

Rod A Wing

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

281 papers	40,267 citations	87 h-index	198 g-index
296 ext. papers	46,623 ext. citations	10.4 avg, IF	7.27 L-index

#	Paper	IF	Citations
281	Rice domestication.. <i>Current Biology</i> , 2022 , 32, R20-R24	6.3	2
280	Long-read genome sequencing of bread wheat facilitates disease resistance gene cloning.. <i>Nature Genetics</i> , 2022 , 54, 227-231	36.3	3
279	A route to de novo domestication of wild allotetraploid rice. <i>Cell</i> , 2021 , 184, 1156-1170.e14	56.2	81
278	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	11.6	9
277	Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021 , 14, 1757-1767	14.4	15
276	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	11.6	30
275	Evolution and diversification of reproductive phased small interfering RNAs in <i>Oryza</i> species. <i>New Phytologist</i> , 2021 , 229, 2970-2983	9.8	4
274	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021 , 590, 438-444	44.4	42
273	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	3.9	6
272	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	8.3	11
271	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	6.2	6
270	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	18.3	31
269	Initial data release and announcement of the 10,000 Fish Genomes Project (Fish10K). <i>GigaScience</i> , 2020 , 9,	7.6	12
268	A platinum standard pan-genome resource that represents the population structure of Asian rice. <i>Scientific Data</i> , 2020 , 7, 113	8.2	33
267	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020 , 10, 61124.9	14.9	13
266	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	3.3	8
265	Structural variants in 3000 rice genomes. <i>Genome Research</i> , 2019 , 29, 870-880	9.7	62

264	The Genomics of Species Provides Insights into Rice Domestication and Heterosis. <i>Annual Review of Plant Biology</i> , 2019 , 70, 639-665	30.7	46
263	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019 , 3, 679-690	12.3	49
262	Genome-wide association mapping of date palm fruit traits. <i>Nature Communications</i> , 2019 , 10, 4680	17.4	45
261	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019 , 20, 905	4.5	21
260	Progress in single-access information systems for wheat and rice crop improvement. <i>Briefings in Bioinformatics</i> , 2019 , 20, 565-571	13.4	4
259	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <i>Nature</i> , 2018 , 557, 43-49	50.4	582
258	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018 , 16, 1904-1917	11.6	77
257	Genotyping by sequencing of rice interspecific backcross inbred lines identifies QTLs for grain weight and grain length. <i>Euphytica</i> , 2018 , 214, 1	2.1	19
256	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	36.3	229
255	Genetic control of seed shattering during African rice domestication. <i>Nature Plants</i> , 2018 , 4, 331-337	11.5	33
254	The rice genome revolution: from an ancient grain to Green Super Rice. <i>Nature Reviews Genetics</i> , 2018 , 19, 505-517	30.1	135
253	Comparison of and Genomes Reveals Selection-Driven Gene Escape from the Centromeric Regions. <i>Plant Cell</i> , 2018 , 30, 1729-1744	11.6	10
252	The Rice Paradox: Multiple Origins but Single Domestication in Asian Rice. <i>Molecular Biology and Evolution</i> , 2017 , 34, 969-979	8.3	124
251	Aflatoxin-free transgenic maize using host-induced gene silencing. <i>Science Advances</i> , 2017 , 3, e1602382	14.3	60
250	Evolutionary analysis of the SUB1 locus across the <i>Oryza</i> genomes. <i>Rice</i> , 2017 , 10, 4	5.8	10
249	A single-nucleotide polymorphism causes smaller grain size and loss of seed shattering during African rice domestication. <i>Nature Plants</i> , 2017 , 3, 17064	11.5	91
248	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017 , 1, 119	12.3	59
247	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017 , 8, 1279	17.4	149

246	Genetic variation for domestication-related traits revealed in a cultivated rice, Nipponbare (<i>Oryza sativa</i> ssp. <i>japonica</i>) and ancestral rice, O. nivara, mapping population. <i>Molecular Breeding</i> , 2017 , 37, 1	3.4	3
245	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	11.5	50
244	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. <i>Plant Biotechnology Journal</i> , 2017 , 15, 765-774	11.6	32
243	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017 , 45, D1075-D1081	11.8	137
242	Extensive sequence divergence between the reference genomes of two elite indica 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	11.5	141
241	DNA transposon activity is associated with increased mutation rates in genes of rice and other grasses. <i>Nature Communications</i> , 2016 , 7, 12790	17.4	39
240	The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016 , 2, 16167	11.5	56
239	Tracing ancestor rice of Suriname Maroons back to its African origin. <i>Nature Plants</i> , 2016 , 2, 16149	11.5	18
238	Building two indica rice reference genomes with PacBio long-read and Illumina paired-end sequencing data. <i>Scientific Data</i> , 2016 , 3, 160076	8.2	19
237	The impact and origin of copy number variations in the <i>Oryza</i> species. <i>BMC Genomics</i> , 2016 , 17, 261	4.5	23
236	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, 1783-94	3.1	9
235	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016 , 17, 37	18.3	213
234	DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements. <i>Genome Biology</i> , 2016 , 17, 92	18.3	11
233	The Dark Side of the Genome: Revealing the Native Transposable Element/Repeat Content of Eukaryotic Genomes. <i>Molecular Plant</i> , 2016 , 9, 1664-1666	14.4	4
232	Genome puzzle master (GPM): an integrated pipeline for building and editing pseudomolecules from fragmented sequences. <i>Bioinformatics</i> , 2016 , 32, 3058-3064	7.2	13
231	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, 1115-27	2.7	80
230	Sequencing of 15622 gene-bearing BACs clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015 , 84, 216-27	6.9	31
229	Harvesting rice's dispensable genome. <i>Genome Biology</i> , 2015 , 16, 217	18.3	1

228	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015 , 16, 538	4.5	56
227	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, 1683-6	14.4	36
226	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015 , 5, 15655	4.9	124
225	Red clover (<i>Trifolium pratense</i> L.) draft genome provides a platform for trait improvement. <i>Scientific Reports</i> , 2015 , 5, 17394	4.9	85
224	Recurrent sequence exchange between homeologous grass chromosomes. <i>Plant Journal</i> , 2015 , 84, 747-59	5.9	3
223	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	6.2	39
222	Comparative BAC-based physical mapping of <i>Oryza sativa</i> ssp. <i>indica</i> var. 93-11 and evaluation of the two rice reference sequence assemblies. <i>Plant Journal</i> , 2014 , 77, 795-805	6.9	14
221	Disentangling methodological and biological sources of gene tree discordance on <i>Oryza</i> (Poaceae) chromosome 3. <i>Systematic Biology</i> , 2014 , 63, 645-59	8.4	37
220	Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. <i>Nature Communications</i> , 2014 , 5, 5269	17.4	69
219	The genome sequence of African rice (<i>Oryza glaberrima</i>) and evidence for independent domestication. <i>Nature Genetics</i> , 2014 , 46, 982-8	36.3	259
218	Global genomic diversity of <i>Oryza sativa</i> varieties revealed by comparative physical mapping. <i>Genetics</i> , 2014 , 196, 937-49	4	9
217	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014 , 46, 707-13	36.3	772
216	Fifteen million years of evolution in the <i>Oryza</i> genus shows extensive gene family expansion. <i>Molecular Plant</i> , 2014 , 7, 642-56	14.4	32
215	Making a living while starving in the dark: metagenomic insights into the energy dynamics of a carbonate cave. <i>ISME Journal</i> , 2014 , 8, 478-91	11.9	82
214	Profiling bacterial diversity and taxonomic composition on speleothem surfaces in Kartchner Caverns, AZ. <i>Microbial Ecology</i> , 2013 , 65, 371-83	4.4	57
213	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	5.3	43
212	The Wild Relative of Rice: Genomes and Genomics 2013 , 9-25		67
211	The Amborella genome and the evolution of flowering plants. <i>Science</i> , 2013 , 342, 1241089	33.3	546

210	Assembly and validation of the genome of the nonmodel basal angiosperm Amborella. <i>Science</i> , 2013 , 342, 1516-7	33.3	79
209	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, 147-56	9.9	108
208	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <i>Nature Communications</i> , 2013 , 4, 1595	17.4	132
207	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. <i>Weed Science</i> , 2013 , 61, 303-309	2	11
206	BAC-end sequences analysis provides first insights into coffee (<i>Coffea canephora</i> P.) genome composition and evolution. <i>Plant Molecular Biology</i> , 2013 , 83, 177-89	4.6	14
205	High occurrence of functional new chimeric genes in survey of rice chromosome 3 short arm genome sequences. <i>Genome Biology and Evolution</i> , 2013 , 5, 1038-48	3.9	8
204	Genomic resources for gene discovery, functional genome annotation, and evolutionary studies of maize and its close relatives. <i>Genetics</i> , 2013 , 195, 723-37	4	13
203	Evolution of a complex locus for terpene biosynthesis in <i>solanum</i> . <i>Plant Cell</i> , 2013 , 25, 2022-36	11.6	103
202	Grain Quality 2013 , 237-254		7
201	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013 , 4, 46	6.2	156
200	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013 , 500, 335-9	50.4	337
199	Aluminum tolerance in maize is associated with higher MATE1 gene copy number. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 5241-6	11.5	199
198	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012 , 491, 711-6	50.4	1124
197	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	2.3	29
196	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012 , 485, 635-41	50.4	2138
195	Life at the hyperarid margin: novel bacterial diversity in arid soils of the Atacama Desert, Chile. <i>Extremophiles</i> , 2012 , 16, 553-66	3	139
194	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, 321-9	3.2	8
193	Dynamic intra-japonica subspecies variation and resource application. <i>Molecular Plant</i> , 2012 , 5, 218-30	14.4	21

192	Ortholog alleles at Xa3/Xa26 locus confer conserved race-specific resistance against <i>Xanthomonas oryzae</i> in rice. <i>Molecular Plant</i> , 2012 , 5, 281-90	14.4	35
191	Comparative sequence analysis of the Ghd7 orthologous regions revealed movement of Ghd7 in the grass genomes. <i>PLoS ONE</i> , 2012 , 7, e50236	3.7	9
190	LysM-type mycorrhizal receptor recruited for rhizobium symbiosis in nonlegume <i>Parasponia</i> . <i>Science</i> , 2011 , 331, 909-12	33.3	213
189	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	18.3	24
188	The genome of <i>Theobroma cacao</i> . <i>Nature Genetics</i> , 2011 , 43, 101-8	36.3	502
187	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	1.6	1
186	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	5.3	66
185	Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. <i>BMC Genomics</i> , 2011 , 12, 137	4.5	37
184	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	4.5	13
183	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, 3139-50	8.3	20
182	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, 1023-30	4	18
181	Conservation and purifying selection of transcribed genes located in a rice centromere. <i>Plant Cell</i> , 2011 , 23, 2821-30	11.6	19
180	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, 476723		9
179	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010 , 463, 178-83	50.4	2997
178	Spatio-temporal patterns of genome evolution in allotetraploid species of the genus <i>Oryza</i> . <i>Plant Journal</i> , 2010 , 63, 430-42	6.9	43
177	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	6.9	38
176	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, 2487-506	8.3	28
175	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, 2437-40	8.3	23

174	The Oryza 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	2	26
173	An integrated physical, genetic and cytogenetic map of Brachypodium distachyon, a model system for grass research. <i>PLoS ONE</i> , 2010 , 5, e13461	3.7	41
172	Phylogenomic Analysis of BAC-end Sequence Libraries in Oryza (Poaceae). <i>Systematic Botany</i> , 2010 , 35, 512-523	0.7	6
171	Genomic structure and evolution of the Pi2/9 locus in wild rice species. <i>Theoretical and Applied Genetics</i> , 2010 , 121, 295-309	6	23
170	Australian Oryza: Utility and Conservation. <i>Rice</i> , 2010 , 3, 235-241	5.8	48
169	Assessing the Extent of Substitution Rate Variation of Retrotransposon Long Terminal Repeat Sequences in Oryza sativa and Oryza glaberrima. <i>Rice</i> , 2010 , 3, 242-250	5.8	4
168	The Future of Rice Genomics: Sequencing the Collective Oryza Genome. <i>Rice</i> , 2010 , 3, 89-97	5.8	15
167	Dynamic Oryza Genomes: Repetitive DNA Sequences as Genome Modeling Agents. <i>Rice</i> , 2010 , 3, 251-263	5.8	12
166	A draft physical map of a D-genome cotton species (Gossypium raimondii). <i>BMC Genomics</i> , 2010 , 11, 395	4.5	45
165	The physical and genetic framework of the maize B73 genome. <i>PLoS Genetics</i> , 2009 , 5, e1000715	6	83
164	Detailed analysis of a contiguous 22-Mb region of the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000728	6	34
163	Hamiltonella defensa, 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, 9063-8	11.5	187
162	Comparative sequence analysis of MONOCULM1-orthologous regions in 14 Oryza genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2071-6	11.5	94
161	Species trees from highly incongruent gene trees in rice. <i>Systematic Biology</i> , 2009 , 58, 489-500	8.4	79
160	De Novo Next Generation Sequencing of Plant Genomes. <i>Rice</i> , 2009 , 2, 35-43	5.8	50
159	A lineage-specific centromere retrotransposon in Oryza brachyantha. <i>Plant Journal</i> , 2009 , 60, 820-31	6.9	34
158	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, 2365-70	11.5	1370
157	Comparative sequence analysis of the SALT OVERLY SENSITIVE1 orthologous region in Thellungiella halophila and Arabidopsis thaliana. <i>Genomics</i> , 2009 , 94, 196-203	4.3	15

156	The B73 maize genome: complexity, diversity, and dynamics. <i>Science</i> , 2009 , 326, 1112-5	33.3	2949
155	A single molecule scaffold for the maize genome. <i>PLoS Genetics</i> , 2009 , 5, e1000711	6	110
154	Dynamic evolution of oryza genomes is revealed by comparative genomic analysis of a genus-wide vertical data set. <i>Plant Cell</i> , 2008 , 20, 3191-209	11.6	104
153	Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. <i>BMC Genomics</i> , 2008 , 9, 621	4.5	8
152	A fruitful outcome to the papaya genome project. <i>Genome Biology</i> , 2008 , 9, 227	18.3	7
151	The Amborella genome: an evolutionary reference for plant biology. <i>Genome Biology</i> , 2008 , 9, 402	18.3	52
150	Construction, alignment and analysis of twelve framework physical maps that represent the ten genome types of the genus Oryza. <i>Genome Biology</i> , 2008 , 9, R45	18.3	72
149	Microsatellite discovery from BAC end sequences and genetic mapping to anchor the soybean physical and genetic maps. <i>Genome</i> , 2008 , 51, 294-302	2.4	48
148	Diploid/polyploid syntenic shuttle mapping and haplotype-specific chromosome walking toward a rust resistance gene (Bru1) in highly polyploid sugarcane (2n approximately 12x approximately 115). <i>Genetics</i> , 2008 , 180, 649-60	4	88
147	A phylogenetic analysis of indel dynamics in the cotton genus. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1415-28	8.3	36
146	The subtelomere of Oryza sativa chromosome 3 short arm as a hot bed of new gene origination in rice. <i>Molecular Plant</i> , 2008 , 1, 839-50	14.4	31
145	A versatile transposon-based activation tag vector system for functional genomics in cereals and other monocot plants. <i>Plant Physiology</i> , 2008 , 146, 189-99	6.6	52
144	Construction of an Amaranthus hypochondriacus Bacterial Artificial Chromosome Library and Genomic Sequencing of Herbicide Target Genes. <i>Crop Science</i> , 2008 , 48, S-85	2.4	20
143	Evidence of multiple horizontal transfers of the long terminal repeat retrotransposon RIRE1 within the genus Oryza. <i>Plant Journal</i> , 2008 , 53, 950-9	6.9	60
142	Rapid and Differential Proliferation of the Ty3-Gypsy LTR Retrotransposon Atlantys in the Genus Oryza. <i>Rice</i> , 2008 , 1, 85-99	5.8	7
141	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	5.8	13
140	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (Phaseolus vulgaris L.) Genome. <i>Tropical Plant Biology</i> , 2008 , 1, 40-48	1.6	49
139	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2008 , 36, D1028-33	30.1	262

138	Changes in regulation of a transcription factor lead to autogamy in cultivated tomatoes. <i>Science</i> , 2007 , 318, 643-5	33.3	109
137	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
136	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (Gossypium). <i>Plant Journal</i> , 2007 , 50, 995-1006	6.9	67
135	Evolutionary dynamics of an ancient retrotransposon family provides insights into evolution of genome size in the genus Oryza. <i>Plant Journal</i> , 2007 , 52, 342-51	6.9	85
134	Transposable element distribution, abundance and role in genome size variation in the genus Oryza. <i>BMC Evolutionary Biology</i> , 2007 , 7, 152	3	84
133	Plant centromere organization: a dynamic structure with conserved functions. <i>Trends in Genetics</i> , 2007 , 23, 134-9	8.5	118
132	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	2.1	24
131	The barley ERF-type transcription factor HvRAF confers enhanced pathogen resistance and salt tolerance in Arabidopsis. <i>Planta</i> , 2007 , 225, 575-88	4.7	105
130	RL-SAGE and microarray analysis of the rice transcriptome after <i>Rhizoctonia solani</i> infection. <i>Molecular Genetics and Genomics</i> , 2007 , 278, 421-31	3.1	43
129	Evolutionary history and positional shift of a rice centromere. <i>Genetics</i> , 2007 , 177, 1217-20	4	28
128	Physical and genetic structure of the maize genome reflects its complex evolutionary history. <i>PLoS Genetics</i> , 2007 , 3, e123	6	234
127	Comparative physical mapping between <i>Oryza sativa</i> (AA genome type) and <i>O. punctata</i> (BB genome type). <i>Genetics</i> , 2007 , 176, 379-90	4	42
126	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, 175-83	9.7	200
125	Magnaporthe grisea infection triggers RNA variation and antisense transcript expression in rice. <i>Plant Physiology</i> , 2007 , 144, 524-33	6.6	25
124	Efficacy of clone fingerprinting methodologies. <i>Genomics</i> , 2007 , 89, 160-5	4.3	20
123	Rice Genome Sequence: The Foundation for Understanding the Genetic Systems 2007 , 5-20		2
122	The Oryza Map Alignment Project (OMAP): A New Resource for Comparative Genome Studies within Oryza 2007 , 395-409		8
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