

# Jun Zhu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6467831/publications.pdf>

Version: 2024-02-01

79  
papers

4,219  
citations

230014

27  
h-index

129628

63  
g-index

79  
all docs

79  
docs citations

79  
times ranked

5982  
citing authors

#	ARTICLE	IF	CITATIONS
1	Subsampling Technique to Estimate Variance Component for UK-Biobank Traits. <i>Frontiers in Genetics</i> , 2021, 12, 612045.	1.1	0
2	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.	1.1	0
3	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.	1.6	2
4	Conditional GWAS revealing genetic impacts of lifestyle behaviors on low-density lipoprotein (LDL). <i>Computational Biology and Chemistry</i> , 2019, 78, 497-503.	1.1	2
5	Genome-wide association study of maize plant architecture using F1 populations. <i>Plant Molecular Biology</i> , 2019, 99, 1-15.	2.0	17
6	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.	2.8	10
7	Dominance and Epistasis Interactions Revealed as Important Variants for Leaf Traits of Maize NAM Population. <i>Frontiers in Plant Science</i> , 2018, 9, 627.	1.7	24
8	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , 2018, 19, 451.	1.2	22
9	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.	1.4	28
10	Comparing GWAS Results of Complex Traits Using Full Genetic Model and Additive Models for Revealing Genetic Architecture. <i>Scientific Reports</i> , 2017, 7, 38600.	1.6	24
11	Dissecting genetic architecture of startle response in <i>Drosophila melanogaster</i> using multi-omics information. <i>Scientific Reports</i> , 2017, 7, 12367.	1.6	5
12	Genomic Prediction of Genotypic Effects with Epistasis and Environment Interactions for Yield-Related Traits of Rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Genetics</i> , 2017, 8, 15.	1.1	36
13	Dissecting Genetic Network of Fruit Branch Traits in Upland Cotton by Association Mapping Using SSR Markers. <i>PLoS ONE</i> , 2017, 12, e0162815.	1.1	8
14	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.	0.5	17
15	Mixed Linear Model Approaches of Association Mapping for Complex Traits Based on Omics Variants. <i>Scientific Reports</i> , 2015, 5, 10298.	1.6	47
16	Combined Analysis with Copy Number Variation Identifies Risk Loci in Lung Cancer. <i>BioMed Research International</i> , 2014, 2014, 1-9.	0.9	4
17	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.	1.1	55
18	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.	2.3	6

#	ARTICLE	IF	CITATIONS
19	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.	1.1	60
20	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. , 2013, , 301-315.		4
21	Simulating superior genotypes for plant height based on QTLs: Towards virtual breeding of rice. , 2012, , .		2
22	Statistical approaches in QTL mapping and molecular breeding for complex traits. <i>Science Bulletin</i> , 2012, 57, 2637-2644.	1.7	12
23	Quantitative genetic analysis station for the genetic analysis of complex traits. <i>Science Bulletin</i> , 2012, 57, 2721-2726.	1.7	13
24	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.	1.7	4
25	Dissecting anxiety-related QTLs in mice by univariate and multivariate mapping. <i>Science Bulletin</i> , 2012, 57, 2727-2732.	1.7	0
26	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, 515-531.	1.8	41
27	Penalized Independence Rule for Testing High-Dimensional Hypotheses. <i>Communications in Statistics - Theory and Methods</i> , 2011, 40, 2424-2435.	0.6	0
28	Practical and Theoretical Considerations in Study Design for Detecting Gene-Gene Interactions Using MDR and GMDR Approaches. <i>PLoS ONE</i> , 2011, 6, e16981.	1.1	45
29	Functional Mapping of Dynamic Traits with Robust t-Distribution. <i>PLoS ONE</i> , 2011, 6, e24902.	1.1	7
30	A functionalâ€“structural model of rice linking quantitative genetic information with morphological development and physiological processes. <i>Annals of Botany</i> , 2011, 107, 817-828.	1.4	71
31	A faster pedigree-based generalized multifactor dimensionality reduction method for detecting gene-gene interactions. <i>Statistics and Its Interface</i> , 2011, 4, 295-304.	0.2	11
32	QTLNetworkR: an interactive R package for QTL visualization. <i>Journal of Zhejiang University: Science B</i> , 2010, 11, 512-515.	1.3	2
33	Analysis of the 3â€“ 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, 708-718.	1.3	6
34	Identifying differentially expressed genes in human acute leukemia and mouse brain microarray datasets utilizing QTModel. <i>Functional and Integrative Genomics</i> , 2009, 9, 59-66.	1.4	2
35	Quantitative analysis and QTL mapping for agronomic and fiber traits in an RI population of upland cotton. <i>Euphytica</i> , 2009, 165, 231-245.	0.6	105
36	Analysis of genetic effects of nuclearâ€“cytoplasmic interaction on quantitative traits: Genetic models for seed traits of plants. <i>Theoretical and Applied Genetics</i> , 2008, 116, 769-776.	1.8	1

#	ARTICLE	IF	CITATIONS
37	Using matrix of thresholding partial correlation coefficients to infer regulatory network. <i>BioSystems</i> , 2008, 91, 158-165.	0.9	21
38	Influence of outliers on QTL mapping for complex traits. <i>Journal of Zhejiang University: Science B</i> , 2008, 9, 931-937.	1.3	6
39	A Combinatorial Approach to Detecting Gene-Gene and Gene-Environment Interactions in Family Studies. <i>American Journal of Human Genetics</i> , 2008, 83, 457-467.	2.6	90
40	QTLNetwork: mapping and visualizing genetic architecture of complex traits in experimental populations. <i>Bioinformatics</i> , 2008, 24, 721-723.	1.8	396
41	Nonparametric Functional Mapping of Quantitative Trait Loci Underlying Programmed Cell Death. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article4.	0.2	9
42	Mapping Interspecific Genetic Architecture in a Host-Parasite Interaction System. <i>Genetics</i> , 2008, 178, 1737-1743.	1.2	6
43	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, 1125-1137.	2.6	533
44	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, 562-568.	1.7	2
45	Mapping the genetic architecture of complex traits in experimental populations. <i>Bioinformatics</i> , 2007, 23, 1527-1536.	1.8	299
46	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.	1.3	1
47	Mapping QTLs with digenic epistasis under multiple environments and predicting heterosis based on QTL effects. <i>Theoretical and Applied Genetics</i> , 2007, 115, 325-333.	1.8	26
48	Functional mapping for genetic control of programmed cell death. <i>Physiological Genomics</i> , 2006, 25, 458-469.	1.0	39
49	A robust statistical procedure to discover expression biomarkers using microarray genomic expression data. <i>Journal of Zhejiang University: Science B</i> , 2006, 7, 603-607.	1.3	10
50	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.	0.8	29
51	Impacts of QTL $\times$ Environment Interactions on Genetic Response to Marker-Assisted Selection. <i>Journal of Genetics and Genomics</i> , 2006, 33, 63-71.	0.3	11
52	Mapping QTL for Biomass Yield and Its Components in Rice ( <i>Oryza sativa</i> L.). <i>Journal of Genetics and Genomics</i> , 2006, 33, 607-616.	0.3	27
53	Improvement of Mapping Accuracy by Unifying Linkage and Association Analysis. <i>Genetics</i> , 2006, 172, 647-661.	1.2	8
54	Clustering Gene Expression Data Based on Predicted Differential Effects of GV Interaction. <i>Genomics, Proteomics and Bioinformatics</i> , 2005, 3, 36-41.	3.0	3

#	ARTICLE	IF	CITATIONS
55	An integrative genomics approach to infer causal associations between gene expression and disease. <i>Nature Genetics</i> , 2005, 37, 710-717.	9.4	967
56	A two-step strategy for detecting differential gene expression in cDNA microarray data. <i>Current Genetics</i> , 2005, 47, 121-131.	0.8	12
57	Methods for predicting superior genotypes under multiple environments based on QTL effects. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1268-1274.	1.8	132
58	Genetic control of the opaque-2 gene and background polygenes over some kernel traits in maize ( <i>Zea mays</i> L.) overlock 1005.	0.5	0
59	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, 6B, 382-388.	0.4	31
60	A Unified Statistical Model for Functional Mapping of Environment-Dependent Genetic Expression and Genotype $\times$ Environment Interactions for Ontogenetic Development. <i>Genetics</i> , 2004, 168, 1751-1762.	1.2	30
61	Genetic association of yield with its component traits in a recombinant inbred line population of cotton. <i>Euphytica</i> , 2004, 140, 171-179.	0.6	25
62	Marker-assisted selection in segregating generations of self-fertilizing crops. <i>Theoretical and Applied Genetics</i> , 2004, 109, 370-376.	1.8	30
63	A method for marker-assisted selection based on QTLs with epistatic effects. <i>Genetica</i> , 2003, 119, 75-86.	0.5	28
64	Title is missing!. <i>Euphytica</i> , 2003, 129, 183-191.	0.6	50
65	Mapping epigenetic quantitative trait loci (QTL) altering a developmental trajectory. <i>Genome</i> , 2002, 45, 28-33.	0.9	21
66	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.	1.8	10
67	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> , 2000, 68, 191-198.	2.3	22
68	MIXED LINEAR MODEL APPROACHES FOR ANALYZING GENETIC MODELS OF COMPLEX QUANTITATIVE TRAITS. <i>Journal of Zhejiang University Science B</i> , 2000, 1, 78.	0.4	5
69	Molecular Marker-Assisted Dissection of Genotype $\times$ Environment Interaction for Plant Type Traits in Rice ( <i>Oryza sativa</i> L.). <i>Crop Science</i> , 1999, 39, 538-544.	0.8	91
70	An approach for predicting heterosis based on an additive, dominance and additive $\times$ additive model with environment interaction. <i>Heredity</i> , 1999, 82, 510-517.	1.2	28
71	Genetic effects of embryo and endosperm for four malting quality traits of barley. <i>Euphytica</i> , 1999, 106, 27-34.	0.6	8
72	Title is missing!. <i>Euphytica</i> , 1999, 109, 9-15.	0.6	13

#	ARTICLE	IF	CITATIONS
73	Genetic analysis for protein content in indica rice. <i>Euphytica</i> , 1999, 107, 135-140.	0.6	29
74	Molecular Dissection of Developmental Behavior of Plant Height in Rice ( <i>Oryza sativa</i> L.). <i>Genetics</i> , 1998, 150, 1257-1265.	1.2	144
75	Advanced Topics in Biomathematics. , 1998, , .		1
76	Developmental Quantitative Genetics, Conditional Epigenetic Variability and Growth in Mice. <i>Genetics</i> , 1997, 147, 765-776.	1.2	152
77	Genetic studies of anther culture ability in rice ( <i>Oryza sativa</i> ). <i>Plant Cell, Tissue and Organ Culture</i> , 1996, 45, 253-258.	1.2	26
78	Mixed model approaches for diallel analysis based on a bio-model. <i>Genetical Research</i> , 1996, 68, 233-240.	0.3	42
79	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.	1.1	105