

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	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	13.7	3,854
2	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
3	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	13.7	3,365
4	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. japonica). <i>Science</i> , 2002, 296, 92-100.	6.0	2,866
5	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
6	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	13.7	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.	3.3	1,641
8	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	13.7	1,416
9	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
10	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018, 557, 43-49.	13.7	1,091
11	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	6.0	743
12	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011, 43, 101-108.	9.4	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.	6.0	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.	2.4	522
15	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013, 500, 335-339.	13.7	468
16	An Integrated Physical and Genetic Map of the Rice Genome. <i>Plant Cell</i> , 2002, 14, 537-545.	3.1	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.	9.4	413
18	Construction and characterization of bacterial artificial chromosome library of <i>Sorghum bicolor</i> . <i>Nucleic Acids Research</i> , 1994, 22, 4922-4931.	6.5	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.	6.5	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.	2.4	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.	9.4	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.	1.2	331
23	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	3.8	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.	3.5	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.	1.0	324
26	JOINTLESS is a MADS-box gene controlling tomato flower abscissionzone development. <i>Nature</i> , 2000, 406, 910-913.	13.7	314
27	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	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.	3.3	290
29	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081.	6.5	290
30	Preparation of megabase-size DNA from plant nuclei. <i>Plant Journal</i> , 1995, 7, 175-184.	2.8	287
31	A New Resource for Cereal Genomics: 22K Barley GeneChip Comes of Age. <i>Plant Physiology</i> , 2004, 134, 960-968.	2.3	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.	2.7	282
33	LysM-Type Mycorrhizal Receptor Recruited for Rhizobium Symbiosis in Nonlegume <i>Parasponia</i> . <i>Science</i> , 2011, 331, 909-912.	6.0	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.	1.5	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.	3.3	265

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37	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021, 184, 1156-1170.e14.	13.5	259
38	The rice genome revolution: from an ancient grain to Green Super Rice. <i>Nature Reviews Genetics</i> , 2018, 19, 505-517.	7.7	251
39	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. <i>Science</i> , 2003, 300, 1566-1569.	6.0	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.	1.2	242
41	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
42	Functional genomics of cell elongation in developing cotton fibers. <i>Plant Molecular Biology</i> , 2004, 54, 911-929.	2.0	237
43	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
44	Genome Dynamics and Evolution of the Mla (Powdery Mildew) Resistance Locus in Barley [W]. <i>Plant Cell</i> , 2002, 14, 1903-1917.	3.1	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.	1.8	224
46	A rapid procedure for the isolation of <i>C</i> -DNA from plants. <i>Genome</i> , 1997, 40, 138-142.	0.9	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.	2.4	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.	3.3	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.	3.3	211
50	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	1.7	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.	2.4	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.	3.3	195
53	Construction and Characterization of a Bovine Bacterial Artificial Chromosome Library. <i>Genomics</i> , 1995, 29, 413-425.	1.3	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.	5.8	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.	1.8	187
56	Rice Transposable Elements: A Survey of 73,000 Sequence-Tagged-Connectors. <i>Genome Research</i> , 2000, 10, 982-990.	2.4	187
57	Toward a Cytological Characterization of the Rice Genome. <i>Genome Research</i> , 2001, 11, 2133-2141.	2.4	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.	0.9	182
59	The rice paradox: Multiple origins but single domestication in Asian rice. <i>Molecular Biology and Evolution</i> , 2017, 34, msx049.	3.5	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.	1.6	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.	2.0	167
62	Structure and Architecture of the Maize Genome. <i>Plant Physiology</i> , 2005, 139, 1612-1624.	2.3	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.	1.7	158
64	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	13.7	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.	1.2	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.	2.0	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.	3.3	141
68	Changes in Regulation of a Transcription Factor Lead to Autogamy in Cultivated Tomatoes. <i>Science</i> , 2007, 318, 643-645.	6.0	141
69	A global assembly of cotton ESTs. <i>Genome Research</i> , 2006, 16, 441-450.	2.4	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.	0.8	137
71	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
72	Genome and evolution of the shade-tolerant medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	4.1	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.	1.0	134
74	Plant centromere organization: a dynamic structure with conserved functions. <i>Trends in Genetics</i> , 2007, 23, 134-139.	2.9	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.	4.7	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.	3.9	133
77	Evolution of a Complex Locus for Terpene Biosynthesis in <i>Solanum</i> . <i>Plant Cell</i> , 2013, 25, 2022-2036.	3.1	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.	3.1	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.	3.5	126
80	A Single Molecule Scaffold for the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000711.	1.5	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.	3.4	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.	3.3	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.	1.6	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.	4.4	114
86	Integrative transformation of the yeast <i>Yarrowia lipolytica</i> . <i>Current Genetics</i> , 1985, 10, 39-48.	0.8	113
87	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019, 29, 870-880.	2.4	112
88	Diploid/Polyploid Syntenic Shuttle Mapping and Haplotype-Specific Chromosome Walking Toward a Rust Resistance Gene (<i>Bru1</i>) in Highly Polyploid Sugarcane ($2n \times 12x$). <i>Genetics</i> , 2008, 180, 649-660.	1.2	110
89	Fluorescent in situ hybridization of a bacterial artificial chromosome. <i>Genome</i> , 1995, 38, 646-651.	0.9	107
90	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

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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.	1.2	106
92	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	2.4	105
93	A bacterial artificial chromosome library for sugarcane. <i>Theoretical and Applied Genetics</i> , 1999, 99, 419-424.	1.8	100
94	An Improved Method for Plant BAC Library Construction. , 2003, 236, 3-20.		100
95	Efficient insertional mutagenesis in rice using the maize En/Spm elements. <i>Plant Journal</i> , 2005, 44, 879-892.	2.8	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.	2.8	99
97	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014, 5, 5269.	5.8	99
98	Species Trees from Highly Incongruent Gene Trees in Rice. <i>Systematic Biology</i> , 2009, 58, 489-500.	2.7	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.	1.0	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.	2.3	96
101	Structural features of the rice chromosome 4 centromere. <i>Nucleic Acids Research</i> , 2004, 32, 2023-2030.	6.5	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.	3.1	95
103	The Physical and Genetic Framework of the Maize B73 Genome. <i>PLoS Genetics</i> , 2009, 5, e1000715.	1.5	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.	2.3	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.	3.4	94
107	Melon bacterial artificial chromosome (BAC) library construction using improved methods and identification of clones linked to the locus conferring resistance to melon <i>Fusarium wilt</i> (<i>Fom-2</i>). <i>Genome</i> , 2001, 44, 154-162.	0.9	92
108	Access to the Maize Genome: An Integrated Physical and Genetic Map: Table I.. <i>Plant Physiology</i> , 2002, 128, 9-12.	2.3	91

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109	The <i>Cardamine hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016, 2, 16167.	4.7	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.	3.3	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.	2.8	89
112	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1516-1517.	6.0	89
113	Aflatoxin-free transgenic maize using host-induced gene silencing. <i>Science Advances</i> , 2017, 3, e1602382.	4.7	88
114	Whole-Genome Validation of High-Information-Content Fingerprinting. <i>Plant Physiology</i> , 2005, 139, 27-38.	2.3	86
115	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
116	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020, 7, 113.	2.4	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.	1.0	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.	13.9	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.	2.3	81
120	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. <i>Genome Research</i> , 2004, 14, 1474-1482.	2.4	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.	8.6	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.	1.6	79
123	Profiling Bacterial Diversity and Taxonomic Composition on Speleothem Surfaces in Kartchner Caverns, AZ. <i>Microbial Ecology</i> , 2013, 65, 371-383.	1.4	78
124	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019, 10, 4680.	5.8	75
125	Sequence, annotation, and analysis of synteny between rice chromosome 3 and diverged grass species. <i>Genome Research</i> , 2005, 15, 1284-1291.	2.4	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.	1.2	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. <i>Theoretical and Applied Genetics</i> , 2004, 108, 190-196.	1.8	71
128	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
129	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
130	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
131	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
132	The Amborella genome: an evolutionary reference for plant biology. <i>Genome Biology</i> , 2008, 9, 402.	13.9	67
133	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
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>Fom-2</i>). <i>Genome</i> , 2001, 44, 154-162.	0.9	66
135	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
136	A Fine Physical Map of the Rice Chromosome 4. <i>Genome Research</i> , 2002, 12, 817-823.	2.4	64
137	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
138	Gene identification in a complex chromosomal continuum by local genomic cross-referencing. <i>Plant Journal</i> , 1996, 10, 1163-1168.	2.8	63
139	Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. <i>Nature Genetics</i> , 2022, 54, 227-231.	9.4	63
140	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
141	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
142	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
143	Map-based cloning in crop plants. Tomato as a model system: I. Genetic and physical mapping of jointless. <i>Molecular Genetics and Genomics</i> , 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. <i>BMC Genomics</i> , 2006, 7, 310.	1.2	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.	4.1	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.	1.8	59
147	De Novo Next Generation Sequencing of Plant Genomes. <i>Rice</i> , 2009, 2, 35-43.	1.7	59
148	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	1.2	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.	0.9	58
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