Rod A Wing

List of Publications by Year
in descending order

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	Rice domestication. Current Biology, 2022, 32, R20-R24.	3.9	14
2	Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	7
3	Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning. Nature Genetics, 2022, 54, 227-231.	21.4	63
4	Gene fusion as an important mechanism to generate new genes in the genus Oryza. Genome Biology, 2022, 23, .	8.8	7
5	A chromosomeâ€scale assembly of allotetraploid Brassica juncea (AABB) elucidates comparative architecture of the A and B genomes. Plant Biotechnology Journal, 2021, 19, 602-614.	8.3	62
6	Evolution and diversification of reproductive phased small interfering RNAs in Oryza species. New Phytologist, 2021, 229, 2970-2983.	7.3	12
7	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. Nature, 2021, 590, 438-444.	27.8	144
8	A route to de novo domestication of wild allotetraploid rice. Cell, 2021, 184, 1156-1170.e14.	28.9	259
9	The chromosomeâ€scale reference genome of safflower (Carthamus tinctorius) provides insights into linoleic acid and flavonoid biosynthesis. Plant Biotechnology Journal, 2021, 19, 1725-1742.	8.3	60
10	Starch Synthesis-Related Genes (SSRG) Evolution in the Genus Oryza. Plants, 2021, 10, 1057.	3.5	0
11	Two gap-free reference genomes and a global view of the centromere architecture in rice. Molecular Plant, 2021, 14, 1757-1767.	8.3	133
12	Potential of Platinum Standard Reference Genomes to Exploit Natural Variation in the Wild Relatives of Rice. Frontiers in Plant Science, 2020, 11, 579980.	3.6	15
13	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial Populus trichocarpa. Genome Biology, 2020, 21, 259.	8.8	68
14	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). GigaScience, 2020, 9, .	6.4	47
15	Evolution and diversity of the wild rice Oryza officinalis complex, across continents genome types, and ploidy levels. Genome Biology and Evolution, 2020, 12, 413-428.	2.5	17
16	Evolutionary Dynamics of Abundant 7-bp Satellites in the Genome ofDrosophila virilis. Molecular Biology and Evolution, 2020, 37, 1362-1375.	8.9	23
17	A platinum standard pan-genome resource that represents the population structure of Asian rice. Scientific Data, 2020, 7, 113.	5.3	86
18	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. Scientific Reports, 2020, 10, 6112.	3.3	30

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19	Genome-wide association mapping of date palm fruit traits. Nature Communications, 2019, 10, 4680.	12.8	75
20	Functional screening of genes from a halophyte wild rice relative Porteresia coarctata in Arabidopsis model identifies candidate genes involved in salt tolerance. Current Plant Biology, 2019, 18, 100107.	4.7	14
21	Structural variants in 3000 rice genomes. Genome Research, 2019, 29, 870-880.	5.5	112
22	The Genomics of Oryza Species Provides Insights into Rice Domestication and Heterosis. Annual Review of Plant Biology, 2019, 70, 639-665.	18.7	80
23	Rapid evolution of protein diversity by de novo origination in Oryza. Nature Ecology and Evolution, 2019, 3, 679-690.	7.8	121
24	Genome sequence of the model rice variety KitaakeX. BMC Genomics, 2019, 20, 905.	2.8	59
25	Progress in single-access information systems for wheat and rice crop improvement. Briefings in Bioinformatics, 2019, 20, 565-571.	6.5	4
26	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. Nature, 2018, 557, 43-49.	27.8	1,091
27	Genome and evolution of the shadeâ€requiring medicinal herb Panax ginseng. Plant Biotechnology Journal, 2018, 16, 1904-1917.	8.3	136
28	Genotyping by sequencing of rice interspecific backcross inbred lines identifies QTLs for grain weight and grain length. Euphytica, 2018, 214, 1.	1.2	29
29	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
30	Comparison of Oryza sativa and Oryza brachyantha Genomes Reveals Selection-Driven Gene Escape from the Centromeric Regions. Plant Cell, 2018, 30, 1729-1744.	6.6	22
31	Genetic control of seed shattering during African rice domestication. Nature Plants, 2018, 4, 331-337.	9.3	55
32	The rice genome revolution: from an ancient grain to Green Super Rice. Nature Reviews Genetics, 2018, 19, 505-517.	16.3	251
33	The rice paradox: Multiple origins but single domestication in Asian rice. Molecular Biology and Evolution, 2017, 34, msx049.	8.9	178
34	Aflatoxin-free transgenic maize using host-induced gene silencing. Science Advances, 2017, 3, e1602382.	10.3	88
35	Evolutionary analysis of the SUB1 locus across the Oryza genomes. Rice, 2017, 10, 4.	4.0	25
36	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. Nature Plants, 2017, 3, 17064.	9.3	133

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37	Young inversion with multiple linked QTLs under selection in a hybrid zone. Nature Ecology and Evolution, 2017, 1, 119.	7.8	94
38	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. Nature Communications, 2017, 8, 1279.	12.8	240
39	Genetic variation for domestication-related traits revealed in a cultivated rice, Nipponbare (Oryza) Tj ETQq1 1 0.784314 rgBT /Overlock	2.1	5
40	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12003-12008.	7.1	90
41	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. Plant Biotechnology Journal, 2017, 15, 765-774.	8.3	51
42	Rice SNP-seek database update: new SNPs, indels, and queries. Nucleic Acids Research, 2017, 45, D1075-D1081.	14.5	290
43	DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. Genome Biology, 2016, 17, 92.	8.8	14
44	The Dark Side of the Genome: Revealing the Native Transposable Element/Repeat Content of Eukaryotic Genomes. Molecular Plant, 2016, 9, 1664-1666.	8.3	4
45	Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. Bioinformatics, 2016, 32, 3058-3064.	4.1	22
46	Extensive sequence divergence between the reference genomes of two elite indica rice varieties Zhenshan 97 and Minghui 63. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5163-71.	7.1	211
47	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. Nature Communications, 2016, 7, 12790.	12.8	51
48	The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. Nature Plants, 2016, 2, 16167.	9.3	90
49	Tracing ancestor rice of Suriname Maroons back to its African origin. Nature Plants, 2016, 2, 16149.	9.3	31
50	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. Scientific Data, 2016, 3, 160076.	5.3	34
51	The impact and origin of copy number variations in the Oryza species. BMC Genomics, 2016, 17, 261.	2.8	30
52	Development and validation of cross-transferable and polymorphic DNA markers for detecting alien genome introgression in Oryza sativa from Oryza brachyantha. Molecular Genetics and Genomics, 2016, 291, 1783-1794.	2.1	10
53	Evolution of plant genome architecture. Genome Biology, 2016, 17, 37.	8.8	331
54	Genome and Comparative Transcriptomics of African Wild Rice Oryza longistaminata Provide Insights into Molecular Mechanism of Rhizomatousness and Self-Incompatibility. Molecular Plant, 2015, 8, 1683-1686.	8.3	49

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55	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of Oryza AA genome species. Scientific Reports, 2015, 5, 15655.	3.3	169
56	Red clover (Trifolium pratense L.) draft genome provides a platform for trait improvement. Scientific Reports, 2015, 5, 17394.	3.3	136
57	Recurrent sequence exchange between homeologous grass chromosomes. Plant Journal, 2015, 84, 747-759.	5.7	5
58	Transposons play an important role in the evolution and diversification of centromeres among closely related species. Frontiers in Plant Science, 2015, 6, 216.	3.6	51
59	Exceptional reduction of the plastid genome of saguaro cactus (Carnegiea gigantea): Loss of the ndh gene suite and inverted repeat. American Journal of Botany, 2015, 102, 1115-1127.	1.7	137
60	Sequencing of 15Â622 geneâ€bearing BAC s clarifies the geneâ€dense regions of the barley genome. Plant Journal, 2015, 84, 216-227.	5.7	36
61	Harvesting riceâ€™s dispensable genome. Genome Biology, 2015, 16, 217.	8.8	6
62	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. BMC Genomics, 2015, 16, 538.	2.8	86
63	Fifteen Million Years of Evolution in the Oryza Genus Shows Extensive Gene Family Expansion. Molecular Plant, 2014, 7, 642-656.	8.3	54
64	Making a living while starving in the dark: metagenomic insights into the energy dynamics of a carbonate cave. ISME Journal, 2014, 8, 478-491.	9.8	114
65	Comparative <scp>BAC</scp>â€based physical mapping of <scp>O</scp>ryza sativa ssp. indica var. 93â€"11 and evaluation of the two rice reference sequence assemblies. Plant Journal, 2014, 77, 795-805.	5.7	16
66	Disentangling Methodological and Biological Sources of Gene Tree Discordance on Oryza (Poaceae) Chromosome 3. Systematic Biology, 2014, 63, 645-659.	5.6	43
67	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. Nature Communications, 2014, 5, 5269.	12.8	99
68	The genome sequence of African rice (Oryza glaberrima) and evidence for independent domestication. Nature Genetics, 2014, 46, 982-988.	21.4	342
69	Global Genomic Diversity of Oryza sativa Varieties Revealed by Comparative Physical Mapping. Genetics, 2014, 196, 937-949.	2.9	10
70	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	21.4	1,159
71	Profiling Bacterial Diversity and Taxonomic Composition on Speleothem Surfaces in Kartchner Caverns, AZ. Microbial Ecology, 2013, 65, 371-383.	2.8	78
72	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

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73	The Wild Relative of Rice: Genomes and Genomics. , 2013, , 9-25.		94
74	The Amborella Genome and the Evolution of Flowering Plants. Science, 2013, 342, 1241089.	12.6	743
75	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm Amborella. Science, 2013, 342, 1516-1517.	12.6	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.	7.1	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.	7.1	126
78	Whole-genome sequencing of Oryza brachyantha reveals mechanisms underlying Oryza genome evolution. Nature Communications, 2013, 4, 1595.	12.8	190
79	BAC Library Development and Clone Characterization for Dormancy-Responsive DREB4A, DAM, and FT from Leafy Spurge (Euphorbia esula) Identifies Differential Splicing and Conserved Promoter Motifs. Weed Science, 2013, 61, 303-309.	1.5	11
80	BAC-end sequences analysis provides first insights into coffee (Coffea canephora P.) genome composition and evolution. Plant Molecular Biology, 2013, 83, 177-189.	3.9	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.	2.5	11
82	Genomic Resources for Gene Discovery, Functional Genome Annotation, and Evolutionary Studies of Maize and Its Close Relatives. Genetics, 2013, 195, 723-737.	2.9	15
83	Evolution of a Complex Locus for Terpene Biosynthesis in Solanum Â Â. Plant Cell, 2013, 25, 2022-2036.	6.6	132
84	Grain Quality. , 2013, , 237-254.		8
85	The Reference Genome of the Halophytic Plant Eutrema salsugineum. Frontiers in Plant Science, 2013, 4, 46.	3.6	198
86	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. Nature, 2013, 500, 335-339.	27.8	468
87	Aluminum tolerance in maize is associated with higherMATE1gene copy number. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5241-5246.	7.1	265
88	Dynamic Intra-Japonica Subspecies Variation and Resource Application. Molecular Plant, 2012, 5, 218-230.	8.3	23
89	Ortholog Alleles at Xa3/Xa26 Locus Confer Conserved Race-Specific Resistance against Xanthomonas oryzae in Rice. Molecular Plant, 2012, 5, 281-290.	8.3	37
90	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416

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91	A BAC library of the SP80-3280 sugarcane variety (saccharum sp.) and its inferred microsynteny with the sorghum genome. BMC Research Notes, 2012, 5, 185.	1.4	47
92	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
93	Life at the hyperarid margin: novel bacterial diversity in arid soils of the Atacama Desert, Chile. Extremophiles, 2012, 16, 553-566.	2.3	182
94	Integration of the Draft Sequence and Physical Map as a Framework for Genomic Research in Soybean (Glycine max (L.) Merr.) and Wild Soybean (Glycine soja Sieb. and Zucc.). G3: Genes, Genomes, Genetics, 2012, 2, 321-329.	1.8	9
95	Comparative Sequence Analysis of the Ghd7 Orthologous Regions Revealed Movement of Ghd7 in the Grass Genomes. PLoS ONE, 2012, 7, e50236.	2.5	14
96	LysM-Type Mycorrhizal Receptor Recruited for Rhizobium Symbiosis in Nonlegume Parasponia. Science, 2011, 331, 909-912.	12.6	273
97	A physical map for the Amborella trichopoda genome sheds light on the evolution of angiosperm genome structure. Genome Biology, 2011, 12, R48.	9.6	28
98	The genome of Theobroma cacao. Nature Genetics, 2011, 43, 101-108.	21.4	656
99	Molecular and Cytological Characterization of Centromeric Retrotransposons in a Wild Relative of Rice, Oryza granulata. Tropical Plant Biology, 2011, 4, 217-227.	1.9	1
100	Gene-based SSR markers for common bean (Phaseolus vulgaris L.) derived from root and leaf tissue ESTs: an integration of the BMc series. BMC Plant Biology, 2011, 11, 50.	3.6	79
101	Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. BMC Genomics, 2011, 12, 137.	2.8	46
102	Exceptional lability of a genomic complex in rice and its close relatives revealed by interspecific and intraspecific comparison and population analysis. BMC Genomics, 2011, 12, 142.	2.8	14
103	Long-Range and Targeted Ectopic Recombination between the Two Homeologous Chromosomes 11 and 12 in Oryza Species. Molecular Biology and Evolution, 2011, 28, 3139-3150.	8.9	23
104	The 19 Genomes of Drosophila: A BAC Library Resource for Genus-Wide and Genome-Scale Comparative Evolutionary Research. Genetics, 2011, 187, 1023-1030.	2.9	22
105	Conservation and Purifying Selection of Transcribed Genes Located in a Rice Centromere. Plant Cell, 2011, 23, 2821-2830.	6.6	22
106	Construction, Characterization, and Preliminary BAC-End Sequence Analysis of a Bacterial Artificial Chromosome Library of the Tea Plant (Camellia sinensis). Journal of Biomedicine and Biotechnology, 2011, 2011, 1-8.	3.0	11
107	Phylogenomic Analysis of BAC-end Sequence Libraries in <I>Oryza</I> (Poaceae). Systematic Botany, 2010, 35, 512-523.	0.5	8
108	Genomic structure and evolution of the Pi2/9 locus in wild rice species. Theoretical and Applied Genetics, 2010, 121, 295-309.	3.6	25

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109	Australian Oryza: Utility and Conservation. Rice, 2010, 3, 235-241.	4.0	57
110	Assessing the Extent of Substitution Rate Variation of Retrotransposon Long Terminal Repeat Sequences in Oryza sativa and Oryza glaberrima. Rice, 2010, 3, 242-250.	4.0	5
111	The Future of Rice Genomics: Sequencing the Collective Oryza Genome. Rice, 2010, 3, 89-97.	4.0	21
112	Dynamic Oryza Genomes: Repetitive DNA Sequences as Genome Modeling Agents. Rice, 2010, 3, 251-269.	4.0	15
113	A draft physical map of a D-genome cotton species (Gossypium raimondii). BMC Genomics, 2010, 11, 395.	2.8	48
114	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	27.8	3,854
115	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus Oryza. Plant Journal, 2010, 63, 430-442.	5.7	48
116	Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus Oryza. Plant Journal, 2010, 63, 990-1003.	5.7	47
117	Orthologous Comparisons of the Hd1 Region across Genera Reveal Hd1 Gene Lability within Diploid Oryza Species and Disruptions to Microsynteny in Sorghum. Molecular Biology and Evolution, 2010, 27, 2487-2506.	8.9	31
118	Extensive Gene Conversion Drives the Concerted Evolution of Paralogous Copies of the SRY Gene in European Rabbits. Molecular Biology and Evolution, 2010, 27, 2437-2440.	8.9	26
119	The Oryza BAC resource: a genus-wide and genome scale tool for exploring rice genome evolution and leveraging useful genetic diversity from wild relatives. Breeding Science, 2010, 60, 536-543.	1.9	34
120	An Integrated Physical, Genetic and Cytogenetic Map of Brachypodium distachyon, a Model System for Grass Research. PLoS ONE, 2010, 5, e13461.	2.5	45
121	The Physical and Genetic Framework of the Maize B73 Genome. PLoS Genetics, 2009, 5, e1000715.	3.5	95
122	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. PLoS Genetics, 2009, 5, e1000728.	3.5	39
123	Hamiltonella defensa , genome evolution of protective bacterial endosymbiont from pathogenic ancestors. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9063-9068.	7.1	214
124	Dynamic Evolution ofOryzaGenomes Is Revealed by Comparative Genomic Analysis of a Genus-Wide Vertical Data Set. Plant Cell, 2009, 20, 3191-3209.	6.6	128
125	Comparative sequence analysis of MONOCULM1 -orthologous regions in 14 Oryza genomes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2071-2076.	7.1	119
126	Species Trees from Highly Incongruent Gene Trees in Rice. Systematic Biology, 2009, 58, 489-500.	5.6	98

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127	De Novo Next Generation Sequencing of Plant Genomes. Rice, 2009, 2, 35-43.	4.0	59
128	A lineageâ€specific centromere retrotransposon in Oryza brachyantha. Plant Journal, 2009, 60, 820-831.	5.7	41
129	Human gut microbiota in obesity and after gastric bypass. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2365-2370.	7.1	1,641
130	Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in Thellungiella halophila and Arabidopsis thaliana. Genomics, 2009, 94, 196-203.	2.9	17
131	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	12.6	3,612
132	A Single Molecule Scaffold for the Maize Genome. PLoS Genetics, 2009, 5, e1000711.	3.5	122
133	Evidence of multiple horizontal transfers of the long terminal repeat retrotransposon RIRE1 within the genus Oryza. Plant Journal, 2008, 53, 950-959.	5.7	70
134	Rapid and Differential Proliferation of the Ty3-Gypsy LTR Retrotransposon Atlantys in the Genus Oryza. Rice, 2008, 1, 85-99.	4.0	7
135	The Promoter Signatures in Rice LEA Genes Can Be Used to Build a Co-expressing LEA Gene Network. Rice, 2008, 1, 177-187.	4.0	14
136	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (Phaseolus vulgaris L.) Genome. Tropical Plant Biology, 2008, 1, 40-48.	1.9	70
137	Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. BMC Genomics, 2008, 9, 621.	2.8	11
138	A fruitful outcome to the papaya genome project. Genome Biology, 2008, 9, 227.	9.6	9
139	The Amborella genome: an evolutionary reference for plant biology. Genome Biology, 2008, 9, 402.	9.6	67
140	Construction, alignment and analysis of 12 framework physical maps that represent the 10 genome types of the genus Oryza. Genome Biology, 2008, 9, R45.	9.6	82
141	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. Genome, 2008, 51, 294-302.	2.0	50
142	Diploid/Polyploid Syntenic Shuttle Mapping and Haplotype-Specific Chromosome Walking Toward a Rust Resistance Gene (Bru1) in Highly Polyploid Sugarcane (2n âˆ¼ 12x âˆ¼ 115). Genetics, 2008, 180, 649-660.	2.9	110
143	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. Molecular Biology and Evolution, 2008, 25, 1415-1428.	8.9	57
144	The Subtelomere of Oryza sativa Chromosome 3 Short Arm as a Hot Bed of New Gene Origination in Rice. Molecular Plant, 2008, 1, 839-850.	8.3	36

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145	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
146	Construction of an Amaranthus hypochondriacus Bacterial Artificial Chromosome Library and Genomic Sequencing of Herbicide Target Genes. Crop Science, 2008, 48, S-85.	1.8	23
147	Evolutionary History and Positional Shift of a Rice Centromere. Genetics, 2007, 177, 1217-1220.	2.9	29
148	The Rice Annotation Project Database (RAP-DB): 2008 update. Nucleic Acids Research, 2007, 36, D1028-D1033.	14.5	295
149	Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. PLoS Genetics, 2007, 3, e123.	3.5	270
150	Comparative Physical Mapping Between Oryza sativa (AA Genome Type) and O. punctata (BB Genome) Tj ETQq0 0 0 rgBT /Overlock 10	2.9	49
151	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. Genome Research, 2007, 17, 175-183.	5.5	218
152	Magnaporthe grisea Infection Triggers RNA Variation and Antisense Transcript Expression in Rice. Plant Physiology, 2007, 144, 524-533.	4.8	29
153	Efficacy of clone fingerprinting methodologies. Genomics, 2007, 89, 160-165.	2.9	21
154	Rice Genome Sequence: The Foundation for Understanding the Genetic Systems. , 2007, , 5-20.		3
155	The Oryza Map Alignment Project (OMAP): A New Resource for Comparative Genome Studies within Oryza. , 2007, , 395-409.		9
156	Changes in Regulation of a Transcription Factor Lead to Autogamy in Cultivated Tomatoes. Science, 2007, 318, 643-645.	12.6	141
157	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
158	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (Gossypium). Plant Journal, 2007, 50, 995-1006.	5.7	89
159	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genusOryza. Plant Journal, 2007, 52, 342-351.	5.7	99
160	Transposable element distribution, abundance and role in genome size variation in the genus Oryza. BMC Evolutionary Biology, 2007, 7, 152.	3.2	115
161	Plant centromere organization: a dynamic structure with conserved functions. Trends in Genetics, 2007, 23, 134-139.	6.7	133
162	Development of a BAC library for yellow-poplar (Liriodendron tulipifera) and the identification of genes associated with flower development and lignin biosynthesis. Tree Genetics and Genomes, 2007, 3, 215-225.	1.6	25

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163	The barley ERF-type transcription factor HvRAF confers enhanced pathogen resistance and salt tolerance in Arabidopsis. Planta, 2007, 225, 575-588.	3.2	115
164	RL-SAGE and microarray analysis of the rice transcriptome after Rhizoctonia solani infection. Molecular Genetics and Genomics, 2007, 278, 421-431.	2.1	50
165	Differential lineage-specific amplification of transposable elements is responsible for genome size variation in Gossypium. Genome Research, 2006, 16, 1252-1261.	5.5	378
166	Utilization of a zebra finch BAC library to determine the structure of an avian androgen receptor genomic region. Genomics, 2006, 87, 181-190.	2.9	25
167	Two highly representative rice BAC libraries of japonica cv Tainung 67 suitable for rice structural and functional genomic research. Plant Science, 2006, 170, 889-896.	3.6	0
168	A bacterial artificial chromosome library for Biomphalaria glabrata, intermediate snail host of Schistosoma mansoni. Memorias Do Instituto Oswaldo Cruz, 2006, 101, 167-177.	1.6	36
169	Single Nucleotide Polymorphisms and Insertionâ€"Deletions for Genetic Markers and Anchoring the Maize Fingerprint Contig Physical Map. Crop Science, 2006, 46, 12-21.	1.8	51
170	MGOS: A Resource for Studying Magnaporthe grisea and Oryza sativa Interactions. Molecular Plant-Microbe Interactions, 2006, 19, 1055-1061.	2.6	24
171	New Resources for Marine Genomics: Bacterial Artificial Chromosome Libraries for the Eastern and Pacific Oysters (Crassostrea virginica and C. gigas). Marine Biotechnology, 2006, 8, 521-533.	2.4	53
172	Construction of a nurse shark (Ginglymostoma cirratum) bacterial artificial chromosome (BAC) library and a preliminary genome survey. BMC Genomics, 2006, 7, 106.	2.8	27
173	Integration of hybridization-based markers (overgos) into physical maps for comparative and evolutionary explorations in the genus Oryza and in Sorghum. BMC Genomics, 2006, 7, 199.	2.8	12
174	Deep and comparative analysis of the mycelium and appressorium transcriptomes of Magnaporthe grisea using MPSS, RL-SAGE, and oligoarray methods. BMC Genomics, 2006, 7, 310.	2.8	60
175	Genomic and Genetic Characterization of Rice Cen3 Reveals Extensive Transcription and Evolutionary Implications of a Complex Centromere. Plant Cell, 2006, 18, 2123-2133.	6.6	95
176	A global assembly of cotton ESTs. Genome Research, 2006, 16, 441-450.	5.5	138
177	Uneven chromosome contraction and expansion in the maize genome. Genome Research, 2006, 16, 1241-1251.	5.5	105
178	Doubling genome size without polyploidization: Dynamics of retrotransposition-driven genomic expansions in Oryza australiensis, a wild relative of rice. Genome Research, 2006, 16, 1262-1269.	5.5	522
179	Efficient insertional mutagenesis in rice using the maize En/Spm elements. Plant Journal, 2005, 44, 879-892.	5.7	100
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