits by combining quantitative trait transcript (QTT) mapping and diallel cross analysis. <i>Science Bulletin</i> , 2012 , 57, 2695-2700		2
13	Identifying differentially expressed genes in human acute leukemia and mouse brain microarray datasets utilizing QTMModel. <i>Functional and Integrative Genomics</i> , 2009 , 9, 59-66	3.8	2
12	Simulating superior genotypes for plant height based on QTLs: Towards virtual breeding of rice 2012 ,		2
11	Analysis of genetic effects of nuclear-cytoplasmic interaction on quantitative traits: genetic model for diploid plants. <i>Journal of Genetics and Genomics</i> , 2007 , 34, 562-8	4	2
10	Clustering gene expression data based on predicted differential effects of GV interaction. <i>Genomics, Proteomics and Bioinformatics</i> , 2005 , 3, 36-41	6.5	2
9	Conditional GWAS revealing genetic impacts of lifestyle behaviors on low-density lipoprotein (LDL). <i>Computational Biology and Chemistry</i> , 2019 , 78, 497-503	3.6	2
8	QTLNetworkR: an interactive R package for QTL visualization. <i>Journal of Zhejiang University: Science B</i> , 2010 , 11, 512-5	4.5	1

7	3D graphical visualization of the genetic architectures underlying complex traits in multiple environments. <i>Journal of Zhejiang University: Science A</i> , 2007 , 8, 563-567	2.1	1
6	Analysis of genetic effects of nuclear-cytoplasmic interaction on quantitative traits: genetic models for seed traits of plants. <i>Theoretical and Applied Genetics</i> , 2008 , 116, 769-76	6	1
5	Conditional and unconditional genome-wide association study reveal complicate genetic architecture of human body weight and impacts of smoking. <i>Scientific Reports</i> , 2020 , 10, 12136	4.9	1
4	Dissecting anxiety-related QTLs in mice by univariate and multivariate mapping. <i>Science Bulletin</i> , 2012 , 57, 2727-2732		
3	Penalized Independence Rule for Testing High-Dimensional Hypotheses. <i>Communications in Statistics - Theory and Methods</i> , 2011 , 40, 2424-2435	0.5	
2	Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , 2021 , 12, 612045	4.5	
1	Genome-wide conditional association study reveals the influences of lifestyle cofactors on genetic regulation of body surface area in MESA population. <i>PLoS ONE</i> , 2021 , 16, e0253167	3.7	