

Rod A Wing

List of Publications by Year in descending order

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284
papers

50,749
citations

3264

94
h-index

1875

215
g-index

296
all docs

296
docs citations

296
times ranked

40381
citing authors

#	ARTICLE	IF	CITATIONS
1	Rice domestication. <i>Current Biology</i> , 2022, 32, R20-R24.	1.8	14
2	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
3	Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. <i>Nature Genetics</i> , 2022, 54, 227-231.	9.4	63
4	Gene fusion as an important mechanism to generate new genes in the genus <i>Oryza</i> . <i>Genome Biology</i> , 2022, 23, .	3.8	7
5	A chromosome-scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. <i>Plant Biotechnology Journal</i> , 2021, 19, 602-614.	4.1	62
6	Evolution and diversification of reproductive phased small interfering RNAs in <i>Oryza</i> species. <i>New Phytologist</i> , 2021, 229, 2970-2983.	3.5	12
7	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	13.7	144
8	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	13.5	259
9	The chromosome-scale reference genome of safflower (<i>Carthamus tinctorius</i>) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
10	Starch Synthesis-Related Genes (SSRG) Evolution in the Genus <i>Oryza</i> . <i>Plants</i> , 2021, 10, 1057.	1.6	0
11	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	3.9	133
12	Potential of Platinum Standard Reference Genomes to Exploit Natural Variation in the Wild Relatives of Rice. <i>Frontiers in Plant Science</i> , 2020, 11, 579980.	1.7	15
13	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	3.8	68
14	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , 2020, 9, .	3.3	47
15	Evolution and diversity of the wild rice <i>Oryza officinalis</i> complex, across continents genome types, and ploidy levels. <i>Genome Biology and Evolution</i> , 2020, 12, 413-428.	1.1	17
16	Evolutionary Dynamics of Abundant 7-bp Satellites in the Genome of <i>Drosophila virilis</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 1362-1375.	3.5	23
17	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	2.4	86
18	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020, 10, 6112.	1.6	30

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19	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019, 10, 4680.	5.8	75
20	Functional screening of genes from a halophyte wild rice relative <i>Porteresia coarctata</i> in <i>Arabidopsis</i> model identifies candidate genes involved in salt tolerance. <i>Current Plant Biology</i> , 2019, 18, 100107.	2.3	14
21	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880.	2.4	112
22	The Genomics of <i>Oryza</i> Species Provides Insights into Rice Domestication and Heterosis. <i>Annual Review of Plant Biology</i> , 2019, 70, 639-665.	8.6	80
23	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	3.4	121
24	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	1.2	59
25	Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019, 20, 565-571.	3.2	4
26	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
27	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	4.1	136
28	Genotyping by sequencing of rice interspecific backcross inbred lines identifies QTLs for grain weight and grain length. <i>Euphytica</i> , 2018, 214, 1.	0.6	29
29	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
30	Comparison of <i>Oryza sativa</i> and <i>Oryza brachyantha</i> Genomes Reveals Selection-Driven Gene Escape from the Centromeric Regions. <i>Plant Cell</i> , 2018, 30, 1729-1744.	3.1	22
31	Genetic control of seed shattering during African rice domestication. <i>Nature Plants</i> , 2018, 4, 331-337.	4.7	55
32	The rice genome revolution: from an ancient grain to Green Super Rice. <i>Nature Reviews Genetics</i> , 2018, 19, 505-517.	7.7	251
33	The rice paradox: Multiple origins but single domestication in Asian rice. <i>Molecular Biology and Evolution</i> , 2017, 34, msx049.	3.5	178
34	Aflatoxin-free transgenic maize using host-induced gene silencing. <i>Science Advances</i> , 2017, 3, e1602382.	4.7	88
35	Evolutionary analysis of the SUB1 locus across the <i>Oryza</i> genomes. <i>Rice</i> , 2017, 10, 4.	1.7	25
36	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017, 3, 17064.	4.7	133

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37	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	3.4	94
38	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	5.8	240
39	Genetic variation for domestication-related traits revealed in a cultivated rice, Nipponbare (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT ₅ /Overloc	1.0	10
40	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12003-12008.	3.3	90
41	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 765-774.	4.1	51
42	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081.	6.5	290
43	DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. <i>Genome Biology</i> , 2016, 17, 92.	3.8	14
44	The Dark Side of the Genome: Revealing the Native Transposable Element/Repeat Content of Eukaryotic Genomes. <i>Molecular Plant</i> , 2016, 9, 1664-1666.	3.9	4
45	Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. <i>Bioinformatics</i> , 2016, 32, 3058-3064.	1.8	22
46	Extensive sequence divergence between the reference genomes of two elite <i>indica</i> rice varieties Zhenshan 97 and Minghui 63. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5163-71.	3.3	211
47	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. <i>Nature Communications</i> , 2016, 7, 12790.	5.8	51
48	The Cardamine <i>hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	4.7	90
49	Tracing ancestor rice of Suriname Maroons back to its African origin. <i>Nature Plants</i> , 2016, 2, 16149.	4.7	31
50	Building two <i>indica</i> rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016, 3, 160076.	2.4	34
51	The impact and origin of copy number variations in the <i>Oryza</i> species. <i>BMC Genomics</i> , 2016, 17, 261.	1.2	30
52	Development and validation of cross-transferable and polymorphic DNA markers for detecting alien genome introgression in <i>Oryza sativa</i> from <i>Oryza brachyantha</i> . <i>Molecular Genetics and Genomics</i> , 2016, 291, 1783-1794.	1.0	10
53	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	3.8	331
54	Genome and Comparative Transcriptomics of African Wild Rice <i>Oryza longistaminata</i> Provide Insights into Molecular Mechanism of Rhizomatousness and Self-Incompatibility. <i>Molecular Plant</i> , 2015, 8, 1683-1686.	3.9	49

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55	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015, 5, 15655.	1.6	169
56	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015, 5, 17394.	1.6	136
57	Recurrent sequence exchange between homeologous grass chromosomes. <i>Plant Journal</i> , 2015, 84, 747-759.	2.8	5
58	Transposons play an important role in the evolution and diversification of centromeres among closely related species. <i>Frontiers in Plant Science</i> , 2015, 6, 216.	1.7	51
59	Exceptional reduction of the plastid genome of saguaro cactus (<i>Carnegiea gigantea</i>): Loss of the <i>ndh</i> gene suite and inverted repeat. <i>American Journal of Botany</i> , 2015, 102, 1115-1127.	0.8	137
60	Sequencing of 15,622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	2.8	36
61	Harvesting rice's dispensable genome. <i>Genome Biology</i> , 2015, 16, 217.	3.8	6
62	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
63	Fifteen Million Years of Evolution in the <i>Oryza</i> Genus Shows Extensive Gene Family Expansion. <i>Molecular Plant</i> , 2014, 7, 642-656.	3.9	54
64	Making a living while starving in the dark: metagenomic insights into the energy dynamics of a carbonate cave. <i>ISME Journal</i> , 2014, 8, 478-491.	4.4	114
65	Comparative BAC-based physical mapping of <i>Oryza sativa</i> ssp. <i>indica</i> var. 9311 and evaluation of the two rice reference sequence assemblies. <i>Plant Journal</i> , 2014, 77, 795-805.	2.8	16
66	Disentangling Methodological and Biological Sources of Gene Tree Discordance on <i>Oryza</i> (Poaceae) Chromosome 3. <i>Systematic Biology</i> , 2014, 63, 645-659.	2.7	43
67	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014, 5, 5269.	5.8	99
68	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014, 46, 982-988.	9.4	342
69	Global Genomic Diversity of <i>Oryza sativa</i> Varieties Revealed by Comparative Physical Mapping. <i>Genetics</i> , 2014, 196, 937-949.	1.2	10
70	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	9.4	1,159
71	Profiling Bacterial Diversity and Taxonomic Composition on Speleothem Surfaces in Kartchner Caverns, AZ. <i>Microbial Ecology</i> , 2013, 65, 371-383.	1.4	78
72	Ginger and turmeric expressed sequence tags identify signature genes for rhizome identity and development and the biosynthesis of curcuminoids, gingerols and terpenoids. <i>BMC Plant Biology</i> , 2013, 13, 27.	1.6	61

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73	The Wild Relative of Rice: Genomes and Genomics. , 2013, , 9-25.		94
74	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	6.0	743
75	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i> . Science, 2013, 342, 1516-1517.	6.0	89
76	Genome studies and molecular genetics: understanding the functional genome based on the rice model. Current Opinion in Plant Biology, 2013, 16, 129-132.	3.5	13
77	The International Oryza Map Alignment Project: development of a genus-wide comparative genomics platform to help solve the 9 billion-people question. Current Opinion in Plant Biology, 2013, 16, 147-156.	3.5	126
78	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. Nature Communications, 2013, 4, 1595.	5.8	190
79	BAC Library Development and Clone Characterization for Dormancy-Responsive DREB4A, DAM, and FT from Leafy Spurge (<i>Euphorbia esula</i>) Identifies Differential Splicing and Conserved Promoter Motifs. Weed Science, 2013, 61, 303-309.	0.8	11
80	BAC-end sequences analysis provides first insights into coffee (<i>Coffea canephora</i> P.) genome composition and evolution. Plant Molecular Biology, 2013, 83, 177-189.	2.0	15
81	High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences. Genome Biology and Evolution, 2013, 5, 1038-1048.	1.1	11
82	Genomic Resources for Gene Discovery, Functional Genome Annotation, and Evolutionary Studies of Maize and Its Close Relatives. Genetics, 2013, 195, 723-737.	1.2	15
83	Evolution of a Complex Locus for Terpene Biosynthesis in <i>Solanum</i> . Plant Cell, 2013, 25, 2022-2036.	3.1	132
84	Grain Quality. , 2013, , 237-254.		8
85	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . Frontiers in Plant Science, 2013, 4, 46.	1.7	198
86	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. Nature, 2013, 500, 335-339.	13.7	468
87	Aluminum tolerance in maize is associated with higher <i>MATE1</i> gene copy number. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5241-5246.	3.3	265
88	Dynamic Intra-Japonica Subspecies Variation and Resource Application. Molecular Plant, 2012, 5, 218-230.	3.9	23
89	Ortholog Alleles at Xa3/Xa26 Locus Confer Conserved Race-Specific Resistance against <i>Xanthomonas oryzae</i> in Rice. Molecular Plant, 2012, 5, 281-290.	3.9	37
90	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	13.7	1,416

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91	A BAC library of the SP80-3280 sugarcane variety (<i>saccharum</i> sp.) and its inferred microsynteny with the sorghum genome. <i>BMC Research Notes</i> , 2012, 5, 185.	0.6	47
92	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
93	Life at the hyperarid margin: novel bacterial diversity in arid soils of the Atacama Desert, Chile. <i>Extremophiles</i> , 2012, 16, 553-566.	0.9	182
94	Integration of the Draft Sequence and Physical Map as a Framework for Genomic Research in Soybean (<i>Glycine max</i> (L.) Merr.) and Wild Soybean (<i>Glycine soja</i> Sieb. and Zucc.). <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 321-329.	0.8	9
95	Comparative Sequence Analysis of the Ghd7 Orthologous Regions Revealed Movement of Ghd7 in the Grass Genomes. <i>PLoS ONE</i> , 2012, 7, e50236.	1.1	14
96	LysM-Type Mycorrhizal Receptor Recruited for Rhizobium Symbiosis in Nonlegume <i>Parasponia</i> . <i>Science</i> , 2011, 331, 909-912.	6.0	273
97	A physical map for the <i>Amborella trichopoda</i> genome sheds light on the evolution of angiosperm genome structure. <i>Genome Biology</i> , 2011, 12, R48.	13.9	28
98	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	9.4	656
99	Molecular and Cytological Characterization of Centromeric Retrotransposons in a Wild Relative of Rice, <i>Oryza granulata</i> . <i>Tropical Plant Biology</i> , 2011, 4, 217-227.	1.0	1
100	Gene-based SSR markers for common bean (<i>Phaseolus vulgaris</i> L.) derived from root and leaf tissue ESTs: an integration of the BMC series. <i>BMC Plant Biology</i> , 2011, 11, 50.	1.6	79
101	Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. <i>BMC Genomics</i> , 2011, 12, 137.	1.2	46
102	Exceptional lability of a genomic complex in rice and its close relatives revealed by interspecific and intraspecific comparison and population analysis. <i>BMC Genomics</i> , 2011, 12, 142.	1.2	14
103	Long-Range and Targeted Ectopic Recombination between the Two Homeologous Chromosomes 11 and 12 in <i>Oryza</i> Species. <i>Molecular Biology and Evolution</i> , 2011, 28, 3139-3150.	3.5	23
104	The 19 Genomes of <i>Drosophila</i> : A BAC Library Resource for Genus-Wide and Genome-Scale Comparative Evolutionary Research. <i>Genetics</i> , 2011, 187, 1023-1030.	1.2	22
105	Conservation and Purifying Selection of Transcribed Genes Located in a Rice Centromere. <i>Plant Cell</i> , 2011, 23, 2821-2830.	3.1	22
106	Construction, Characterization, and Preliminary BAC-End Sequence Analysis of a Bacterial Artificial Chromosome Library of the Tea Plant (<i>Camellia sinensis</i>). <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-8.	3.0	11
107	Phylogenomic Analysis of BAC-end Sequence Libraries in <i>Oryza</i> (Poaceae). <i>Systematic Botany</i> , 2010, 35, 512-523.	0.2	8
108	Genomic structure and evolution of the Pi2/9 locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010, 121, 295-309.	1.8	25

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109	Australian <i>Oryza</i> : Utility and Conservation. <i>Rice</i> , 2010, 3, 235-241.	1.7	57
110	Assessing the Extent of Substitution Rate Variation of Retrotransposon Long Terminal Repeat Sequences in <i>Oryza sativa</i> and <i>Oryza glaberrima</i> . <i>Rice</i> , 2010, 3, 242-250.	1.7	5
111	The Future of Rice Genomics: Sequencing the Collective <i>Oryza</i> Genome. <i>Rice</i> , 2010, 3, 89-97.	1.7	21
112	Dynamic <i>Oryza</i> Genomes: Repetitive DNA Sequences as Genome Modeling Agents. <i>Rice</i> , 2010, 3, 251-269.	1.7	15
113	A draft physical map of a D-genome cotton species (<i>Gossypium raimondii</i>). <i>BMC Genomics</i> , 2010, 11, 395.	1.2	48
114	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	13.7	3,854
115	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 430-442.	2.8	48
116	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010, 63, 990-1003.	2.8	47
117	Orthologous Comparisons of the Hd1 Region across Genera Reveal Hd1 Gene Lability within Diploid <i>Oryza</i> Species and Disruptions to Microsynteny in <i>Sorghum</i> . <i>Molecular Biology and Evolution</i> , 2010, 27, 2487-2506.	3.5	31
118	Extensive Gene Conversion Drives the Concerted Evolution of Paralogous Copies of the SRY Gene in European Rabbits. <i>Molecular Biology and Evolution</i> , 2010, 27, 2437-2440.	3.5	26
119	The <i>Oryza</i> BAC resource: a genus-wide and genome scale tool for exploring rice genome evolution and leveraging useful genetic diversity from wild relatives. <i>Breeding Science</i> , 2010, 60, 536-543.	0.9	34
120	An Integrated Physical, Genetic and Cytogenetic Map of <i>Brachypodium distachyon</i> , a Model System for Grass Research. <i>PLoS ONE</i> , 2010, 5, e13461.	1.1	45
121	The Physical and Genetic Framework of the Maize B73 Genome. <i>PLoS Genetics</i> , 2009, 5, e1000715.	1.5	95
122	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
123	<i>Hamiltonella defensa</i> , genome evolution of protective bacterial endosymbiont from pathogenic ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9063-9068.	3.3	214
124	Dynamic Evolution of <i>Oryza</i> Genomes Is Revealed by Comparative Genomic Analysis of a Genus-Wide Vertical Data Set. <i>Plant Cell</i> , 2009, 20, 3191-3209.	3.1	128
125	Comparative sequence analysis of <i>MONOCULM1</i> -orthologous regions in 14 <i>Oryza</i> genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2071-2076.	3.3	119
126	Species Trees from Highly Incongruent Gene Trees in Rice. <i>Systematic Biology</i> , 2009, 58, 489-500.	2.7	98

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127	De Novo Next Generation Sequencing of Plant Genomes. <i>Rice</i> , 2009, 2, 35-43.	1.7	59
128	A lineage-specific centromere retrotransposon in <i>Oryza brachyantha</i> . <i>Plant Journal</i> , 2009, 60, 820-831.	2.8	41
129	Human gut microbiota in obesity and after gastric bypass. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 2365-2370.	3.3	1,641
130	Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in <i>Thellungiella halophila</i> and <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2009, 94, 196-203.	1.3	17
131	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
132	A Single Molecule Scaffold for the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000711.	1.5	122
133	Evidence of multiple horizontal transfers of the long terminal repeat retrotransposon <i>RIRE1</i> within the genus <i>Oryza</i> . <i>Plant Journal</i> , 2008, 53, 950-959.	2.8	70
134	Rapid and Differential Proliferation of the Ty3-Gypsy LTR Retrotransposon <i>Atlantys</i> in the Genus <i>Oryza</i> . <i>Rice</i> , 2008, 1, 85-99.	1.7	7
135	The Promoter Signatures in Rice LEA Genes Can Be Used to Build a Co-expressing LEA Gene Network. <i>Rice</i> , 2008, 1, 177-187.	1.7	14
136	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. <i>Tropical Plant Biology</i> , 2008, 1, 40-48.	1.0	70
137	Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. <i>BMC Genomics</i> , 2008, 9, 621.	1.2	11
138	A fruitful outcome to the papaya genome project. <i>Genome Biology</i> , 2008, 9, 227.	13.9	9
139	The Amborella genome: an evolutionary reference for plant biology. <i>Genome Biology</i> , 2008, 9, 402.	13.9	67
140	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Biology</i> , 2008, 9, R45.	13.9	82
141	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. <i>Genome</i> , 2008, 51, 294-302.	0.9	50
142	Diploid/Polyploid Syntenic Shuttle Mapping and Haplotype-Specific Chromosome Walking Toward a Rust Resistance Gene (<i>Bru1</i>) in Highly Polyploid Sugarcane ($2n \times 12x$). <i>Genetics</i> , 2008, 180, 649-660.	1.2	110
143	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1415-1428.	3.5	57
144	The Subtelomere of <i>Oryza sativa</i> Chromosome 3 Short Arm as a Hot Bed of New Gene Origination in Rice. <i>Molecular Plant</i> , 2008, 1, 839-850.	3.9	36

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145	A Versatile Transposon-Based Activation Tag Vector System for Functional Genomics in Cereals and Other Monocot Plants. <i>Plant Physiology</i> , 2008, 146, 189-199.	2.3	64
146	Construction of an <i>Amaranthus hypochondriacus</i> Bacterial Artificial Chromosome Library and Genomic Sequencing of Herbicide Target Genes. <i>Crop Science</i> , 2008, 48, S-85.	0.8	23
147	Evolutionary History and Positional Shift of a Rice Centromere. <i>Genetics</i> , 2007, 177, 1217-1220.	1.2	29
148	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	295
149	Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. <i>PLoS Genetics</i> , 2007, 3, e123.	1.5	270
150	Comparative Physical Mapping Between <i>Oryza sativa</i> (AA Genome Type) and <i>O. punctata</i> (BB Genome) Tj ETQq0 0,0,rgBT /Overlock 10	1.2	49
151	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
152	Magnaporthe grisea Infection Triggers RNA Variation and Antisense Transcript Expression in Rice. <i>Plant Physiology</i> , 2007, 144, 524-533.	2.3	29
153	Efficacy of clone fingerprinting methodologies. <i>Genomics</i> , 2007, 89, 160-165.	1.3	21
154	Rice Genome Sequence: The Foundation for Understanding the Genetic Systems. , 2007, , 5-20.		3
155	The <i>Oryza</i> Map Alignment Project (OMAP): A New Resource for Comparative Genome Studies within <i>Oryza</i> . , 2007, , 395-409.		9
156	Changes in Regulation of a Transcription Factor Lead to Autogamy in Cultivated Tomatoes. <i>Science</i> , 2007, 318, 643-645.	6.0	141
157	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	1,886
158	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (<i>Gossypium</i>). <i>Plant Journal</i> , 2007, 50, 995-1006.	2.8	89
159	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus <i>Oryza</i> . <i>Plant Journal</i> , 2007, 52, 342-351.	2.8	99
160	Transposable element distribution, abundance and role in genome size variation in the genus <i>Oryza</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 152.	3.2	115
161	Plant centromere organization: a dynamic structure with conserved functions. <i>Trends in Genetics</i> , 2007, 23, 134-139.	2.9	133
162	Development of a BAC library for yellow-poplar (<i>Liriodendron tulipifera</i>) and the identification of genes associated with flower development and lignin biosynthesis. <i>Tree Genetics and Genomes</i> , 2007, 3, 215-225.	0.6	25

#	ARTICLE	IF	CITATIONS
163	The barley ERF-type transcription factor HvRAF confers enhanced pathogen resistance and salt tolerance in Arabidopsis. <i>Planta</i> , 2007, 225, 575-588.	1.6	115
164	RL-SAGE and microarray analysis of the rice transcriptome after <i>Rhizoctonia solani</i> infection. <i>Molecular Genetics and Genomics</i> , 2007, 278, 421-431.	1.0	50
165	Differential lineage-specific amplification of transposable elements is responsible for genome size variation in <i>Gossypium</i> . <i>Genome Research</i> , 2006, 16, 1252-1261.	2.4	378
166	Utilization of a zebra finch BAC library to determine the structure of an avian androgen receptor genomic region. <i>Genomics</i> , 2006, 87, 181-190.	1.3	25
167	Two highly representative rice BAC libraries of japonica cv Tainung 67 suitable for rice structural and functional genomic research. <i>Plant Science</i> , 2006, 170, 889-896.	1.7	0
168	A bacterial artificial chromosome library for <i>Biomphalaria glabrata</i> , intermediate snail host of <i>Schistosoma mansoni</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2006, 101, 167-177.	0.8	36
169	Single Nucleotide Polymorphisms and Insertion-Deletions for Genetic Markers and Anchoring the Maize Fingerprint Contig Physical Map. <i>Crop Science</i> , 2006, 46, 12-21.	0.8	51
170	MGOS: A Resource for Studying <i>Magnaporthe grisea</i> and <i>Oryza sativa</i> Interactions. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1055-1061.	1.4	24
171	New Resources for Marine Genomics: Bacterial Artificial Chromosome Libraries for the Eastern and Pacific Oysters (<i>Crassostrea virginica</i> and <i>C. gigas</i>). <i>Marine Biotechnology</i> , 2006, 8, 521-533.	1.1	53
172	Construction of a nurse shark (<i>Ginglymostoma cirratum</i>) bacterial artificial chromosome (BAC) library and a preliminary genome survey. <i>BMC Genomics</i> , 2006, 7, 106.	1.2	27
173	Integration of hybridization-based markers (overgos) into physical maps for comparative and evolutionary explorations in the genus <i>Oryza</i> and in <i>Sorghum</i> . <i>BMC Genomics</i> , 2006, 7, 199.	1.2	12
174	Deep and comparative analysis of the mycelium and appressorium transcriptomes of <i>Magnaporthe grisea</i> using MPSS, RL-SAGE, and oligoarray methods. <i>BMC Genomics</i> , 2006, 7, 310.	1.2	60
175	Genomic and Genetic Characterization of Rice Cen3 Reveals Extensive Transcription and Evolutionary Implications of a Complex Centromere. <i>Plant Cell</i> , 2006, 18, 2123-2133.	3.1	95
176	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	2.4	138
177	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105
178	Doubling genome size without polyploidization: Dynamics of retrotransposition-driven genomic expansions in <i>Oryza australiensis</i> , a wild relative of rice. <i>Genome Research</i> , 2006, 16, 1262-1269.	2.4	522
179	Efficient insertional mutagenesis in rice using the maize En/Spm elements. <i>Plant Journal</i> , 2005, 44, 879-892.	2.8	100
180	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	13.7	3,365

#	ARTICLE	IF	CITATIONS
181	Construction of a bacterial artificial chromosome library from the spikemoss <i>Selaginella moellendorffii</i> : a new resource for plant comparative genomics. <i>BMC Plant Biology</i> , 2005, 5, 10.	1.6	53
182	Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf euchromatic portions of the genome. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1596-1607.	1.8	36
183	Candidate gene database and transcript map for peach, a model species for fruit trees. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1419-1428.	1.8	71
184	Toward closing rice telomere gaps: mapping and sequence characterization of rice subtelomere regions. <i>Theoretical and Applied Genetics</i> , 2005, 111, 467-478.	1.8	21
185	In-depth sequence analysis of the tomato chromosome 12 centromeric region: identification of a large CAA block and characterization of pericentromere retrotransposons. <i>Chromosoma</i> , 2005, 114, 103-117.	1.0	52
186	The <i>Oryza</i> Map Alignment Project: The Golden Path to Unlocking the Genetic Potential of Wild Rice Species. <i>Plant Molecular Biology</i> , 2005, 59, 53-62.	2.0	143
187	The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. <i>BMC Biology</i> , 2005, 3, 20.	1.7	158
188	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	2.4	73
189	Structure and Architecture of the Maize Genome. <i>Plant Physiology</i> , 2005, 139, 1612-1624.	2.3	159
190	Large-Scale Identification of Expressed Sequence Tags Involved in Rice and Rice Blast Fungus Interaction. <i>Plant Physiology</i> , 2005, 138, 105-115.	2.3	96
191	Sorghum Expressed Sequence Tags Identify Signature Genes for Drought, Pathogenesis, and Skotomorphogenesis from a Milestone Set of 16,801 Unique Transcripts. <i>Plant Physiology</i> , 2005, 139, 869-884.	2.3	66
192	Comparative physical mapping links conservation of microsynteny to chromosome structure and recombination in grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13206-13211.	3.3	141
193	The <i>Oryza</i> bacterial artificial chromosome library resource: Construction and analysis of 12 deep-coverage large-insert BAC libraries that represent the 10 genome types of the genus <i>Oryza</i> . <i>Genome Research</i> , 2005, 16, 140-147.	2.4	197
194	Whole-Genome Validation of High-Information-Content Fingerprinting. <i>Plant Physiology</i> , 2005, 139, 27-38.	2.3	86
195	Comparative Population Genetics of the Panicoid Grasses: Sequence Polymorphism, Linkage Disequilibrium and Selection in a Diverse Sample of <i>Sorghum bicolor</i> . <i>Genetics</i> , 2004, 167, 471-483.	1.2	106
196	A 3347-Locus Genetic Recombination Map of Sequence-Tagged Sites Reveals Features of Genome Organization, Transmission and Evolution of Cotton (<i>Gossypium</i>). <i>Genetics</i> , 2004, 166, 389-417.	1.2	331
197	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.	2.4	80
198	Structural features of the rice chromosome 4 centromere. <i>Nucleic Acids Research</i> , 2004, 32, 2023-2030.	6.5	95

#	ARTICLE	IF	CITATIONS
199	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	2.3	287
200	The <i>Ashbya gossypii</i> Genome as a Tool for Mapping the Ancient <i>Saccharomyces cerevisiae</i> Genome. <i>Science</i> , 2004, 304, 304-307.	6.0	599
201	Anchoring 9,371 Maize Expressed Sequence Tagged Unigenes to the Bacterial Artificial Chromosome Contig Map by Two-Dimensional Overgo Hybridization. <i>Plant Physiology</i> , 2004, 134, 1317-1326.	2.3	94
202	Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. <i>Functional and Integrative Genomics</i> , 2004, 4, 102-117.	1.4	44
203	Functional genomics of cell elongation in developing cotton fibers. <i>Plant Molecular Biology</i> , 2004, 54, 911-929.	2.0	237
204	Bacterial artificial chromosome (BAC) library resource for positional cloning of pest and disease resistance genes in cassava (<i>Manihot esculenta</i> Crantz). <i>Plant Molecular Biology</i> , 2004, 56, 555-561.	2.0	19
205	Localization of jointless-2 gene in the centromeric region of tomato chromosome 12 based on high resolution genetic and physical mapping. <i>Theoretical and Applied Genetics</i> , 2004, 108, 190-196.	1.8	71
206	Sequence composition and genome organization of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14349-14354.	3.3	290
207	BAC end sequences and a physical map reveal transposable element content and clustering patterns in the genome of <i>Magnaporthe grisea</i> . <i>Fungal Genetics and Biology</i> , 2004, 41, 657-666.	0.9	27
208	Genetic Conservation of Genomic Resources. , 2004, , 1-5.		1
209	Whole Genome Sequencing: Methodology and Progress in Cereals. , 2004, , 385-423.		0
210	Construction and utility of 10-kb libraries for efficient clone-gap closure for rice genome sequencing. <i>Theoretical and Applied Genetics</i> , 2003, 107, 652-660.	1.8	18
211	Rate Variation Among Nuclear Genes and the Age of Polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 633-643.	3.5	325
212	Comparison of peach and <i>Arabidopsis</i> genomic sequences: fragmentary conservation of gene neighborhoods. <i>Genome</i> , 2003, 46, 268-276.	0.9	30
213	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	6.0	245
214	An Improved Method for Plant BAC Library Construction. , 2003, 236, 3-20.		100
215	Mapping Sequence to Rice FPC. , 2003, , 59-79.		2
216	A Fine Physical Map of the Rice Chromosome 4. <i>Genome Research</i> , 2002, 12, 817-823.	2.4	64

#	ARTICLE	IF	CITATIONS
217	MagnaportheDB: a federated solution for integrating physical and genetic map data with BAC end derived sequences for the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nucleic Acids Research</i> , 2002, 30, 121-124.	6.5	38
218	Genetic, Physical, and Informatics Resources for Maize. On the Road to an Integrated Map. <i>Plant Physiology</i> , 2002, 130, 1598-1605.	2.3	106
219	Genome Dynamics and Evolution of the <i>Mla</i> (Powdery Mildew) Resistance Locus in Barley [W]. <i>Plant Cell</i> , 2002, 14, 1903-1917.	3.1	229
220	Access to the Maize Genome: An Integrated Physical and Genetic Map: Table I.. <i>Plant Physiology</i> , 2002, 128, 9-12.	2.3	91
221	An Integrated Physical and Genetic Map of the Rice Genome. <i>Plant Cell</i> , 2002, 14, 537-545.	3.1	422
222	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>japonica</i>). <i>Science</i> , 2002, 296, 92-100.	6.0	2,866
223	Construction of BAC libraries from two apomictic grasses to study the microcolinearity of their apospory-specific genomic regions. <i>Theoretical and Applied Genetics</i> , 2002, 104, 804-812.	1.8	41
224	Resolution of fluorescence in-situ hybridization mapping on rice mitotic prometaphase chromosomes, meiotic pachytene chromosomes and extended DNA fibers. <i>Chromosome Research</i> , 2002, 10, 379-387.	1.0	84
225	<i>Dasheng</i> : A Recently Amplified Nonautonomous Long Terminal Repeat Element That Is a Major Component of Pericentromeric Regions in Rice. <i>Genetics</i> , 2002, 161, 1293-1305.	1.2	73
226	Access to the maize genome: an integrated physical and genetic map. <i>Plant Physiology</i> , 2002, 128, 9-12.	2.3	57
227	Pulsed-Field Gel Electrophoresis for Long-Range Restriction Mapping. <i>Current Protocols in Human Genetics</i> , 2001, 31, Unit5.1.	3.5	1
228	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon <i>Fusarium</i> wilt (<i>Fom-2</i>). <i>Genome</i> , 2001, 44, 154-162.	0.9	92
229	Complete Nucleotide Sequence and Organization of the Atrazine Catabolic Plasmid pADP-1 from <i>Pseudomonas</i> sp. Strain ADP. <i>Journal of Bacteriology</i> , 2001, 183, 5684-5697.	1.0	324
230	Evaluation of genetic variation in the daylily (<i>Hemerocallis</i> spp.) using AFLP markers. <i>Theoretical and Applied Genetics</i> , 2001, 102, 489-496.	1.8	61
231	Title is missing!. <i>Molecular Breeding</i> , 2001, 8, 255-261.	1.0	45
232	Sequence and Analysis of the Tomato <i>JOINTLESS</i> Locus. <i>Plant Physiology</i> , 2001, 126, 1331-1340.	2.3	36
233	Construction of a 1.2-Mb contig including the citrus tristeza virus resistance gene locus using a bacterial artificial chromosome library of <i>Poncirus trifoliata</i> (L.) Raf.. <i>Genome</i> , 2001, 44, 382-393.	0.9	36
234	Toward Integration of Comparative Genetic, Physical, Diversity, and Cytomolecular Maps for Grasses and Grains, Using the Sorghum Genome as a Foundation. <i>Plant Physiology</i> , 2001, 125, 1325-1341.	2.3	81

#	ARTICLE	IF	CITATIONS
235	A Marker-Dense Physical Map of the <i>Bradyrhizobium japonicum</i> Genome. <i>Genome Research</i> , 2001, 11, 1434-1440.	2.4	11
236	Toward a Cytological Characterization of the Rice Genome. <i>Genome Research</i> , 2001, 11, 2133-2141.	2.4	182
237	A Framework for Sequencing the Rice Genome. <i>Novartis Foundation Symposium</i> , 2001, 236, 13-27.	1.2	2
238	High-Resolution Pachytene Chromosome Mapping of Bacterial Artificial Chromosomes Anchored by Genetic Markers Reveals the Centromere Location and the Distribution of Genetic Recombination Along Chromosome 10 of Rice. <i>Genetics</i> , 2001, 157, 1749-1757.	1.2	144
239	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon <i>Fusarium</i> wilt (<i>Fom</i>-<i>2</i>). <i>Genome</i> , 2001, 44, 154-162.	0.9	66
240	Construction of a 1.2-Mb contig including the citrus tristeza virus resistance gene locus using a bacterial artificial chromosome library of <i>Poncirus trifoliata</i> (L.) Raf.. <i>Genome</i> , 2001, 44, 382-393.	0.9	26
241	JOINTLESS is a MADS-box gene controlling tomato flower abscissionzone development. <i>Nature</i> , 2000, 406, 910-913.	13.7	314
242	Genetic mapping of jointless-2 to tomato chromosome 12 using RFLP and RAPD markers. <i>Theoretical and Applied Genetics</i> , 2000, 100, 1183-1189.	1.8	21
243	A bacterial artificial chromosome library for barley (<i>Hordeum vulgare</i> L.) and the identification of clones containing putative resistance genes. <i>Theoretical and Applied Genetics</i> , 2000, 101, 1093-1099.	1.8	187
244	A new approach for the identification and cloning of genes: the pBACwich system using Cre/lox site-specific recombination. <i>Nucleic Acids Research</i> , 2000, 28, 19e-19.	6.5	35
245	Rice Transposable Elements: A Survey of 73,000 Sequence-Tagged-Connectors. <i>Genome Research</i> , 2000, 10, 982-990.	2.4	187
246	The Construction of Bacterial Artificial Chromosome (BAC) Libraries. , 2000, , 1-28.		12
247	Physical Map and Gene Survey of the <i>Ochrobactrum anthropi</i> Genome Using Bacterial Artificial Chromosome Contigs. <i>Microbial & Comparative Genomics</i> , 1999, 4, 203-217.	0.6	7
248	A bacterial artificial chromosome library for soybean PI 437654 and identification of clones associated with cyst nematode resistance. <i>Plant Molecular Biology</i> , 1999, 41, 25-32.	2.0	65
249	A bacterial artificial chromosome library for sugarcane. <i>Theoretical and Applied Genetics</i> , 1999, 99, 419-424.	1.8	100
250	The Mla (Powdery Mildew) Resistance Cluster Is Associated With Three NBS-LRR Gene Families and Suppressed Recombination Within a 240-kb DNA Interval on Chromosome 5S (1HS) of Barley. <i>Genetics</i> , 1999, 153, 1929-1948.	1.2	242
251	Gene expression induced by physical impedance in maize roots. <i>Plant Molecular Biology</i> , 1998, 37, 921-930.	2.0	14
252	Cloning and characterization of a centromere-specific repetitive DNA element from <i>Sorghum bicolor</i> . <i>Theoretical and Applied Genetics</i> , 1998, 96, 832-839.	1.8	59

#	ARTICLE	IF	CITATIONS
253	Brief communication. Tetraploid nature of <i>Sorghum bicolor</i> (L.) Moench. <i>Journal of Heredity</i> , 1998, 89, 188-190.	1.0	36
254	Physical Mapping of the liguleless Linkage Group in <i>Sorghum bicolor</i> Using Rice RFLP-Selected <i>Sorghum</i> BACs. <i>Genetics</i> , 1998, 148, 1983-1992.	1.2	51
255	Microcolinearity in sh2-homologous regions of the maize, rice, and sorghum genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 3431-3435.	3.3	231
256	FISH of a maize sh2-selected sorghum BAC to chromosomes of <i>Sorghum bicolor</i> . <i>Genome</i> , 1997, 40, 475-478.	0.9	33
257	A Large-Insert (130 kbp) Bacterial Artificial Chromosome Library of the Rice Blast Fungus <i>Magnaporthe grisea</i> : Genome Analysis, Contig Assembly, and Gene Cloning. <i>Fungal Genetics and Biology</i> , 1997, 21, 337-347.	0.9	58
258	A rapid procedure for the isolation of <i>C</i> -DNA from plants. <i>Genome</i> , 1997, 40, 138-142.	0.9	219
259	Physical mapping of the rice genome with BACs. , 1997, 35, 115-127.		55
260	Physical mapping of the rice genome with BACs. , 1997, , 115-127.		27
261	A conserved repetitive DNA element located in the centromeres of cereal chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 14210-14213.	3.3	195
262	Gene identification in a complex chromosomal continuum by local genomic cross-referencing. <i>Plant Journal</i> , 1996, 10, 1163-1168.	2.8	63
263	Comparative gene expression in sexual and apomictic ovaries of <i>Pennisetum ciliare</i> (L.) Link.. <i>Plant Molecular Biology</i> , 1996, 32, 1085-1092.	2.0	56
264	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.	1.0	134
265	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.	2.8	287
266	Isolation of megabase-size DNA from sorghum and applications for physical mapping and bacterial and yeast artificial chromosome library construction. <i>Plant Molecular Biology Reporter</i> , 1995, 13, 82-94.	1.0	15
267	Construction and characterization of a bacterial artificial chromosome library of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology Reporter</i> , 1995, 13, 124-128.	1.0	97
268	Construction and Characterization of a Bovine Bacterial Artificial Chromosome Library. <i>Genomics</i> , 1995, 29, 413-425.	1.3	193
269	Fluorescent in situ hybridization of a bacterial artificial chromosome. <i>Genome</i> , 1995, 38, 646-651.	0.9	107
270	Cloning and characterization of the majority of repetitive DNA in cotton (<i>Gossypium</i> L.). <i>Genome</i> , 1995, 38, 1177-1188.	0.9	28

#	ARTICLE	IF	CITATIONS
271	Construction and characterization of bacterial artificial chromosome library of Sorghum bicolor. Nucleic Acids Research, 1994, 22, 4922-4931.	6.5	389
272	A detailed RFLP map of Sorghum bicolor x S. prostratum, suitable for high-density mapping, suggests ancestral duplication of Sorghum chromosomes or chromosomal segments. Theoretical and Applied Genetics, 1994, 87, 925-933.	1.8	224
273	Map-based cloning in crop plants: tomato as a model system II. Isolation and characterization of a set of overlapping yeast artificial chromosomes encompassing the jointless locus. Molecular Genetics and Genomics, 1994, 244, 613-621.	2.4	32
274	Map-based cloning in crop plants. Tomato as a model system: I. Genetic and physical mapping of jointless. Molecular Genetics and Genomics, 1994, 242, 681-688.	2.4	60
275	A simple method for isolation of megabase DNA from cotton. Plant Molecular Biology Reporter, 1994, 12, 110-115.	1.0	8
276	Genome mapping in plants. Current Opinion in Biotechnology, 1993, 4, 142-147.	3.3	41
277	An improved method of plant megabase DNA isolation in agarose microbeads suitable for physical mapping and YAC cloning. Plant Journal, 1993, 4, 893-898.	2.8	41
278	PCR amplification from single seeds, facilitating DNA marker-assisted breeding. Nucleic Acids Research, 1993, 21, 2527-2527.	6.5	13
279	Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. Nucleic Acids Research, 1991, 19, 6553-6568.	6.5	381
280	Promoter analysis of genes that are coordinately expressed during pollen development reveals pollen-specific enhancer sequences and shared regulatory elements. Genes and Development, 1991, 5, 496-507.	2.7	282
281	Molecular and genetic characterization of two pollen-expressed genes that have sequence similarity to pectate lyases of the plant pathogen Erwinia. Plant Molecular Biology, 1990, 14, 17-28.	2.0	167
282	Isolation and expression of an anther-specific gene from tomato. Molecular Genetics and Genomics, 1989, 217, 240-245.	2.4	270
283	Integrative transformation of the yeast Yarrowia lipolytica. Current Genetics, 1985, 10, 39-48.	0.8	113
284	Construction and Application of Genomic DNA Libraries. , 0, , .		1