Zhao-Bang Zeng

List of Publications by Year
in descending order

34
papers	3,178
citations	331670
21
h-index	414414
32
g-index
41
all docs	41
docs citations	41
times ranked	2466
citing authors

#	Article	IF	Citations
1	Multiple Interval Mapping for Quantitative Trait Loci. Genetics, 1999, 152, 1203-1216.	2.9	797
2	Genotype-Environment Interaction for Quantitative Trait Loci Affecting Life Span in Drosophila melanogaster. Genetics, 2000, 154, 213-227.	2.9	303
3	Estimating the genetic architecture of quantitative traits. Genetical Research, 1999, 74, 279-289.	0.9	286
4	Genetic Analysis of a Morphological Shape Difference in the Male Genitalia of *Drosophila simulans* and *D. mauritiana*. Genetics, 1996, 142, 1129-1145.	2.9	209
5	Mapping quantitative trait loci with dominant and missing markers in various crosses from two inbred lines. Genetica, 1997, 101, 47-58.	1.1	200
6	Genetic Architecture of a Morphological Shape Difference Between Two Drosophila Species. Genetics, 2000, 154, 299-310.	2.9	180
7	Modeling Quantitative Trait Loci and Interpretation of Models. Genetics, 2005, 169, 1711-1725.	2.9	146
8	An Analysis of Polygenes Affecting Wing Shape on Chromosome 3 in Drosophila melanogaster. Genetics, 1999, 153, 773-786.	2.9	117
9	QUANTITATIVE GENETIC ANALYSIS OF DIVERGENCE IN MALE SECONDARY SEXUAL TRAITS BETWEEN *DROSOPHILA SIMULANS* AND *DROSOPHILA MAURITIANA*. Evolution; International Journal of Organic Evolution, 1997, 51, 816-832.	2.3	97
10	Composite Interval Mapping and Multiple Interval Mapping: Procedures and Guidelines for Using Windows QTL Cartographer. Methods in Molecular Biology, 2012, 871, 75-119.	0.9	95
11	A General Polyploid Model for Analyzing Gene Segregation in Outcrossing Tetraploid Species. Genetics, 2001, 159, 869-882.	2.9	84
12	Joint Linkage and Linkage Disequilibrium Mapping in Natural Populations. Genetics, 2001, 157, 899-909.	2.9	72
13	Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping. G3: Genes, Genomes, Genetics, 2020, 10, 281-292.	1.8	65
14	An Analysis of Polygenes Affecting Wing Shape on Chromosome 2 in *Drosophila melanogaster*. Genetics, 2001, 159, 1045-1057.	2.9	61
15	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β-carotene and starch content in hexaploid sweetpotato [Ipomoea batatas (L.) Lam.]. Theoretical and Applied Genetics, 2020, 133, 23-36.	3.6	59
16	Genomic Selection with Allele Dosage in *Panicum maximum* Jacq.. G3: Genes, Genomes, Genetics, 2019, 9, 2463-2475.	1.8	57
17	A general mixture model approach for mapping quantitative trait loci from diverse cross designs involving multiple inbred lines. Genetical Research, 2000, 75, 345-355.	0.9	56
18	Multiple QTL Mapping in Autopolyploids: A Random-Effect Model Approach with Application in a Hexaploid Sweetpotato Full-Sib Population. Genetics, 2020, 215, 579-595.	2.9	42

#	Article	IF	Citations
19	A Multivalent Pairing Model of Linkage Analysis in Autotetraploids. Genetics, 2001, 159, 1339-1350.	2.9	31
20	Mapping epistatic quantitative trait loci. BMC Genetics, 2014, 15, 112.	2.7	24
21	Sequencing depth and genotype quality: accuracy and breeding operation considerations for genomic selection applications in autopolyploid crops. Theoretical and Applied Genetics, 2020, 133, 3345-3363.	3.6	24
22	Multiple trait multiple interval mapping of quantitative trait loci from inbred line crosses. BMC Genetics, 2012, 13, 67.	2.7	23
23	Linkage map construction and QTL analysis for internal heat necrosis in autotetraploid potato. Theoretical and Applied Genetics, 2017, 130, 2045-2056.	3.6	22
24	QTL mapping and the genetic basis of adaptation: recent developments. Genetica, 2005, 123, 25-37.	1.1	20
25	Multiple trait multiple interval mapping of quantitative trait loci from inbred line crosses. BMC Genetics, 2012, 13, 67.	2.7	18
26	Discovery of a major QTL for root-knot nematode (Meloidogyne incognita) resistance in cultivated sweetpotato (Ipomoea batatas). Theoretical and Applied Genetics, 2021, 134, 1945-1955.	3.6	14
27	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. Nature Genetics, 2020, 52, 1256-1264.	21.4	13
28	Genetic Architecture of Natural Variation Underlying Adult Foraging Behavior That Is Essential for Survival of Drosophila melanogaster. Genome Biology and Evolution, 2017, 9, 1357-1369.	2.5	11
29	The recombination landscape and multiple QTL mapping in a Solanum tuberosum cv. â€˜Atlanticâ€™-derived F1 population. Heredity, 2021, 126, 817-830.	2.6	10
30	Quantitative trait loci influencing forking defects in an outbred pedigree of loblolly pine. BMC Genetics, 2016, 17, 138.	2.7	5
31	A genetic model of interpopulation variation and covariation of quantitative characters. Genetical Research, 1989, 53, 215-221.	0.9	3
32	Quantitative Trait Locus Mapping for Common Scab Resistance in a Tetraploid Potato Full-Sib Population. Plant Disease, 2021, 105, 3048-3054.	1.4	3
33	VIEWpoly: a visualization tool to integrate and explore results of polyploid genetic analysis. Journal of Open Source Software, 2022, 7, 4242.	4.6	2
34	The Hillâ€"Robertson effect is a consequence of interplay between linkage, selection and drift: a commentary on â€˜The effect of linkage on limits to artificial selectionâ€™ by W.ÂG. Hill and A. Robertson. Genetical Research, 2007, 89, 309-310.	0.9	0