

Shizhong Xu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/856291/publications.pdf>

Version: 2024-02-01

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 | 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 |
| 2 | Theoretical Basis of the Beavis Effect. Genetics, 2003, 165, 2259-2268. | 2.9 | 399 |
| 3 | Estimating Polygenic Effects Using Markers of the Entire Genome. Genetics, 2003, 163, 789-801. | 2.9 | 337 |
| 4 | Bayesian LASSO for Quantitative Trait Loci Mapping. Genetics, 2008, 179, 1045-1055. | 2.9 | 291 |
| 5 | Quantitative Trait Locus Mapping Can Benefit From Segregation Distortion. Genetics, 2008, 180, 2201-2208. | 2.9 | 197 |
| 6 | 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 |
| 7 | Mapping quantitative trait loci using four-way crosses. Genetical Research, 1996, 68, 175-181. | 0.9 | 190 |
| 8 | An Empirical Bayes Method for Estimating Epistatic Effects of Quantitative Trait Loci. Biometrics, 2007, 63, 513-521. | 1.4 | 154 |
| 9 | Bayesian Shrinkage Estimation of Quantitative Trait Loci Parameters. Genetics, 2005, 170, 465-480. | 2.9 | 145 |
| 10 | Genome-wide dissection of the maize ear genetic architecture using multiple populations. New Phytologist, 2016, 210, 1095-1106. | 7.3 | 142 |
| 11 | Mapping Quantitative Trait Loci Using Naturally Occurring Genetic Variance Among Commercial Inbred Lines of Maize (<i>Zea mays</i> L.). Genetics, 2005, 169, 2267-2275. | 2.9 | 138 |
| 12 | A multi-parent advanced generation inter-cross (<sc>MAGIC</sc>) population for genetic analysis and improvement of cowpea (<i>Vigna unguiculata</i> L. Walp.). Plant Journal, 2018, 93, 1129-1142. | 5.7 | 132 |
| 13 | Metabolomic prediction of yield in hybrid rice. Plant Journal, 2016, 88, 219-227. | 5.7 | 120 |
| 14 | Mapping Quantitative Trait Loci for Complex Binary Diseases Using Line Crosses. Genetics, 1996, 143, 1417-1424. | 2.9 | 116 |
| 15 | Mapping Quantitative Trait Loci by Controlling Polygenic Background Effects. Genetics, 2013, 195, 1209-1222. | 2.9 | 111 |
| 16 | Genomewide Analysis of Epistatic Effects for Quantitative Traits in Barley. Genetics, 2007, 175, 1955-1963. | 2.9 | 107 |
| 17 | Identification of QTL controlling domestication-related traits in cowpea (<i>Vigna unguiculata</i> L. Walp.). Scientific Reports, 2018, 8, 6261. | 3.3 | 105 |
| 18 | Bayesian Mapping of Quantitative Trait Loci for Complex Binary Traits. Genetics, 2000, 155, 1391-1403. | 2.9 | 105 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Multipoint Mapping of Viability and Segregation Distorting Loci Using Molecular Markers. <i>Genetics</i> , 2000, 155, 1439-1447. | 2.9 | 105 |
| 20 | Mapping Quantitative Trait Loci Using Multiple Families of Line Crosses. <i>Genetics</i> , 1998, 148, 517-524. | 2.9 | 93 |
| 21 | Hybrid breeding of rice via genomic selection. <i>Plant Biotechnology Journal</i> , 2020, 18, 57-67. | 8.3 | 87 |
| 22 | Genetic control of the rate of wound healing in mice. <i>Heredity</i> , 2001, 86, 668-674. | 2.6 | 83 |
| 23 | 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. | 5.7 | 80 |
| 24 | 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. | 3.6 | 78 |
| 25 | 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. | 1.8 | 75 |
| 26 | Mapping quantitative trait loci with epistatic effects. <i>Genetical Research</i> , 2002, 79, 185-198. | 0.9 | 73 |
| 27 | Mapping Quantitative Trait Loci Using Distorted Markers. <i>International Journal of Plant Genomics</i> , 2009, 2009, 1-11. | 2.2 | 73 |
| 28 | A Random-Model Approach to QTL Mapping in Multiparent Advanced Generation Intercross (MAGIC) Populations. <i>Genetics</i> , 2016, 202, 471-486. | 2.9 | 71 |
| 29 | Bayesian Mapping of Quantitative Trait Loci Under Complicated Mating Designs. <i>Genetics</i> , 2001, 157, 1759-1771. | 2.9 | 70 |
| 30 | Statistical power in genome-wide association studies and quantitative trait locus mapping. <i>Heredity</i> , 2019, 123, 287-306. | 2.6 | 68 |
| 31 | Further investigation on the regression method of mapping quantitative trait loci. <i>Heredity</i> , 1998, 80, 364-373. | 2.6 | 67 |
| 32 | Iteratively reweighted least squares mapping of quantitative trait loci. <i>Behavior Genetics</i> , 1998, 28, 341-355. | 2.1 | 61 |
| 33 | Bayesian Shrinkage Analysis of Quantitative Trait Loci for Dynamic Traits. <i>Genetics</i> , 2007, 176, 1169-1185. | 2.9 | 59 |
| 34 | Genetic Mapping and Genomic Selection Using Recombination Breakpoint Data. <i>Genetics</i> , 2013, 195, 1103-1115. | 2.9 | 59 |
| 35 | Mapping quantitative trait loci for ordered categorical traits in four-way crosses. <i>Heredity</i> , 1998, 81, 214-224. | 2.6 | 58 |
| 36 | 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. | 2.9 | 58 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | PROC QTL—A SAS Procedure for Mapping Quantitative Trait Loci. International Journal of Plant Genomics, 2009, 2009, 1-3. | 2.2 | 57 |
| 38 | Genomic selection: A breakthrough technology in rice breeding. Crop Journal, 2021, 9, 669-677. | 5.2 | 55 |
| 39 | Efficiency of multistage marker-assisted selection in the improvement of multiple quantitative traits. Heredity, 1998, 80, 489-498. | 2.6 | 51 |
| 40 | A Random Model Approach to Mapping Quantitative Trait Loci for Complex Binary Traits in Outbred Populations. Genetics, 1999, 153, 1029-1040. | 2.9 | 50 |
| 41 | Bayesian Mapping of Quantitative Trait Loci Under the Identity-by-Descent-Based Variance Component Model. Genetics, 2000, 156, 411-422. | 2.9 | 50 |
| 42 | 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 |
| 43 | Significance Test and Genome Selection in Bayesian Shrinkage Analysis. International Journal of Plant Genomics, 2010, 2010, 1-11. | 2.2 | 42 |
| 44 | Detection of additive and additive×environment interaction effects of QTLs for yield—component traits of rice using single—segment substitution lines (SSSLs). Plant Breeding, 2016, 135, 452-458. | 1.9 | 42 |
| 45 | 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 |
| 46 | Generalized linear model for interval mapping of quantitative trait loci. Theoretical and Applied Genetics, 2010, 121, 47-63. | 3.6 | 37 |
| 47 | 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 |
| 48 | Meiosis and the Evolution of Recombination at Low Mutation Rates. Genetics, 2000, 156, 449-456. | 2.9 | 33 |
| 49 | Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. Genomics, 2020, 112, 225-236. | 2.9 | 32 |
| 50 | An Infinitesimal Model for Quantitative Trait Genomic Value Prediction. PLoS ONE, 2012, 7, e41336. | 2.5 | 30 |
| 51 | 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 |
| 52 | Mapping quantitative trait loci for complex binary traits in outbred populations. Heredity, 1999, 82, 668-676. | 2.6 | 29 |
| 53 | A directed learning strategy integrating multiple omic data improves genomic prediction. Plant Biotechnology Journal, 2019, 17, 2011-2020. | 8.3 | 29 |
| 54 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 55 | Mapping Environment-Specific Quantitative Trait Loci. <i>Genetics</i> , 2010, 186, 1053-1066. | 2.9 | 24 |
| 56 | Multiple locus genome-wide association studies for important economic traits of oil palm. <i>Tree Genetics and Genomes</i> , 2017, 13, 1. | 1.6 | 24 |
| 57 | On the evolution of recombination and meiosis. <i>Genetical Research</i> , 1999, 73, 119-131. | 0.9 | 23 |
| 58 | Maximum likelihood analysis of quantitative trait loci under selective genotyping. <i>Heredity</i> , 2000, 84, 525-537. | 2.6 | 23 |
| 59 | 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. | 3.2 | 23 |
| 60 | Mapping quantitative trait loci in tetraploid populations. <i>Genetical Research</i> , 2000, 76, 105-115. | 0.9 | 22 |
| 61 | Whole-Genome Quantitative Trait Locus Mapping Reveals Major Role of Epistasis on Yield of Rice. <i>PLoS ONE</i> , 2014, 9, e87330. | 2.5 | 21 |
| 62 | Multipoint genetic mapping of quantitative trait loci using a variable number of sibs per family. <i>Genetical Research</i> , 1998, 71, 73-83. | 0.9 | 20 |
| 63 | Methods of plant breeding in the genome era. <i>Genetical Research</i> , 2010, 92, 423-441. | 0.9 | 20 |
| 64 | Principles of Statistical Genomics. , 2013, , . | | 19 |
| 65 | 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. | 4.1 | 19 |
| 66 | Simultaneous Improvement and Genetic Dissection of Drought Tolerance Using Selected Breeding Populations of Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 320. | 3.6 | 19 |
| 67 | Efficient multivariate analysis algorithms for longitudinal genome-wide association studies. <i>Bioinformatics</i> , 2019, 35, 4879-4885. | 4.1 | 19 |
| 68 | Generalized linear mixed model for segregation distortion analysis. <i>BMC Genetics</i> , 2011, 12, 97. | 2.7 | 18 |
| 69 | A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values. <i>Bioinformatics</i> , 2018, 34, 1817-1825. | 4.1 | 18 |
| 70 | GWASpro: a high-performance genome-wide association analysis server. <i>Bioinformatics</i> , 2019, 35, 2512-2514. | 4.1 | 18 |
| 71 | Genomic prediction using subsampling. <i>BMC Bioinformatics</i> , 2017, 18, 191. | 2.6 | 17 |
| 72 | Correcting the bias in estimation of genetic variances contributed by individual QTL. <i>Genetica</i> , 2003, 119, 107-114. | 1.1 | 16 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 73 | 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. | 2.9 | 15 |
| 74 | Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. <i>Genetics</i> , 2020, 216, 781-804. | 2.9 | 15 |
| 75 | Mapping Quantitative Trait Loci in F2 Incorporating Phenotypes of F3 Progeny. <i>Genetics</i> , 2004, 166, 1981-1993. | 2.9 | 15 |
| 76 | Genetic Dissection of Hybrid Performance and Heterosis for Yield-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 774478. | 3.6 | 15 |
| 77 | 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. | 3.6 | 14 |
| 78 | Rapid epistatic mixed-model association studies by controlling multiple polygenic effects. <i>Bioinformatics</i> , 2020, 36, 4833-4837. | 4.1 | 14 |
| 79 | Derivation of the Shrinkage Estimates of Quantitative Trait Locus Effects. <i>Genetics</i> , 2007, 177, 1255-1258. | 2.9 | 13 |
| 80 | Strategies of Marker-Aided Recurrent Selection. <i>Crop Science</i> , 1998, 38, 1526-1535. | 1.8 | 11 |
| 81 | QTL Analysis in Plants. , 2002, 195, 283-310. | | 11 |
| 82 | Multipoint genetic mapping of quantitative trait loci with dominant markers in outbred populations. <i>Genetica</i> , 1999, 105, 281-291. | 1.1 | 8 |
| 83 | Adaptive Ridge Regression for Rare Variant Detection. <i>PLoS ONE</i> , 2012, 7, e44173. | 2.5 | 7 |
| 84 | Statistics of Mendelian segregation—A mixture model. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 341-350. | 2.0 | 7 |
| 85 | Deshrinking ridge regression for genome-wide association studies. <i>Bioinformatics</i> , 2020, 36, 4154-4162. | 4.1 | 6 |
| 86 | Genetic control of the rate of wound healing in mice. <i>Heredity</i> , 2001, 86, 668-674. | 2.6 | 6 |
| 87 | Genome-wide association studies using binned genotypes. <i>Heredity</i> , 2020, 124, 288-298. | 2.6 | 5 |
| 88 | 2D association and integrative omics analysis in rice provides systems biology view in trait analysis. <i>Communications Biology</i> , 2018, 1, 153. | 4.4 | 4 |
| 89 | Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. <i>Genetics</i> , 2021, 219, . | 2.9 | 4 |
| 90 | Efficiency of multistage marker-assisted selection in the improvement of multiple quantitative traits. <i>Heredity</i> , 1998, 80, 489-498. | 2.6 | 4 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|-----|-----------|
| 91 | Sib mating designs for mapping quantitative trait loci. <i>Genetica</i> , 1998, 104, 9-19. | 1.1 | 3 |
| 92 | Testing Hardy-Weinberg disequilibrium using the generalized linear model. <i>Genetical Research</i> , 2012, 94, 319-330. | 0.9 | 3 |
| 93 | An expectation and maximization algorithm for estimating Q \times E interaction effects. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1375-1387. | 3.6 | 3 |
| 94 | Mapping QTL for Multiple Traits. , 2013, , 209-222. | | 3 |
| 95 | Recombination Fraction. , 2013, , 11-22. | | 2 |
| 96 | Genome Scanning for Quantitative Trait Loci. , 2013, , 95-108. | | 2 |
| 97 | Mapping quantitative trait loci using binned genotypes. <i>Journal of Genetics and Genomics</i> , 2019, 46, 343-352. | 3.9 | 2 |
| 98 | 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. | 4.1 | 2 |
| 99 | 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. | 3.2 | 2 |
| 100 | QTL Mapping in Other Populations. , 2013, , 171-185. | | 1 |
| 101 | Hierarchical Clustering of Microarray Data. , 2013, , 303-319. | | 1 |
| 102 | Time-Course Microarray Data Analysis. , 2013, , 365-382. | | 1 |
| 103 | An alternative derivation of Harville's restricted log likelihood function for variance component estimation. <i>Biometrical Journal</i> , 2019, 61, 157-161. | 1.0 | 1 |
| 104 | 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. | 3.2 | 1 |
| 105 | Estimating genetic variance contributed by a quantitative trait locus: A random model approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009923. | 3.2 | 1 |
| 106 | An embarrassment of riches: the stochastic generation of beneficial mutations. <i>Genetica</i> , 1998, 102/103, 145-155. | 1.1 | 0 |
| 107 | Random Model Approach to QTL Mapping. , 2013, , 187-207. | | 0 |
| 108 | Bayesian Multiple QTL Mapping. , 2013, , 223-256. | | 0 |

| # | ARTICLE | IF | CITATIONS |
|-----|--|----|-----------|
| 109 | Empirical Bayesian QTL Mapping. , 2013, , 257-279. | | 0 |
| 110 | Microarray Differential Expression Analysis. , 2013, , 283-302. | | 0 |
| 111 | Model-Based Clustering of Microarray Data. , 2013, , 321-333. | | 0 |
| 112 | Gene-Specific Analysis of Variances. , 2013, , 335-342. | | 0 |
| 113 | Genetic Map Construction. , 2013, , 23-33. | | 0 |
| 114 | Multipoint Analysis of Mendelian Loci. , 2013, , 35-49. | | 0 |
| 115 | Basic Concepts of Quantitative Genetics. , 2013, , 53-60. | | 0 |
| 116 | Map Functions. , 2013, , 3-10. | | 0 |
| 117 | Major Gene Detection. , 2013, , 61-78. | | 0 |
| 118 | Segregation Analysis. , 2013, , 79-93. | | 0 |
| 119 | Interval Mapping. , 2013, , 109-129. | | 0 |
| 120 | Interval Mapping for Ordinal Traits. , 2013, , 131-149. | | 0 |
| 121 | Mapping Segregation Distortion Loci. , 2013, , 151-170. | | 0 |
| 122 | Factor Analysis of Microarray Data. , 2013, , 343-353. | | 0 |
| 123 | Classification of Tissue Samples Using Microarrays. , 2013, , 355-363. | | 0 |
| 124 | Quantitative Trait-Associated Microarray Data Analysis. , 2013, , 383-394. | | 0 |
| 125 | Mapping Expression Quantitative Trait Loci. , 2013, , 395-411. | | 0 |