

Rod A Wing

List of Publications by Year in descending order

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284
papers

50,749
citations

2802
94
h-index

1634
215
g-index

296
all docs

296
docs citations

296
times ranked

36346
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
2	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.6	3,612
3	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	27.8	3,365
4	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>japonica</i>). <i>Science</i> , 2002, 296, 92-100.	12.6	2,866
5	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	27.8	2,860
6	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
7	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.	7.1	1,641
8	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
9	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
10	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	27.8	1,091
11	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	12.6	743
12	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	21.4	656
13	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.	12.6	599
14	Doubling genome size without polyploidization: Dynamics of retrotransposon-driven genomic expansions in <i>Oryza australiensis</i> , a wild relative of rice. <i>Genome Research</i> , 2006, 16, 1262-1269.	5.5	522
15	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013, 500, 335-339.	27.8	468
16	An Integrated Physical and Genetic Map of the Rice Genome. <i>Plant Cell</i> , 2002, 14, 537-545.	6.6	422
17	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.	21.4	413
18	Construction and characterization of bacterial artificial chromosome library of <i>Sorghum bicolor</i> . <i>Nucleic Acids Research</i> , 1994, 22, 4922-4931.	14.5	389

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19	Isolation of molecular markers from specific chromosomal intervals using DNA pools from existing mapping populations. <i>Nucleic Acids Research</i> , 1991, 19, 6553-6568.	14.5	381
20	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.	5.5	378
21	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014, 46, 982-988.	21.4	342
22	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.	2.9	331
23	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	8.8	331
24	Rate Variation Among Nuclear Genes and the Age of Polyploidy in <i>Gossypium</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 633-643.	8.9	325
25	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.	2.2	324
26	JOINTLESS is a MADS-box gene controlling tomato flower abscissionzone development. <i>Nature</i> , 2000, 406, 910-913.	27.8	314
27	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	14.5	295
28	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.	7.1	290
29	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081.	14.5	290
30	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.	5.7	287
31	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	4.8	287
32	Promoter analysis of genes that are coordinately expressed during pollen development reveals pollen-specific enhancer sequences and shared regulatory elements.. <i>Genes and Development</i> , 1991, 5, 496-507.	5.9	282
33	LysM-Type Mycorrhizal Receptor Recruited for Rhizobium Symbiosis in Nonlegume <i>Parasponia</i> . <i>Science</i> , 2011, 331, 909-912.	12.6	273
34	Isolation and expression of an anther-specific gene from tomato. <i>Molecular Genetics and Genomics</i> , 1989, 217, 240-245.	2.4	270
35	Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. <i>PLoS Genetics</i> , 2007, 3, e123.	3.5	270
36	Aluminum tolerance in maize is associated with higher <i>MATE1</i> gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5241-5246.	7.1	265

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37	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	28.9	259
38	The rice genome revolution: from an ancient grain to Green Super Rice. <i>Nature Reviews Genetics</i> , 2018, 19, 505-517.	16.3	251
39	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	12.6	245
40	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.	2.9	242
41	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	12.8	240
42	Functional genomics of cell elongation in developing cotton fibers. <i>Plant Molecular Biology</i> , 2004, 54, 911-929.	3.9	237
43	Microcolinearity in <i>sh2</i> -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.	7.1	231
44	Genome Dynamics and Evolution of the <i>Mla</i> (Powdery Mildew) Resistance Locus in Barley[W]. <i>Plant Cell</i> , 2002, 14, 1903-1917.	6.6	229
45	A detailed RFLP map of <i>Sorghum bicolor</i> x <i>S. propinquum</i> , suitable for high-density mapping, suggests ancestral duplication of <i>Sorghum</i> chromosomes or chromosomal segments. <i>Theoretical and Applied Genetics</i> , 1994, 87, 925-933.	3.6	224
46	A rapid procedure for the isolation of <i>C₀t</i> -1 DNA from plants. <i>Genome</i> , 1997, 40, 138-142.	2.0	219
47	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.	5.5	218
48	<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.	7.1	214
49	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.	7.1	211
50	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
51	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.	5.5	197
52	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.	7.1	195
53	Construction and Characterization of a Bovine Bacterial Artificial Chromosome Library. <i>Genomics</i> , 1995, 29, 413-425.	2.9	193
54	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013, 4, 1595.	12.8	190

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55	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.	3.6	187
56	Rice Transposable Elements: A Survey of 73,000 Sequence-Tagged-Connectors. <i>Genome Research</i> , 2000, 10, 982-990.	5.5	187
57	Toward a Cytological Characterization of the Rice Genome. <i>Genome Research</i> , 2001, 11, 2133-2141.	5.5	182
58	Life at the hyperarid margin: novel bacterial diversity in arid soils of the Atacama Desert, Chile. <i>Extremophiles</i> , 2012, 16, 553-566.	2.3	182
59	The rice paradox: Multiple origins but single domestication in Asian rice. <i>Molecular Biology and Evolution</i> , 2017, 34, msx049.	8.9	178
60	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015, 5, 15655.	3.3	169
61	Molecular and genetic characterization of two pollen-expressed genes that have sequence similarity to pectate lyases of the plant pathogen <i>Erwinia</i> . <i>Plant Molecular Biology</i> , 1990, 14, 17-28.	3.9	167
62	Structure and Architecture of the Maize Genome. <i>Plant Physiology</i> , 2005, 139, 1612-1624.	4.8	159
63	The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. <i>BMC Biology</i> , 2005, 3, 20.	3.8	158
64	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
65	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.	2.9	144
66	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.	3.9	143
67	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.	7.1	141
68	Changes in Regulation of a Transcription Factor Lead to Autogamy in Cultivated Tomatoes. <i>Science</i> , 2007, 318, 643-645.	12.6	141
69	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	5.5	138
70	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.	1.7	137
71	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015, 5, 17394.	3.3	136
72	Genome and evolution of the shade-tolerant medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	8.3	136

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73	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
74	Plant centromere organization: a dynamic structure with conserved functions. <i>Trends in Genetics</i> , 2007, 23, 134-139.	6.7	133
75	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017, 3, 17064.	9.3	133
76	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767.	8.3	133
77	Evolution of a Complex Locus for Terpene Biosynthesis in <i>Solanum</i> . <i>Plant Cell</i> , 2013, 25, 2022-2036.	6.6	132
78	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.	6.6	128
79	The International Oryza Map Alignment Project: development of a genus-wide comparative genomics platform to help solve the 9 billion-people question. <i>Current Opinion in Plant Biology</i> , 2013, 16, 147-156.	7.1	126
80	A Single Molecule Scaffold for the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000711.	3.5	122
81	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	7.8	121
82	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.	7.1	119
83	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
84	The barley ERF-type transcription factor HvRAF confers enhanced pathogen resistance and salt tolerance in <i>Arabidopsis</i> . <i>Planta</i> , 2007, 225, 575-588.	3.2	115
85	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.	9.8	114
86	Integrative transformation of the yeast <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 1985, 10, 39-48.	1.7	113
87	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880.	5.5	112
88	Diploid/Polyploid Syntenic Shuttle Mapping and Haplotype-Specific Chromosome Walking Toward a Rust Resistance Gene (<i>Bru1</i>) in Highly Polyploid Sugarcane (2n ^x 12x 115). <i>Genetics</i> , 2008, 180, 649-660.	2.9	110
89	Fluorescent in situ hybridization of a bacterial artificial chromosome. <i>Genome</i> , 1995, 38, 646-651.	2.0	107
90	Genetic, Physical, and Informatics Resources for Maize. On the Road to an Integrated Map. <i>Plant Physiology</i> , 2002, 130, 1598-1605.	4.8	106

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91	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.	2.9	106
92	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	5.5	105
93	A bacterial artificial chromosome library for sugarcane. <i>Theoretical and Applied Genetics</i> , 1999, 99, 419-424.	3.6	100
94	An Improved Method for Plant BAC Library Construction. , 2003, 236, 3-20.		100
95	Efficient insertional mutagenesis in rice using the maize <i>En1/Spm</i> elements. <i>Plant Journal</i> , 2005, 44, 879-892.	5.7	100
96	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.	5.7	99
97	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014, 5, 5269.	12.8	99
98	Species Trees from Highly Incongruent Gene Trees in Rice. <i>Systematic Biology</i> , 2009, 58, 489-500.	5.6	98
99	Construction and characterization of a bacterial artificial chromosome library of <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology Reporter</i> , 1995, 13, 124-128.	1.8	97
100	Large-Scale Identification of Expressed Sequence Tags Involved in Rice and Rice Blast Fungus Interaction. <i>Plant Physiology</i> , 2005, 138, 105-115.	4.8	96
101	Structural features of the rice chromosome 4 centromere. <i>Nucleic Acids Research</i> , 2004, 32, 2023-2030.	14.5	95
102	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.	6.6	95
103	The Physical and Genetic Framework of the Maize B73 Genome. <i>PLoS Genetics</i> , 2009, 5, e1000715.	3.5	95
104	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.	4.8	94
105	The Wild Relative of Rice: Genomes and Genomics. , 2013, , 9-25.		94
106	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	7.8	94
107	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon Fusarium wilt (<i>Fom2</i>). <i>Genome</i> , 2001, 44, 154-162.	2.0	92
108	Access to the Maize Genome: An Integrated Physical and Genetic Map: Table I.. <i>Plant Physiology</i> , 2002, 128, 9-12.	4.8	91

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109	The Cardamine <i>hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	9.3	90
110	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.	7.1	90
111	Microcolinearity and genome evolution in the <i>AdhA</i> region of diploid and polyploid cotton (<i>Gossypium</i>). <i>Plant Journal</i> , 2007, 50, 995-1006.	5.7	89
112	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1516-1517.	12.6	89
113	Aflatoxin-free transgenic maize using host-induced gene silencing. <i>Science Advances</i> , 2017, 3, e1602382.	10.3	88
114	Whole-Genome Validation of High-Information-Content Fingerprinting. <i>Plant Physiology</i> , 2005, 139, 27-38.	4.8	86
115	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	2.8	86
116	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	5.3	86
117	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.	2.2	84
118	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.	9.6	82
119	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.	4.8	81
120	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.	5.5	80
121	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.	18.7	80
122	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.	3.6	79
123	Profiling Bacterial Diversity and Taxonomic Composition on Speleothem Surfaces in Kartchner Caverns, AZ. <i>Microbial Ecology</i> , 2013, 65, 371-383.	2.8	78
124	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019, 10, 4680.	12.8	75
125	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	5.5	73
126	<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.	2.9	73

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127	Localization of jointless-2 gene in the centromeric region of tomato chromosome 12 based on high resolution genetic and physical mapping. Theoretical and Applied Genetics, 2004, 108, 190-196.	3.6	71
128	Candidate gene database and transcript map for peach, a model species for fruit trees. Theoretical and Applied Genetics, 2005, 110, 1419-1428.	3.6	71
129	Evidence of multiple horizontal transfers of the long terminal repeat retrotransposon <i>RIRE1</i> within the genus <i>Oryza</i> . Plant Journal, 2008, 53, 950-959.	5.7	70
130	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (<i>Phaseolus vulgaris</i> L.) Genome. Tropical Plant Biology, 2008, 1, 40-48.	1.9	70
131	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . Genome Biology, 2020, 21, 259.	8.8	68
132	The Amborella genome: an evolutionary reference for plant biology. Genome Biology, 2008, 9, 402.	9.6	67
133	Sorghum Expressed Sequence Tags Identify Signature Genes for Drought, Pathogenesis, and Skotomorphogenesis from a Milestone Set of 16,801 Unique Transcripts. Plant Physiology, 2005, 139, 869-884.	4.8	66
134	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon Fusarium wilt (<i>Fom2</i>). Genome, 2001, 44, 154-162.	2.0	66
135	A bacterial artificial chromosome library for soybean PI 437654 and identification of clones associated with cyst nematode resistance. Plant Molecular Biology, 1999, 41, 25-32.	3.9	65
136	A Fine Physical Map of the Rice Chromosome 4. Genome Research, 2002, 12, 817-823.	5.5	64
137	A Versatile Transposon-Based Activation Tag Vector System for Functional Genomics in Cereals and Other Monocot Plants. Plant Physiology, 2008, 146, 189-199.	4.8	64
138	Gene identification in a complex chromosomal continuum by local genomic cross-referencing. Plant Journal, 1996, 10, 1163-1168.	5.7	63
139	Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. Nature Genetics, 2022, 54, 227-231.	21.4	63
140	A chromosome-scale assembly of allotetraploid <i>Brassica juncea</i> (AABB) elucidates comparative architecture of the A and B genomes. Plant Biotechnology Journal, 2021, 19, 602-614.	8.3	62
141	Evaluation of genetic variation in the daylily (<i>Hemerocallis</i> spp.) using AFLP markers. Theoretical and Applied Genetics, 2001, 102, 489-496.	3.6	61
142	Ginger and turmeric expressed sequence tags identify signature genes for rhizome identity and development and the biosynthesis of curcuminoids, gingerols and terpenoids. BMC Plant Biology, 2013, 13, 27.	3.6	61
143	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
144	Deep and comparative analysis of the mycelium and appressorium transcriptomes of <i>Magnaporthe grisea</i> using MPSS, RL-SAGE, and oligoarray methods. BMC Genomics, 2006, 7, 310.	2.8	60

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145	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.	8.3	60
146	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.	3.6	59
147	De Novo Next Generation Sequencing of Plant Genomes. <i>Rice</i> , 2009, 2, 35-43.	4.0	59
148	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59
149	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.	2.1	58
150	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. <i>Molecular Biology and Evolution</i> , 2008, 25, 1415-1428.	8.9	57
151	Australian <i>Oryza</i> : Utility and Conservation. <i>Rice</i> , 2010, 3, 235-241.	4.0	57
152	Access to the Maize Genome: An Integrated Physical and Genetic Map. <i>Plant Physiology</i> , 2002, 128, 9-12.	4.8	57
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