

# Jun Zhu

## List of Publications by Year in Descending Order

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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	Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 612045	4.5	
77	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> , <b>2021</b> , 16, e0253167	3.7	
76	Conditional and unconditional genome-wide association study reveal complicate genetic architecture of human body weight and impacts of smoking. <i>Scientific Reports</i> , <b>2020</b> , 10, 12136	4.9	1
75	Conditional GWAS revealing genetic impacts of lifestyle behaviors on low-density lipoprotein (LDL). <i>Computational Biology and Chemistry</i> , <b>2019</b> , 78, 497-503	3.6	2
74	Genome-wide association study of maize plant architecture using F populations. <i>Plant Molecular Biology</i> , <b>2019</b> , 99, 1-15	4.6	8
73	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> , <b>2018</b> , 39, 906-911	8	5
72	Dominance and Epistasis Interactions Revealed as Important Variants for Leaf Traits of Maize NAM Population. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 627	6.2	16
71	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , <b>2018</b> , 19, 451	4.5	16
70	An association study revealed substantial effects of dominance, epistasis and substance dependence co-morbidity on alcohol dependence symptom count. <i>Addiction Biology</i> , <b>2017</b> , 22, 1475-1483	4.6	9
69	Comparing GWAS Results of Complex Traits Using Full Genetic Model and Additive Models for Revealing Genetic Architecture. <i>Scientific Reports</i> , <b>2017</b> , 7, 38600	4.9	12
68	Dissecting genetic architecture of startle response in <i>Drosophila melanogaster</i> using multi-omics information. <i>Scientific Reports</i> , <b>2017</b> , 7, 12367	4.9	3
67	Genomic Prediction of Genotypic Effects with Epistasis and Environment Interactions for Yield-Related Traits of Rapeseed (L.). <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 15	4.5	14
66	Dissecting Genetic Network of Fruit Branch Traits in Upland Cotton by Association Mapping Using SSR Markers. <i>PLoS ONE</i> , <b>2017</b> , 12, e0162815	3.7	6
65	Gene Polymorphism Association with Type 2 Diabetes and Related Gene-Gene and Gene-Environment Interactions in a Uyghur Population. <i>Medical Science Monitor</i> , <b>2016</b> , 22, 474-87	3.2	13
64	Mixed Linear Model Approaches of Association Mapping for Complex Traits Based on Omics Variants. <i>Scientific Reports</i> , <b>2015</b> , 5, 10298	4.9	28
63	Combined analysis with copy number variation identifies risk loci in lung cancer. <i>BioMed Research International</i> , <b>2014</b> , 2014, 469103	3	3
62	Association mapping for epistasis and environmental interaction of yield traits in 323 cotton cultivars under 9 different environments. <i>PLoS ONE</i> , <b>2014</b> , 9, e95882	3.7	30

61	Mapping epistasis and environmentQTX interaction based on four -omics genotypes for the detected QTX loci controlling complex traits in tobacco. <i>Crop Journal</i> , <b>2013</b> , 1, 151-159	4.6	6
60	Development of GMDR-GPU for gene-gene interaction analysis and its application to WTCCC GWAS data for type 2 diabetes. <i>PLoS ONE</i> , <b>2013</b> , 8, e61943	3.7	43
59	Large Population with Low Marker Density Verse Small Population with High Marker Density for QTL Mapping: A Case Study for Mapping QTL Controlling Barley Net Blotch Resistance <b>2013</b> , 301-315		4
58	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> , <b>2012</b> , 124, 515-31	6	31
57	Statistical approaches in QTL mapping and molecular breeding for complex traits. <i>Science Bulletin</i> , <b>2012</b> , 57, 2637-2644		8
56	Quantitative genetic analysis station for the genetic analysis of complex traits. <i>Science Bulletin</i> , <b>2012</b> , 57, 2721-2726		7
55	A new approach to dissecting complex traits by combining quantitative trait transcript (QTT) mapping and diallel cross analysis. <i>Science Bulletin</i> , <b>2012</b> , 57, 2695-2700		2
54	Dissecting anxiety-related QTLs in mice by univariate and multivariate mapping. <i>Science Bulletin</i> , <b>2012</b> , 57, 2727-2732		
53	Simulating superior genotypes for plant height based on QTLs: Towards virtual breeding of rice <b>2012</b> ,		2
52	Practical and theoretical considerations in study design for detecting gene-gene interactions using MDR and GMDR approaches. <i>PLoS ONE</i> , <b>2011</b> , 6, e16981	3.7	43
51	Functional mapping of dynamic traits with robust t-distribution. <i>PLoS ONE</i> , <b>2011</b> , 6, e24902	3.7	4
50	Penalized Independence Rule for Testing High-Dimensional Hypotheses. <i>Communications in Statistics - Theory and Methods</i> , <b>2011</b> , 40, 2424-2435	0.5	
49	A functional-structural model of rice linking quantitative genetic information with morphological development and physiological processes. <i>Annals of Botany</i> , <b>2011</b> , 107, 817-28	4.1	63
48	A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. <i>Statistics and Its Interface</i> , <b>2011</b> , 4, 295-304	0.4	9
47	QTLNetworkR: an interactive R package for QTL visualization. <i>Journal of Zhejiang University: Science B</i> , <b>2010</b> , 11, 512-5	4.5	1
46	Analysis of the 3Vends of tRNA as the cause of insertion sites of foreign DNA in <i>Prochlorococcus</i> . <i>Journal of Zhejiang University: Science B</i> , <b>2010</b> , 11, 708-18	4.5	4
45	Identifying differentially expressed genes in human acute leukemia and mouse brain microarray datasets utilizing QTModel. <i>Functional and Integrative Genomics</i> , <b>2009</b> , 9, 59-66	3.8	2
44	Quantitative analysis and QTL mapping for agronomic and fiber traits in an RI population of upland cotton. <i>Euphytica</i> , <b>2009</b> , 165, 231-245	2.1	72

43	QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations. <i>Bioinformatics</i> , <b>2008</b> , 24, 721-3	7.2	339
42	Nonparametric functional mapping of quantitative trait loci underlying programmed cell death. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2008</b> , 7, Article4	1.2	8
41	Mapping interspecific genetic architecture in a host-parasite interaction system. <i>Genetics</i> , <b>2008</b> , 178, 1737-43	4	6
40	Analysis of genetic effects of nuclear-cytoplasmic interaction on quantitative traits: genetic models for seed traits of plants. <i>Theoretical and Applied Genetics</i> , <b>2008</b> , 116, 769-76	6	1
39	Using matrix of thresholding partial correlation coefficients to infer regulatory network. <i>BioSystems</i> , <b>2008</b> , 91, 158-65	1.9	19
38	Influence of outliers on QTL mapping for complex traits. <i>Journal of Zhejiang University: Science B</i> , <b>2008</b> , 9, 931-7	4.5	6
37	A combinatorial approach to detecting gene-gene and gene-environment interactions in family studies. <i>American Journal of Human Genetics</i> , <b>2008</b> , 83, 457-67	11	77
36	Mapping the genetic architecture of complex traits in experimental populations. <i>Bioinformatics</i> , <b>2007</b> , 23, 1527-36	7.2	253
35	3D graphical visualization of the genetic architectures underlying complex traits in multiple environments. <i>Journal of Zhejiang University: Science A</i> , <b>2007</b> , 8, 563-567	2.1	1
34	Mapping QTLs with digenic epistasis under multiple environments and predicting heterosis based on QTL effects. <i>Theoretical and Applied Genetics</i> , <b>2007</b> , 115, 325-33	6	24
33	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> , <b>2007</b> , 80, 1125-37	11	470
32	Analysis of genetic effects of nuclear-cytoplasmic interaction on quantitative traits: genetic model for diploid plants. <i>Journal of Genetics and Genomics</i> , <b>2007</b> , 34, 562-8	4	2
31	Impacts of QTL x environment interactions on genetic response to marker-assisted selection. <i>Journal of Genetics and Genomics</i> , <b>2006</b> , 33, 63-71		9
30	Mapping QTL for biomass yield and its components in rice ( <i>Oryza sativa</i> L.). <i>Journal of Genetics and Genomics</i> , <b>2006</b> , 33, 607-16		15
29	Improvement of mapping accuracy by unifying linkage and association analysis. <i>Genetics</i> , <b>2006</b> , 172, 647-61		6
28	Functional mapping for genetic control of programmed cell death. <i>Physiological Genomics</i> , <b>2006</b> , 25, 458-69		34
27	A robust statistical procedure to discover expression biomarkers using microarray genomic expression data. <i>Journal of Zhejiang University: Science B</i> , <b>2006</b> , 7, 603-7	4.5	10
26	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> , <b>2006</b> , 53, 515-521	2	25

25	Clustering gene expression data based on predicted differential effects of GV interaction. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2005</b> , 3, 36-41	6.5	2
24	An integrative genomics approach to infer causal associations between gene expression and disease. <i>Nature Genetics</i> , <b>2005</b> , 37, 710-7	36.3	820
23	A two-step strategy for detecting differential gene expression in cDNA microarray data. <i>Current Genetics</i> , <b>2005</b> , 47, 121-31	2.9	12
22	Methods for predicting superior genotypes under multiple environments based on QTL effects. <i>Theoretical and Applied Genetics</i> , <b>2005</b> , 110, 1268-74	6	114
21	Genetic control of the opaque-2 gene and background polygenes over some kernel traits in maize ( <i>Zea mays</i> L.). <i>Genetica</i> , <b>2005</b> , 124, 291-300	1.5	7
20	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> , <b>2005</b> , 6, 382-8		25
19	A unified statistical model for functional mapping of environment-dependent genetic expression and genotype x environment interactions for ontogenetic development. <i>Genetics</i> , <b>2004</b> , 168, 1751-62	4	25
18	Genetic association of yield with its component traits in a recombinant inbred line population of cotton. <i>Euphytica</i> , <b>2004</b> , 140, 171-179	2.1	24
17	Marker-assisted selection in segregating generations of self-fertilizing crops. <i>Theoretical and Applied Genetics</i> , <b>2004</b> , 109, 370-6	6	28
16	A method for marker-assisted selection based on QTLs with epistatic effects. <i>Genetica</i> , <b>2003</b> , 119, 75-86	1.5	23
15	Genetic analysis for developmental behavior of some seed quality traits in Upland cotton ( <i>Gossypum hirsutum</i> L.). <i>Euphytica</i> , <b>2003</b> , 129, 183-191	2.1	45
14	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> , <b>2002</b> , 105, 964-971	6	10
13	Mapping epigenetic quantitative trait loci (QTL) altering a developmental trajectory. <i>Genome</i> , <b>2002</b> , 45, 28-33	2.4	20
12	Genetic and genotype $\times$ environment interaction effects from embryo, endosperm, cytoplasm and maternal plant for rice grain shape traits of indica rice. <i>Field Crops Research</i> , <b>2000</b> , 68, 191-198	5.5	17
11	MIXED LINEAR MODEL APPROACHES FOR ANALYZING GENETIC MODELS OF COMPLEX QUANTITATIVE TRAITS. <i>Journal of Zhejiang University Science B</i> , <b>2000</b> , 1, 78		4
10	Molecular Marker-Assisted Dissection of Genotype $\times$ Environment Interaction for Plant Type Traits in Rice ( <i>Oryza sativa</i> L.). <i>Crop Science</i> , <b>1999</b> , 39, 538-544	2.4	77
9	An approach for predicting heterosis based on an additive, dominance and additive $\times$ additive model with environment interaction. <i>Heredity</i> , <b>1999</b> , 82 ( Pt 5), 510-7	3.6	27
8	Genetic effects of embryo and endosperm for four malting quality traits of barley. <i>Euphytica</i> , <b>1999</b> , 106, 27-34	2.1	7

7	Genetic effects and genotype × environment interactions for cooking quality traits in Indica-japonica crosses of rice ( <i>Oryza sativa</i> L.). <i>Euphytica</i> , <b>1999</b> , 109, 9-15	2.1	12
6	Genetic analysis for protein content in indica rice. <i>Euphytica</i> , <b>1999</b> , 107, 135-140	2.1	23
5	Molecular dissection of developmental behavior of plant height in rice ( <i>Oryza sativa</i> L.). <i>Genetics</i> , <b>1998</b> , 150, 1257-65	4	127
4	Developmental quantitative genetics, conditional epigenetic variability and growth in mice. <i>Genetics</i> , <b>1997</b> , 147, 765-76	4	126
3	Genetic studies of anther culture ability in rice ( <i>Oryza sativa</i> ). <i>Plant Cell, Tissue and Organ Culture</i> , <b>1996</b> , 45, 253-258	2.7	18
2	Mixed model approaches for diallel analysis based on a bio-model. <i>Genetical Research</i> , <b>1996</b> , 68, 233-40	1.1	34
1	THE GENETIC BASIS OF LIFE-HISTORY CHARACTERS IN A POLYCHAETE EXHIBITING PLANKTOTROPHY AND LECITHOTROPHY. <i>Evolution; International Journal of Organic Evolution</i> , <b>1991</b> , 45, 380-397	3.8	94