

Shizhong Xu

List of Publications by Year in descending order

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125
papers

6,063
citations

66234

42
h-index

76769

74
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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. <i>PLoS Computational Biology</i> , 2022, 18, e1009923.	1.5	1
2	Incorporation of parental phenotypic data into multi-omic models improves prediction of yield-related traits in hybrid rice. <i>Plant Biotechnology Journal</i> , 2021, 19, 261-272.	4.1	27
3	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab060.	1.5	1
4	Genomic selection: A breakthrough technology in rice breeding. <i>Crop Journal</i> , 2021, 9, 669-677.	2.3	55
5	Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. <i>Genetics</i> , 2021, 219, .	1.2	4
6	Genetic Dissection of Hybrid Performance and Heterosis for Yield-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 774478.	1.7	15
7	Hybrid breeding of rice via genomic selection. <i>Plant Biotechnology Journal</i> , 2020, 18, 57-67.	4.1	87
8	Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. <i>Genomics</i> , 2020, 112, 225-236.	1.3	32
9	GPU empowered pipelines for calculating genome-wide kinship matrices with ultra-high dimensional genetic variants and facilitating 1D and 2D GWAS. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz009.	1.5	2
10	Genome-wide association studies using binned genotypes. <i>Heredity</i> , 2020, 124, 288-298.	1.2	5
11	Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. <i>Genetics</i> , 2020, 216, 781-804.	1.2	15
12	Accurate Prediction of a Quantitative Trait Using the Genes Controlling the Trait for Gene-Based Breeding in Cotton. <i>Frontiers in Plant Science</i> , 2020, 11, 583277.	1.7	14
13	Deshrinking ridge regression for genome-wide association studies. <i>Bioinformatics</i> , 2020, 36, 4154-4162.	1.8	6
14	Rapid epistatic mixed-model association studies by controlling multiple polygenic effects. <i>Bioinformatics</i> , 2020, 36, 4833-4837.	1.8	14
15	A genome-wide association and meta-analysis reveal regions associated with seed size in cowpea [<i>Vigna unguiculata</i> (L.) Walp]. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3079-3087.	1.8	42
16	Mapping quantitative trait loci using binned genotypes. <i>Journal of Genetics and Genomics</i> , 2019, 46, 343-352.	1.7	2
17	Efficient multivariate analysis algorithms for longitudinal genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 4879-4885.	1.8	19
18	Statistics of Mendelian segregation—A mixture model. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 341-350.	0.8	7

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19	Statistical power in genome-wide association studies and quantitative trait locus mapping. <i>Heredity</i> , 2019, 123, 287-306.	1.2	68
20	A directed learning strategy integrating multiple omic data improves genomic prediction. <i>Plant Biotechnology Journal</i> , 2019, 17, 2011-2020.	4.1	29
21	A coordinate descent approach for sparse Bayesian learning in high dimensional QTL mapping and genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 4327-4335.	1.8	2
22	An alternative derivation of Harville's restricted log likelihood function for variance component estimation. <i>Biometrical Journal</i> , 2019, 61, 157-161.	0.6	1
23	CWASpro: a high-performance genome-wide association analysis server. <i>Bioinformatics</i> , 2019, 35, 2512-2514.	1.8	18
24	Identification of QTL controlling domestication-related traits in cowpea (<i>Vigna unguiculata</i> L. Walp). <i>Scientific Reports</i> , 2018, 8, 6261.	1.6	105
25	A multi-parent advanced generation inter-cross (MAGIC) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). <i>Plant Journal</i> , 2018, 93, 1129-1142.	2.8	132
26	A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values. <i>Bioinformatics</i> , 2018, 34, 1817-1825.	1.8	18
27	JRmGRN: joint reconstruction of multiple gene regulatory networks with common hub genes using data from multiple tissues or conditions. <i>Bioinformatics</i> , 2018, 34, 3470-3478.	1.8	19
28	Genome-Wide Analysis of Grain Yield Stability and Environmental Interactions in a Multiparental Soybean Population. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 519-529.	0.8	75
29	2D association and integrative omics analysis in rice provides systems biology view in trait analysis. <i>Communications Biology</i> , 2018, 1, 153.	2.0	4
30	Simultaneous Improvement and Genetic Dissection of Drought Tolerance Using Selected Breeding Populations of Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 320.	1.7	19
31	Predicted Residual Error Sum of Squares of Mixed Models: An Application for Genomic Prediction. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 895-909.	0.8	34
32	Multiple locus genome-wide association studies for important economic traits of oil palm. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	24
33	A Mixed Model Approach to Genome-Wide Association Studies for Selection Signatures, with Application to Mice Bred for Voluntary Exercise Behavior. <i>Genetics</i> , 2017, 207, 785-799.	1.2	15
34	Genomic prediction using subsampling. <i>BMC Bioinformatics</i> , 2017, 18, 191.	1.2	17
35	High Density Linkage Map Construction and Mapping of Yield Trait QTLs in Maize (<i>Zea mays</i>) Using the Genotyping-by-Sequencing (GBS) Technology. <i>Frontiers in Plant Science</i> , 2017, 8, 706.	1.7	78
36	PEPIS: A Pipeline for Estimating Epistatic Effects in Quantitative Trait Locus Mapping and Genome-Wide Association Studies. <i>PLoS Computational Biology</i> , 2016, 12, e1004925.	1.5	23

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37	Detection of additive and additive×environment interaction effects of QTLs for yield component traits of rice using single segment substitution lines (SSSLs). <i>Plant Breeding</i> , 2016, 135, 452-458.	1.0	42
38	Metabolomic prediction of yield in hybrid rice. <i>Plant Journal</i> , 2016, 88, 219-227.	2.8	120
39	Improving power and accuracy of genome-wide association studies via a multi-locus mixed linear model methodology. <i>Scientific Reports</i> , 2016, 6, 19444.	1.6	479
40	Genome-wide dissection of the maize ear genetic architecture using multiple populations. <i>New Phytologist</i> , 2016, 210, 1095-1106.	3.5	142
41	A Random-Model Approach to QTL Mapping in Multiparent Advanced Generation Intercross (MAGIC) Populations. <i>Genetics</i> , 2016, 202, 471-486.	1.2	71
42	Population genomic analyses from low coverage RAD-seq data: a case study on the non-model cucurbit bottle gourd. <i>Plant Journal</i> , 2014, 77, 430-442.	2.8	80
43	Predicting hybrid performance in rice using genomic best linear unbiased prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12456-12461.	3.3	194
44	Whole-Genome Quantitative Trait Locus Mapping Reveals Major Role of Epistasis on Yield of Rice. <i>PLoS ONE</i> , 2014, 9, e87330.	1.1	21
45	Mapping Quantitative Trait Loci by Controlling Polygenic Background Effects. <i>Genetics</i> , 2013, 195, 1209-1222.	1.2	111
46	<i>Principles of Statistical Genomics</i> . , 2013, , .		19
47	Genetic Mapping and Genomic Selection Using Recombination Breakpoint Data. <i>Genetics</i> , 2013, 195, 1103-1115.	1.2	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. <i>Genetical Research</i> , 2012, 94, 319-330.	0.3	3
74	An Infinitesimal Model for Quantitative Trait Genomic Value Prediction. <i>PLoS ONE</i> , 2012, 7, e41336.	1.1	30
75	Adaptive Ridge Regression for Rare Variant Detection. <i>PLoS ONE</i> , 2012, 7, e44173.	1.1	7
76	An expectation and maximization algorithm for estimating Q \times E interaction effects. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1375-1387.	1.8	3
77	Generalized linear mixed model for segregation distortion analysis. <i>BMC Genetics</i> , 2011, 12, 97.	2.7	18
78	Generalized linear model for interval mapping of quantitative trait loci. <i>Theoretical and Applied Genetics</i> , 2010, 121, 47-63.	1.8	37
79	Mapping Environment-Specific Quantitative Trait Loci. <i>Genetics</i> , 2010, 186, 1053-1066.	1.2	24
80	Methods of plant breeding in the genome era. <i>Genetical Research</i> , 2010, 92, 423-441.	0.3	20
81	Significance Test and Genome Selection in Bayesian Shrinkage Analysis. <i>International Journal of Plant Genomics</i> , 2010, 2010, 1-11.	2.2	42
82	PROC QTL—A SAS Procedure for Mapping Quantitative Trait Loci. <i>International Journal of Plant Genomics</i> , 2009, 2009, 1-3.	2.2	57
83	Mapping Quantitative Trait Loci Using Distorted Markers. <i>International Journal of Plant Genomics</i> , 2009, 2009, 1-11.	2.2	73
84	Quantitative Trait Locus Mapping Can Benefit From Segregation Distortion. <i>Genetics</i> , 2008, 180, 2201-2208.	1.2	197
85	Bayesian LASSO for Quantitative Trait Loci Mapping. <i>Genetics</i> , 2008, 179, 1045-1055.	1.2	291
86	Genomewide Analysis of Epistatic Effects for Quantitative Traits in Barley. <i>Genetics</i> , 2007, 175, 1955-1963.	1.2	107
87	Derivation of the Shrinkage Estimates of Quantitative Trait Locus Effects. <i>Genetics</i> , 2007, 177, 1255-1258.	1.2	13
88	Bayesian Shrinkage Analysis of Quantitative Trait Loci for Dynamic Traits. <i>Genetics</i> , 2007, 176, 1169-1185.	1.2	59
89	An Empirical Bayes Method for Estimating Epistatic Effects of Quantitative Trait Loci. <i>Biometrics</i> , 2007, 63, 513-521.	0.8	154
90	Bayesian Shrinkage Estimation of Quantitative Trait Loci Parameters. <i>Genetics</i> , 2005, 170, 465-480.	1.2	145

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91	Mapping Quantitative Trait Loci Using Naturally Occurring Genetic Variance Among Commercial Inbred Lines of Maize (<i>Zea mays</i> L.). <i>Genetics</i> , 2005, 169, 2267-2275.	1.2	138
92	Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. <i>Genetics</i> , 2004, 166, 1981-1993.	1.2	15
93	Correcting the bias in estimation of genetic variances contributed by individual QTL. <i>Genetica</i> , 2003, 119, 107-114.	0.5	16
94	An EM algorithm for mapping binary disease loci: application to fibrosarcoma in a four-way cross mouse family. <i>Genetical Research</i> , 2003, 82, 127-138.	0.3	43
95	Estimating Polygenic Effects Using Markers of the Entire Genome. <i>Genetics</i> , 2003, 163, 789-801.	1.2	337
96	Theoretical Basis of the Beavis Effect. <i>Genetics</i> , 2003, 165, 2259-2268.	1.2	399
97	QTL Analysis in Plants. , 2002, 195, 283-310.		11
98	Mapping quantitative trait loci with epistatic effects. <i>Genetical Research</i> , 2002, 79, 185-198.	0.3	73
99	Genetic control of the rate of wound healing in mice. <i>Heredity</i> , 2001, 86, 668-674.	1.2	83
100	Bayesian Mapping of Quantitative Trait Loci Under Complicated Mating Designs. <i>Genetics</i> , 2001, 157, 1759-1771.	1.2	70
101	Mapping quantitative trait loci in tetraploid populations. <i>Genetical Research</i> , 2000, 76, 105-115.	0.3	22
102	Maximum likelihood analysis of quantitative trait loci under selective genotyping. <i>Heredity</i> , 2000, 84, 525-537.	1.2	23
103	Bayesian Mapping of Quantitative Trait Loci for Complex Binary Traits. <i>Genetics</i> , 2000, 155, 1391-1403.	1.2	105
104	Multipoint Mapping of Viability and Segregation Distorting Loci Using Molecular Markers. <i>Genetics</i> , 2000, 155, 1439-1447.	1.2	105
105	Bayesian Mapping of Quantitative Trait Loci Under the Identity-by-Descent-Based Variance Component Model. <i>Genetics</i> , 2000, 156, 411-422.	1.2	50
106	Meiosis and the Evolution of Recombination at Low Mutation Rates. <i>Genetics</i> , 2000, 156, 449-456.	1.2	33
107	Mapping quantitative trait loci for complex binary traits in outbred populations. <i>Heredity</i> , 1999, 82, 668-676.	1.2	29
108	Multipoint genetic mapping of quantitative trait loci with dominant markers in outbred populations. <i>Genetica</i> , 1999, 105, 281-291.	0.5	8

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109	On the evolution of recombination and meiosis. <i>Genetical Research</i> , 1999, 73, 119-131.	0.3	23
110	A Random Model Approach to Mapping Quantitative Trait Loci for Complex Binary Traits in Outbred Populations. <i>Genetics</i> , 1999, 153, 1029-1040.	1.2	50
111	An embarrassment of riches: the stochastic generation of beneficial mutations. <i>Genetica</i> , 1998, 102/103, 145-155.	0.5	0
112	Iteratively reweighted least squares mapping of quantitative trait loci. <i>Behavior Genetics</i> , 1998, 28, 341-355.	1.4	61
113	Sib mating designs for mapping quantitative trait loci. <i>Genetica</i> , 1998, 104, 9-19.	0.5	3
114	Mapping quantitative trait loci for binary traits using a heterogeneous residual variance model: an application to Marek's disease susceptibility in chickens. <i>Genetica</i> , 1998, 104, 171-178.	0.5	29
115	Further investigation on the regression method of mapping quantitative trait loci. <i>Heredity</i> , 1998, 80, 364-373.	1.2	67
116	Efficiency of multistage marker-assisted selection in the improvement of multiple quantitative traits. <i>Heredity</i> , 1998, 80, 489-498.	1.2	51
117	Mapping quantitative trait loci for ordered categorical traits in four-way crosses. <i>Heredity</i> , 1998, 81, 214-224.	1.2	58
118	Strategies of Marker-Aided Recurrent Selection. <i>Crop Science</i> , 1998, 38, 1526-1535.	0.8	11
119	Multipoint genetic mapping of quantitative trait loci using a variable number of sibs per family. <i>Genetical Research</i> , 1998, 71, 73-83.	0.3	20
120	Efficiency of multistage marker-assisted selection in the improvement of multiple quantitative traits. <i>Heredity</i> , 1998, 80, 489-498.	1.2	4
121	Mapping Quantitative Trait Loci Using Multiple Families of Line Crosses. <i>Genetics</i> , 1998, 148, 517-524.	1.2	93
122	Combining Different Line Crosses for Mapping Quantitative Trait Loci Using the Identical by Descent-Based Variance Component Method. <i>Genetics</i> , 1998, 149, 1139-1146.	1.2	58
123	Mapping quantitative trait loci using four-way crosses. <i>Genetical Research</i> , 1996, 68, 175-181.	0.3	190
124	Mapping Quantitative Trait Loci for Complex Binary Diseases Using Line Crosses. <i>Genetics</i> , 1996, 143, 1417-1424.	1.2	116
125	Genetic control of the rate of wound healing in mice. , 0, .		6