Shizhong Xu

List of Publications by Year
in descending order

125 papers	6,063 citations	66343 42 h-index	76900 74 g-index
136 all docs	136 docs citations	136 times ranked	4898 citing authors

#	Article	IF	Citations
1	Estimating genetic variance contributed by a quantitative trait locus: A random model approach. PLoS Computational Biology, 2022, 18, e1009923.	3.2	1
2	Incorporation of parental phenotypic data into multi‐omic models improves prediction of yield‐related traits in hybrid rice. Plant Biotechnology Journal, 2021, 19, 261-272.	8.3	27
3	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. NAR Genomics and Bioinformatics, 2021, 3, lqab060.	3.2	1
4	Genomic selection: A breakthrough technology in rice breeding. Crop Journal, 2021, 9, 669-677.	5.2	55
5	Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. Genetics, 2021, 219, .	2.9	4
6	Genetic Dissection of Hybrid Performance and Heterosis for Yield-Related Traits in Maize. Frontiers in Plant Science, 2021, 12, 774478.	3.6	15
7	Hybrid breeding of rice via genomic selection. Plant Biotechnology Journal, 2020, 18, 57-67.	8.3	87
8	Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. Genomics, 2020, 112, 225-236.	2.9	32
9	GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. NAR Genomics and Bioinformatics, 2020, 2, lqz009.	3.2	2
10	Genome-wide association studies using binned genotypes. Heredity, 2020, 124, 288-298.	2.6	5
11	Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. Genetics, 2020, 216, 781-804.	2.9	15
12	Accurate Prediction of a Quantitative Trait Using the Genes Controlling the Trait for Gene-Based Breeding in Cotton. Frontiers in Plant Science, 2020, 11, 583277.	3.6	14
13	Deshrinking ridge regression for genome-wide association studies. Bioinformatics, 2020, 36, 4154-4162.	4.1	6
14	Rapid epistatic mixed-model association studies by controlling multiple polygenic effects. Bioinformatics, 2020, 36, 4833-4837.	4.1	14
15	A genome-wide association and meta-analysis reveal regions associated with seed size in cowpea [Vigna unguiculata (L.) Walp]. Theoretical and Applied Genetics, 2019, 132, 3079-3087.	3.6	42
16	Mapping quantitative trait loci using binned genotypes. Journal of Genetics and Genomics, 2019, 46, 343-352.	3.9	2
17	Efficient multivariate analysis algorithms for longitudinal genome-wide association studies. Bioinformatics, 2019, 35, 4879-4885.	4.1	19
18	Statistics of Mendelian segregation—A mixture model. Journal of Animal Breeding and Genetics, 2019, 136, 341-350.	2.0	7

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19	Statistical power in genome-wide association studies and quantitative trait locus mapping. Heredity, 2019, 123, 287-306.	2.6	68
20	A directed learning strategy integrating multiple omic data improves genomic prediction. Plant Biotechnology Journal, 2019, 17, 2011-2020.	8.3	29
21	A coordinate descent approach for sparse Bayesian learning in high dimensional QTL mapping and genome-wide association studies. Bioinformatics, 2019, 35, 4327-4335.	4.1	2
22	An alternative derivation of Harville's restricted log likelihood function for variance component estimation. Biometrical Journal, 2019, 61, 157-161.	1.0	1
23	GWASpro: a high-performance genome-wide association analysis server. Bioinformatics, 2019, 35, 2512-2514.	4.1	18
24	Identification of QTL controlling domestication-related traits in cowpea (Vigna unguiculata L. Walp). Scientific Reports, 2018, 8, 6261.	3.3	105
25	A multiâ€parent advanced generation interâ€cross (<scp>MAGIC</scp>) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). Plant Journal, 2018, 93, 1129-1142.	5.7	132
26	A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values. Bioinformatics, 2018, 34, 1817-1825.	4.1	18
27	JRmGRN: joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. Bioinformatics, 2018, 34, 3470-3478.	4.1	19
28	Genome-Wide Analysis of Grain Yield Stability and Environmental Interactions in a Multiparental Soybean Population. G3: Genes, Genomes, Genetics, 2018, 8, 519-529.	1.8	75
29	2D association and integrative omics analysis in rice provides systems biology view in trait analysis. Communications Biology, 2018, 1, 153.	4.4	4
30	Simultaneous Improvement and Genetic Dissection of Drought Tolerance Using Selected Breeding Populations of Rice. Frontiers in Plant Science, 2018, 9, 320.	3.6	19
31	Predicted Residual Error Sum of Squares of Mixed Models: An Application for Genomic Prediction. G3: Genes, Genomes, Genetics, 2017, 7, 895-909.	1.8	34
32	Multiple locus genome-wide association studies for important economic traits of oil palm. Tree Genetics and Genomes, 2017, 13, 1.	1.6	24
33	A Mixed Model Approach to Genome-Wide Association Studies for Selection Signatures, with Application to Mice Bred for Voluntary Exercise Behavior. Genetics, 2017, 207, 785-799.	2.9	15
34	Genomic prediction using subsampling. BMC Bioinformatics, 2017, 18, 191.	2.6	17
35	High Density Linkage Map Construction and Mapping of Yield Trait QTLs in Maize (Zea mays) Using the Genotyping-by-Sequencing (GBS) Technology. Frontiers in Plant Science, 2017, 8, 706.	3.6	78
36	PEPIS: A Pipeline for Estimating Epistatic Effects in Quantitative Trait Locus Mapping and Genome-Wide Association Studies. PLoS Computational Biology, 2016, 12, e1004925.	3.2	23

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37	Detection of additive and additiveÃ—environment interaction effects of QTLs for yieldâ€component traits of rice using singleâ€segment substitution lines (SSSLs). Plant Breeding, 2016, 135, 452-458.	1.9	42
38	Metabolomic prediction of yield in hybrid rice. Plant Journal, 2016, 88, 219-227.	5.7	120
39	Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. Scientific Reports, 2016, 6, 19444.	3.3	479
40	Genomeâ€wide dissection of the maize ear genetic architecture using multiple populations. New Phytologist, 2016, 210, 1095-1106.	7.3	142
41	A Random-Model Approach to QTL Mapping in Multiparent Advanced Generation Intercross (MAGIC) Populations. Genetics, 2016, 202, 471-486.	2.9	71
42	Population genomic analyses from lowâ€coverage <scp>RAD</scp>â€Seq data: a case study on the nonâ€model cucurbit bottle gourd. Plant Journal, 2014, 77, 430-442.	5.7	80
43	Predicting hybrid performance in rice using genomic best linear unbiased prediction. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12456-12461.	7.1	194
44	Whole-Genome Quantitative Trait Locus Mapping Reveals Major Role of Epistasis on Yield of Rice. PLoS ONE, 2014, 9, e87330.	2.5	21
45	Mapping Quantitative Trait Loci by Controlling Polygenic Background Effects. Genetics, 2013, 195, 1209-1222.	2.9	111
46	Principles of Statistical Genomics. , 2013, , .		19
47	Genetic Mapping and Genomic Selection Using Recombination Breakpoint Data. Genetics, 2013, 195, 1103-1115.	2.9	59
48	Random Model Approach to QTL Mapping. , 2013, , 187-207.		0
49	Bayesian Multiple QTL Mapping. , 2013, , 223-256.		0
50	Empirical Bayesian QTL Mapping. , 2013, , 257-279.		0
51	QTL Mapping in Other Populations. , 2013, , 171-185.		1
52	Microarray Differential Expression Analysis. , 2013, , 283-302.		0
53	Hierarchical Clustering of Microarray Data. , 2013, , 303-319.		1
54	Model-Based Clustering of Microarray Data. , 2013, , 321-333.		0

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55	Gene-Specific Analysis of Variances. , 2013, , 335-342.		0
56	Recombination Fraction. , 2013, , 11-22.		2
57	Genetic Map Construction. , 2013, , 23-33.		0
58	Multipoint Analysis of Mendelian Loci. , 2013, , 35-49.		0
59	Basic Concepts of Quantitative Genetics. , 2013, , 53-60.		0
60	Map Functions. , 2013, , 3-10.		0
61	Major Gene Detection. , 2013, , 61-78.		0
62	Segregation Analysis. , 2013, , 79-93.		0
63	Genome Scanning for Quantitative Trait Loci. , 2013, , 95-108.		2
64	Interval Mapping. , 2013, , 109-129.		0
65	Interval Mapping for Ordinal Traits. , 2013, , 131-149.		0
66	Mapping Segregation Distortion Loci. , 2013, , 151-170.		0
67	Mapping QTL for Multiple Traits. , 2013, , 209-222.		3
68	Factor Analysis of Microarray Data. , 2013, , 343-353.		0
69	Classification of Tissue Samples Using Microarrays. , 2013, , 355-363.		0
70	Time-Course Microarray Data Analysis. , 2013, , 365-382.		1
71	Quantitative Trait-Associated Microarray Data Analysis. , 2013, , 383-394.		0
72	Mapping Expression Quantitative Trait Loci. , 2013, , 395-411.		0

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73	Testing Hardy–Weinberg disequilibrium using the generalized linear model. Genetical Research, 2012, 94, 319-330.	0.9	3
74	An Infinitesimal Model for Quantitative Trait Genomic Value Prediction. PLoS ONE, 2012, 7, e41336.	2.5	30
75	Adaptive Ridge Regression for Rare Variant Detection. PLoS ONE, 2012, 7, e44173.	2.5	7
76	An expectation and maximization algorithm for estimating QÂÃ—ÂE interaction effects. Theoretical and Applied Genetics, 2012, 124, 1375-1387.	3.6	3
77	Generalized linear mixed model for segregation distortion analysis. BMC Genetics, 2011, 12, 97.	2.7	18
78	Generalized linear model for interval mapping of quantitative trait loci. Theoretical and Applied Genetics, 2010, 121, 47-63.	3.6	37
79	Mapping Environment-Specific Quantitative Trait Loci. Genetics, 2010, 186, 1053-1066.	2.9	24
80	Methods of plant breeding in the genome era. Genetical Research, 2010, 92, 423-441.	0.9	20
81	Significance Test and Genome Selection in Bayesian Shrinkage Analysis. International Journal of Plant Genomics, 2010, 2010, 1-11.	2.2	42
82	PROC QTL–A SAS Procedure for Mapping Quantitative Trait Loci. International Journal of Plant Genomics, 2009, 2009, 1-3.	2.2	57
83	Mapping Quantitative Trait Loci Using Distorted Markers. International Journal of Plant Genomics, 2009, 2009, 1-11.	2.2	73
84	Quantitative Trait Locus Mapping Can Benefit From Segregation Distortion. Genetics, 2008, 180, 2201-2208.	2.9	197
85	Bayesian LASSO for Quantitative Trait Loci Mapping. Genetics, 2008, 179, 1045-1055.	2.9	291
86	Genomewide Analysis of Epistatic Effects for Quantitative Traits in Barley. Genetics, 2007, 175, 1955-1963.	2.9	107
87	Derivation of the Shrinkage Estimates of Quantitative Trait Locus Effects. Genetics, 2007, 177, 1255-1258.	2.9	13
88	Bayesian Shrinkage Analysis of Quantitative Trait Loci for Dynamic Traits. Genetics, 2007, 176, 1169-1185.	2.9	59
89	An Empirical Bayes Method for Estimating Epistatic Effects of Quantitative Trait Loci. Biometrics, 2007, 63, 513-521.	1.4	154
90	Bayesian Shrinkage Estimation of Quantitative Trait Loci Parameters. Genetics, 2005, 170, 465-480.	2.9	145

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91	Mapping Quantitative Trait Loci Using Naturally Occurring Genetic Variance Among Commercial Inbred Lines of Maize (Zea mays L.). Genetics, 2005, 169, 2267-2275.	2.9	138
92	Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. Genetics, 2004, 166, 1981-1993.	2.9	15
93	Correcting the bias in estimation of genetic variances contributed by individual QTL. Genetica, 2003, 119, 107-114.	1.1	16
94	An EM algorithm for mapping binary disease loci: application to fibrosarcoma in a four-way cross mouse family. Genetical Research, 2003, 82, 127-138.	0.9	43
95	Estimating Polygenic Effects Using Markers of the Entire Genome. Genetics, 2003, 163, 789-801.	2.9	337
96	Theoretical Basis of the Beavis Effect. Genetics, 2003, 165, 2259-2268.	2.9	399
97	QTL Analysis in Plants. , 2002, 195, 283-310.		11
98	Mapping quantitative trait loci with epistatic effects. Genetical Research, 2002, 79, 185-198.	0.9	73
99	Genetic control of the rate of wound healing in mice. Heredity, 2001, 86, 668-674.	2.6	83
100	Genetic control of the rate of wound healing in mice. Heredity, 2001, 86, 668-674.	2.6	6
101	Bayesian Mapping of Quantitative Trait Loci Under Complicated Mating Designs. Genetics, 2001, 157, 1759-1771.	2.9	70
102	Mapping quantitative trait loci in tetraploid populations. Genetical Research, 2000, 76, 105-115.	0.9	22
103	Maximum likelihood analysis of quantitative trait loci under selective genotyping. Heredity, 2000, 84, 525-537.	2.6	23
104	Bayesian Mapping of Quantitative Trait Loci for Complex Binary Traits. Genetics, 2000, 155, 1391-1403.	2.9	105
105	Multipoint Mapping of Viability and Segregation Distorting Loci Using Molecular Markers. Genetics, 2000, 155, 1439-1447.	2.9	105
106	Bayesian Mapping of Quantitative Trait Loci Under the Identity-by-Descent-Based Variance Component Model. Genetics, 2000, 156, 411-422.	2.9	50
107	Meiosis and the Evolution of Recombination at Low Mutation Rates. Genetics, 2000, 156, 449-456.	2.9	33
108	Mapping quantitative trait loci for complex binary traits in outbred populations. Heredity, 1999, 82, 668-676.	2.6	29

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109	Multipoint genetic mapping of quantitative trait loci with dominant markers in outbred populations. Genetica, 1999, 105, 281-291.	1.1	8
110	On the evolution of recombination and meiosis. Genetical Research, 1999, 73, 119-131.	0.9	23
111	A Random Model Approach to Mapping Quantitative Trait Loci for Complex Binary Traits in Outbred Populations. Genetics, 1999, 153, 1029-1040.	2.9	50
112	An embarrassment of riches: the stochastic generation of beneficial mutations. Genetica, 1998, 102/103, 145-155.	1.1	0
113	Iteratively reweighted least squares mapping of quantitative trait loci. Behavior Genetics, 1998, 28, 341-355.	2.1	61
114	Sib mating designs for mapping quantitative trait loci. Genetica, 1998, 104, 9-19.	1.1	3
115	Mapping quantitative trait loci for binary traits using a heterogeneous residual variance model: an application to Marek's disease susceptibility in chickens. Genetica, 1998, 104, 171-178.	1.1	29
116	Further investigation on the regression method of mapping quantitative trait loci. Heredity, 1998, 80, 364-373.	2.6	67
117	Efficiency of multistage marker-assisted selection in the improvement of multiple quantitative traits. Heredity, 1998, 80, 489-498.	2.6	51
118	Mapping quantitative trait loci for ordered categorical traits in four-way crosses. Heredity, 1998, 81, 214-224.	2.6	58
119	Strategies of Marker–Aided Recurrent Selection. Crop Science, 1998, 38, 1526-1535.	1.8	11
120	Multipoint genetic mapping of quantitative trait loci using a variable number of sibs per family. Genetical Research, 1998, 71, 73-83.	0.9	20
121	Efficiency of multistage marker-assisted selection in the improvement of multiple quantitative traits. Heredity, 1998, 80, 489-498.	2.6	4
122	Mapping Quantitative Trait Loci Using Multiple Families of Line Crosses. Genetics, 1998, 148, 517-524.	2.9	93
123	Combining Different Line Crosses for Mapping Quantitative Trait Loci Using the Identical by Descent-Based Variance Component Method. Genetics, 1998, 149, 1139-1146.	2.9	58
124	Mapping quantitative trait loci using four-way crosses. Genetical Research, 1996, 68, 175-181.	0.9	190
125	Mapping Quantitative Trait Loci for Complex Binary Diseases Using Line Crosses. Genetics, 1996, 143, 1417-1424.	2.9	116