

Hong-Bin Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3986586/publications.pdf>

Version: 2024-02-01

52
papers

2,713
citations

218677

26
h-index

197818

49
g-index

53
all docs

53
docs citations

53
times ranked

3467
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate prediction of complex traits for individuals and offspring from parents using a simple, rapid, and efficient method for gene-based breeding in cotton and maize. <i>Plant Science</i> , 2022, 316, 111153.	3.6	5
2	Analysis of the genes controlling cotton fiber length reveals the molecular basis of plant breeding and the genetic potential of current cultivars for continued improvement. <i>Plant Science</i> , 2022, 321, 111318.	3.6	4
3	Molecular and genetic dissection of the USDA rice mini-core collection using high-density SNP markers. <i>Plant Science</i> , 2021, 308, 110910.	3.6	5
4	Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. <i>Genomics</i> , 2020, 112, 225-236.	2.9	32
5	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
6	Quantitative trait loci influencing days to flowering and plant height in cowpea, <i>Vigna unguiculata</i> (L.) Walp. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1187-1195.	2.1	4
7	Analysis of the genes controlling three quantitative traits in three diverse plant species reveals the molecular basis of quantitative traits. <i>Scientific Reports</i> , 2020, 10, 10074.	3.3	37
8	Phenotypic and molecular dissection of grain quality using the USDA rice mini-core collection. <i>Food Chemistry</i> , 2019, 284, 312-322.	8.2	11
9	Quantification of gene expression while taking into account RNA alternative splicing. <i>Genomics</i> , 2019, 111, 1517-1528.	2.9	39
10	Genetic Relationship in <i>Cicer Sp.</i> Expose Evidence for Geneflow between the Cultigen and Its Wild Progenitor. <i>PLoS ONE</i> , 2015, 10, e0139789.	2.5	17
11	Phylogenetic analysis of <i>Gossypium L.</i> using restriction fragment length polymorphism of repeated sequences. <i>Molecular Genetics and Genomics</i> , 2015, 290, 1859-1872.	2.1	1
12	A plant-transformation-competent BIBAC library of ginseng (<i>Panax ginseng</i> C. A. Meyer) for functional genomics research and characterization of genes involved in ginsenoside biosynthesis. <i>Molecular Breeding</i> , 2013, 31, 685-692.	2.1	6
13	Construction of a plant-transformation-competent BIBAC library and genome sequence analysis of polyploid Upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2013, 14, 208.	2.8	15
14	Identification and characterization of a repertoire of genes differentially expressed in developing top ear shoots between a superior hybrid and its parental inbreds in <i>Zea mays</i> L.. <i>Molecular Genetics and Genomics</i> , 2013, 288, 691-705.	2.1	10
15	Construction of BIBAC and BAC libraries from a variety of organisms for advanced genomics research. <i>Nature Protocols</i> , 2012, 7, 479-499.	12.0	24
16	Genome Physical Mapping of Polyploids: A BIBAC Physical Map of Cultivated Tetraploid Cotton, <i>Gossypium hirsutum</i> L. <i>PLoS ONE</i> , 2012, 7, e33644.	2.5	11
17	Preparation of megabase-sized DNA from a variety of organisms using the nuclei method for advanced genomics research. <i>Nature Protocols</i> , 2012, 7, 467-478.	12.0	115
18	Construction and characterization of a BIBAC library of <i>Jatropha curcas</i> L. and identification of BIBAC clones containing genes associated with fatty acid metabolism. <i>Molecular Breeding</i> , 2011, 28, 559-567.	2.1	3

#	ARTICLE	IF	CITATIONS
19	A comparative physical map reveals the pattern of chromosomal evolution between the turkey (<i>Meleagris gallopavo</i>) and chicken (<i>Gallus gallus</i>) genomes. <i>BMC Genomics</i> , 2011, 12, 447.	2.8	24
20	Characterization of a plant-transformation-ready large-insert BIBAC library of <i>Arabidopsis</i> and bombardment transformation of a large-insert BIBAC of the library into tobacco. <i>Genome</i> , 2011, 54, 437-447.	2.0	13
21	A BAC-Based Physical Map of Zhikong Scallop (<i>Chlamys farreri</i> Jones et Preston). <i>PLoS ONE</i> , 2011, 6, e27612.	2.5	29
22	Construction and Characterization of a Bacterial Artificial Chromosome (BAC) Library of Pacific White Shrimp, <i>Litopenaeus vannamei</i> . <i>Marine Biotechnology</i> , 2010, 12, 141-149.	2.4	33
23	Construction of Two BAC Libraries from Half-Smooth Tongue Sole <i>Cynoglossus semilaevis</i> and Identification of Clones Containing Candidate Sex-Determination Genes. <i>Marine Biotechnology</i> , 2010, 12, 558-568.	2.4	51
24	A BAC/BIBAC-based physical map of chickpea, <i>Cicer arietinum</i> L. <i>BMC Genomics</i> , 2010, 11, 501.	2.8	29
25	Numbers of genes in the NBS and RLK families vary by more than four-fold within a plant species and are regulated by multiple factors. <i>Nucleic Acids Research</i> , 2010, 38, 6513-6525.	14.5	60
26	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	5.6	348
27	Construction and sequence sampling of deep-coverage, large-insert BAC libraries for three model lepidopteran species. <i>BMC Genomics</i> , 2009, 10, 283.	2.8	12
28	Construction and Characterization of Two Bacterial Artificial Chromosome Libraries of Zhikong Scallop, <i>Chlamys farreri</i> Jones et Preston, and Identification of BAC Clones Containing the Genes Involved in Its Innate Immune System. <i>Marine Biotechnology</i> , 2008, 10, 358-365.	2.4	34
29	Recent Advances in Cotton Genomics. <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-20.	2.2	126
30	A plant-transformation-competent BIBAC/BAC-based map of rice for functional analysis and genetic engineering of its genomic sequence. <i>Genome</i> , 2007, 50, 278-288.	2.0	13
31	Interactions among genomic structure, function, and evolution revealed by comprehensive analysis of the <i>Arabidopsis thaliana</i> genome. <i>Genomics</i> , 2006, 88, 394-406.	2.9	8
32	An Integrated BAC and Genome Sequence Physical Map of <i>Phytophthora sojae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1302-1310.	2.6	29
33	Construction of BAC and BIBAC libraries from sunflower and identification of linkage group-specific clones by overgo hybridization. <i>Theoretical and Applied Genetics</i> , 2006, 113, 23-32.	3.6	31
34	Genome physical mapping from large-insert clones by fingerprint analysis with capillary electrophoresis: a robust physical map of <i>Penicillium chrysogenum</i> . <i>Nucleic Acids Research</i> , 2005, 33, e50-e50.	14.5	28
35	Whole-Genome Physical Mapping: An Overview on Methods for DNA Fingerprinting. , 2005, , 257-283.		9
36	Genomic DNA Libraries and Physical Mapping. , 2005, , 173-213.		21

#	ARTICLE	IF	CITATIONS
37	A BAC- and BIBAC-Based Physical Map of the Soybean Genome. <i>Genome Research</i> , 2004, 14, 319-326.	5.5	111
38	Construction of a binary BAC library for an apomictic monosomic addition line of <i>Beta corolliflora</i> in sugar beet and identification of the clones derived from the alien chromosome. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1420-1425.	3.6	16
39	Genome physical mapping with large-insert bacterial clones by fingerprint analysis: methodologies, source clone genome coverage, and contig map quality. <i>Genomics</i> , 2004, 84, 941-951.	2.9	34
40	A BAC-Based Physical Map of the Chicken Genome. <i>Genome Research</i> , 2003, 13, 2754-2758.	5.5	72
41	BAC as tools for genome sequencing. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 195-209.	5.8	74
42	Bacterial Artificial Chromosome-Based Physical Map of the Rice Genome Constructed by Restriction Fingerprint Analysis. <i>Genetics</i> , 2001, 158, 1711-1724.	2.9	92
43	An Integrated Map of <i>Arabidopsis thaliana</i> for Functional Analysis of Its Genome Sequence. <i>Genetics</i> , 2001, 159, 1231-1242.	2.9	48
44	A binary vector-based large insert library for <i>Brassica napus</i> and identification of clones linked to a fertility restorer locus for <i>Ogura</i> cytoplasmic male sterility (CMS). <i>Genome</i> , 2000, 43, 102-109.	2.0	16
45	A binary vector-based large insert library for <i>Brassica napus</i> and identification of clones linked to a fertility restorer locus for <i>Ogura</i> cytoplasmic male sterility (CMS). <i>Genome</i> , 2000, 43, 102-109.	2.0	7
46	Construction of tomato genomic DNA libraries in a binary-BAC (BIBAC) vector. <i>Plant Journal</i> , 1999, 18, 223-229.	5.7	65
47	Physical mapping of the rice genome with BACs. , 1997, 35, 115-127.		55
48	Construction and characterization of two rice bacterial artificial chromosome libraries from the parents of a permanent recombinant inbred mapping population. <i>Molecular Breeding</i> , 1996, 2, 11.	2.1	134
49	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.	5.7	287
50	The evolution of polyploid wheats: identification of the A genome donor species. <i>Genome</i> , 1993, 36, 21-31.	2.0	389
51	Diploid ancestry and evolution of <i>Triticum kotschyi</i> and <i>T. peregrinum</i> examined using variation in repeated nucleotide sequences. <i>Genome</i> , 1992, 35, 182-191.	2.0	30
52	The genome origin and evolution of hexaploid <i>Triticum crassum</i> and <i>Triticum syriacum</i> determined from variation in repeated nucleotide sequences. <i>Genome</i> , 1992, 35, 806-814.	2.0	31