Hong-Bin Zhang

List of Publications by Year
in descending order

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	The evolution of polyploid wheats: identification of the A genome donor species. Genome, 1993, 36, 21-31.	2.0	389
2	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	5.6	348
3	Preparation of megabase-size DNA from plant nuclei. Plant Journal, 1995, 7, 175-184.	5.7	287
4	Construction and characterization of two rice bacterial artificial chromosome libraries from the parents of a permanent recombinant inbred mapping population. Molecular Breeding, 1996, 2, 11.	2.1	134
5	Recent Advances in Cotton Genomics. International Journal of Plant Genomics, 2008, 2008, 1-20.	2.2	126
6	Preparation of megabase-sized DNA from a variety of organisms using the nuclei method for advanced genomics research. Nature Protocols, 2012, 7, 467-478.	12.0	115
7	A BAC- and BIBAC-Based Physical Map of the Soybean Genome. Genome Research, 2004, 14, 319-326.	5.5	111
8	Bacterial Artificial Chromosome-Based Physical Map of the Rice Genome Constructed by Restriction Fingerprint Analysis. Genetics, 2001, 158, 1711-1724.	2.9	92
9	BAC as tools for genome sequencing. Plant Physiology and Biochemistry, 2001, 39, 195-209.	5.8	74
10	A BAC-Based Physical Map of the Chicken Genome. Genome Research, 2003, 13, 2754-2758.	5.5	72
11	Construction of tomato genomic DNA libraries in a binary-BAC (BIBAC) vector. Plant Journal, 1999, 18, 223-229.	5.7	65
12	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. Nucleic Acids Research, 2010, 38, 6513-6525.	14.5	60
13	Physical mapping of the rice genome with BACs. , 1997, 35, 115-127.		55
14	Construction of Two BAC Libraries from Half-Smooth Tongue Sole Cynoglossus semilaevis and Identification of Clones Containing Candidate Sex-Determination Genes. Marine Biotechnology, 2010, 12, 558-568.	2.4	51
15	An Integrated Map of <i>Arabidopsis thaliana</i> for Functional Analysis of Its Genome Sequence. Genetics, 2001, 159, 1231-1242.	2.9	48
16	Quantification of gene expression while taking into account RNA alternative splicing. Genomics, 2019, 111, 1517-1528.	2.9	39
17	Analysis of the genes controlling three quantitative traits in three diverse plant species reveals the molecular basis of quantitative traits. Scientific Reports, 2020, 10, 10074.	3.3	37
18	Genome physical mapping with large-insert bacterial clones by fingerprint analysis: methodologies, source clone genome coverage, and contig map quality. Genomics, 2004, 84, 941-951.	2.9	34

#	Article	IF	Citations
19	Construction and Characterization of Two Bacterial Artificial Chromosome Libraries of Zhikong Scallop, Chlamys farreri Jones et Preston, and Identification of BAC Clones Containing the Genes Involved in Its Innate Immune System. Marine Biotechnology, 2008, 10, 358-365.	2.4	34
20	Construction and Characterization of a Bacterial Artificial Chromosome (BAC) Library of Pacific White Shrimp, Litopenaeus vannamei. Marine Biotechnology, 2010, 12, 141-149.	2.4	33
21	Accurate prediction of maize grain yield using its contributing genes for gene-based breeding. Genomics, 2020, 112, 225-236.	2.9	32
22	The genome origin and evolution of hexaploid *Triticum crassum* and *Triticum syriacum* determined from variation in repeated nucleotide sequences. Genome, 1992, 35, 806-814.	2.0	31
23	Construction of BAC and BIBAC libraries from sunflower and identification of linkage group-specific clones by overgo hybridization. Theoretical and Applied Genetics, 2006, 113, 23-32.	3.6	31
24	Diploid ancestry and evolution of Triticum kotschyi and T. peregrinum examined using variation in repeated nucleotide sequences. Genome, 1992, 35, 182-191.	2.0	30
25	An Integrated BAC and Genome Sequence Physical Map of Phytophthora sojae. Molecular Plant-Microbe Interactions, 2006, 19, 1302-1310.	2.6	29
26	A BAC/BIBAC-based physical map of chickpea, Cicer arietinum L. BMC Genomics, 2010, 11, 501.	2.8	29
27	A BAC-Based Physical Map of Zhikong Scallop (Chlamys farreri Jones et Preston). PLoS ONE, 2011, 6, e27612.	2.5	29
28	Genome physical mapping from large-insert clones by fingerprint analysis with capillary electrophoresis: a robust physical map of Penicillium chrysogenum. Nucleic Acids Research, 2005, 33, e50-e50.	14.5	28
29	A comparative physical map reveals the pattern of chromosomal evolution between the turkey (Meleagris gallopavo) and chicken (Gallus gallus) genomes. BMC Genomics, 2011, 12, 447.	2.8	24
30	Construction of BIBAC and BAC libraries from a variety of organisms for advanced genomics research. Nature Protocols, 2012, 7, 479-499.	12.0	24
31	Genomic DNA Libraries and Physical Mapping. , 2005, , 173-213.		21
32	Genetic Relationship in Cicer Sp. Expose Evidence for Geneflow between the Cultigen and Its Wild Progenitor. PLoS ONE, 2015, 10, e0139789.	2.5	17
33	A binary vector-based large insert library for Brassica napus and identification of clones linked to a fertility restorer locus for Ogura cytoplasmic male sterility (CMS). Genome, 2000, 43, 102-109.	2.0	16
34	Construction of a binary BAC library for an apomictic monosomic addition line of Beta corolliflora in sugar beet and identification of the clones derived from the alien chromosome. Theoretical and Applied Genetics, 2004, 108, 1420-1425.	3.6	16
35	Construction of a plant-transformation-competent BIBAC library and genome sequence analysis of polyploid Upland cotton (Gossypium hirsutumL.). BMC Genomics, 2013, 14, 208.	2.8	15
36	Accurate Prediction of a Quantitative Trait Using the Genes Controlling the Trait for Gene-Based Breeding in Cotton. Frontiers in Plant Science, 2020, 11, 583277.	3.6	14

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37	A plant-transformation-competent BIBAC/BAC-based map of rice for functional analysis and genetic engineering of its genomic sequence. Genome, 2007, 50, 278-288.	2.0	13
38	Characterization of a plant-transformation-ready large-insert BIBAC library of *Arabidopsis* and bombardment transformation of a large-insert BIBAC of the library into tobacco. Genome, 2011, 54, 437-447.	2.0	13
39	Construction and sequence sampling of deep-coverage, large-insert BAC libraries for three model lepidopteran species. BMC Genomics, 2009, 10, 283.	2.8	12
40	Genome Physical Mapping of Polyploids: A BIBAC Physical Map of Cultivated Tetraploid Cotton, Gossypium hirsutum L. PLoS ONE, 2012, 7, e33644.	2.5	11
41	Phenotypic and molecular dissection of grain quality using the USDA rice mini-core collection. Food Chemistry, 2019, 284, 312-322.	8.2	11
42	Identification and characterization of a repertoire of genes differentially expressed in developing top ear shoots between a superior hybrid and its parental inbreds in Zea mays L.. Molecular Genetics and Genomics, 2013, 288, 691-705.	2.1	10
43	Whole-Genome Physical Mapping: An Overview on Methods for DNA Fingerprinting. , 2005, , 257-283.		9
44	Interactions among genomic structure, function, and evolution revealed by comprehensive analysis of the Arabidopsis thaliana genome. Genomics, 2006, 88, 394-406.	2.9	8
45	A binary vector-based large insert library for *Brassica napus* and identification of clones linked to a fertility restorer locus for *Ogura* cytoplasmic male sterility (CMS). Genome, 2000, 43, 102-109.	2.0	7
46	A plant-transformation-competent BIBAC library of ginseng (Panax ginseng C. A. Meyer) for functional genomics research and characterization of genes involved in ginsenoside biosynthesis. Molecular Breeding, 2013, 31, 685-692.	2.1	6
47	Molecular and genetic dissection of the USDA rice mini-core collection using high-density SNP markers. Plant Science, 2021, 308, 110910.	3.6	5
48	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. Plant Science, 2022, 316, 111153.	3.6	5
49	Quantitative trait loci influencing days to flowering and plant height in cowpea, Vigna unguiculata (L.) Walp. Molecular Genetics and Genomics, 2020, 295, 1187-1195.	2.1	4
50	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. Plant Science, 2022, 321, 111318.	3.6	4
51	Construction and characterization of a BIBAC library of Jatropha curcas L. and identification of BIBAC clones containing genes associated with fatty acid metabolism. Molecular Breeding, 2011, 28, 559-567.	2.1	3
52	Phylogenetic analysis of Gossypium L. using restriction fragment length polymorphism of repeated sequences. Molecular Genetics and Genomics, 2015, 290, 1859-1872.	2.1	1