

Zhao-Bang Zeng

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

3,178
citations

331670

21
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414414

32
g-index

41
all docs

41
docs citations

41
times ranked

2466
citing authors

#	ARTICLE	IF	CITATIONS
1	VIEWpoly: a visualization tool to integrate and explore results of polyploid genetic analysis. Journal of Open Source Software, 2022, 7, 4242.	4.6	2
2	The recombination landscape and multiple QTL mapping in a <i>Solanum tuberosum</i> cv. "Atlantic"-derived F1 population. Heredity, 2021, 126, 817-830.	2.6	10
3	Quantitative Trait Locus Mapping for Common Scab Resistance in a Tetraploid Potato Full-Sib Population. Plant Disease, 2021, 105, 3048-3054.	1.4	3
4	Discovery of a major QTL for root-knot nematode (<i>Meloidogyne incognita</i>) resistance in cultivated sweetpotato (<i>Ipomoea batatas</i>). Theoretical and Applied Genetics, 2021, 134, 1945-1955.	3.6	14
5	Quantitative trait loci and differential gene expression analyses reveal the genetic basis for negatively associated β -carotene and starch content in hexaploid sweetpotato [<i>Ipomoea batatas</i> (L.) Lam.]. Theoretical and Applied Genetics, 2020, 133, 23-36.	3.6	59
6	Assembly of whole-chromosome pseudomolecules for polyploid plant genomes using outbred mapping populations. Nature Genetics, 2020, 52, 1256-1264.	21.4	13
7	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
8	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
9	Unraveling the Hexaploid Sweetpotato Inheritance Using Ultra-Dense Multilocus Mapping. G3: Genes, Genomes, Genetics, 2020, 10, 281-292.	1.8	65
10	Genomic Selection with Allele Dosage in <i>Panicum maximum</i> Jacq.. G3: Genes, Genomes, Genetics, 2019, 9, 2463-2475.	1.8	57
11	Genetic Architecture of Natural Variation Underlying Adult Foraging Behavior That Is Essential for Survival of <i>Drosophila melanogaster</i> . Genome Biology and Evolution, 2017, 9, 1357-1369.	2.5	11
12	Linkage map construction and QTL analysis for internal heat necrosis in autotetraploid potato. Theoretical and Applied Genetics, 2017, 130, 2045-2056.	3.6	22
13	Quantitative trait loci influencing forking defects in an outbred pedigree of loblolly pine. BMC Genetics, 2016, 17, 138.	2.7	5
14	Mapping epistatic quantitative trait loci. BMC Genetics, 2014, 15, 112.	2.7	24
15	Multiple trait multiple interval mapping of quantitative trait loci from inbred line crosses. BMC Genetics, 2012, 13, 67.	2.7	23
16	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
17	Multiple trait multiple interval mapping of quantitative trait loci from inbred line crosses. BMC Genetics, 2012, 13, 67.	2.7	18
18	The Hill-Robertson effect is a consequence of interplay between linkage, selection and drift: a commentary on "The effect of linkage on limits to artificial selection" by W.Â.G. Hill and A. Robertson. Genetical Research, 2007, 89, 309-310.	0.9	0

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19	QTL mapping and the genetic basis of adaptation: recent developments. <i>Genetica</i> , 2005, 123, 25-37.	1.1	20
20	Modeling Quantitative Trait Loci and Interpretation of Models. <i>Genetics</i> , 2005, 169, 1711-1725.	2.9	146
21	Joint Linkage and Linkage Disequilibrium Mapping in Natural Populations. <i>Genetics</i> , 2001, 157, 899-909.	2.9	72
22	A General Polyploid Model for Analyzing Gene Segregation in Outcrossing Tetraploid Species. <i>Genetics</i> , 2001, 159, 869-882.	2.9	84
23	An Analysis of Polygenes Affecting Wing Shape on Chromosome 2 in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2001, 159, 1045-1057.	2.9	61
24	A Multivalent Pairing Model of Linkage Analysis in Autotetraploids. <i>Genetics</i> , 2001, 159, 1339-1350.	2.9	31
25	A general mixture model approach for mapping quantitative trait loci from diverse cross designs involving multiple inbred lines. <i>Genetical Research</i> , 2000, 75, 345-355.	0.9	56
26	Genotype-Environment Interaction for Quantitative Trait Loci Affecting Life Span in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2000, 154, 213-227.	2.9	303
27	Genetic Architecture of a Morphological Shape Difference Between Two <i>Drosophila</i> Species. <i>Genetics</i> , 2000, 154, 299-310.	2.9	180
28	Estimating the genetic architecture of quantitative traits. <i>Genetical Research</i> , 1999, 74, 279-289.	0.9	286
29	Multiple Interval Mapping for Quantitative Trait Loci. <i>Genetics</i> , 1999, 152, 1203-1216.	2.9	797
30	An Analysis of Polygenes Affecting Wing Shape on Chromosome 3 in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1999, 153, 773-786.	2.9	117
31	QUANTITATIVE GENETIC ANALYSIS OF DIVERGENCE IN MALE SECONDARY SEXUAL TRAITS BETWEEN <i>DROSOPHILA SIMULANS</i> AND <i>DROSOPHILA MAURITIANA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 816-832.	2.3	97
32	Mapping quantitative trait loci with dominant and missing markers in various crosses from two inbred lines. <i>Genetica</i> , 1997, 101, 47-58.	1.1	200
33	Genetic Analysis of a Morphological Shape Difference in the Male Genitalia of <i>Drosophila simulans</i> and <i>D. mauritiana</i> . <i>Genetics</i> , 1996, 142, 1129-1145.	2.9	209
34	A genetic model of interpopulation variation and covariation of quantitative characters. <i>Genetical Research</i> , 1989, 53, 215-221.	0.9	3