

The map-based sequence of the rice genome

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Scanning Probe Microscope as a Novel Genomic Analysis Tool. <i>Nanobiotechnology</i> , 2005, 1, 369-378.	1.2	3
2	Plant Ontology (PO): a Controlled Vocabulary of Plant Structures and Growth Stages. <i>Comparative and Functional Genomics</i> , 2005, 6, 388-397.	2.0	129
3	Random sheared fosmid library as a new genomic tool to accelerate complete finishing of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf euchromatic portions of the genome. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1596-1607.	1.8	36
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805	High-throughput identification of genetic markers using representational oligonucleotide microarray analysis. <i>Theoretical and Applied Genetics</i> , 2010, 121, 549-565.	1.8	6
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1090	Transposition behavior of nonautonomous a hAT superfamily transposon nDart in rice (<i>Oryza sativa</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 EO		3
1091	Relationship between transmission ratio distortion and genetic divergence in intraspecific rice crosses. <i>Molecular Genetics and Genomics</i> , 2011, 286, 307-319.	1.0	26
1092	Genetic and molecular analysis of a purple sheath somaclonal mutant in japonica rice. <i>Plant Cell Reports</i> , 2011, 30, 901-911.	2.8	36
1093	The chromosome number, karyotype and genome size of the desert plant diploid <i>Reaumuria soongorica</i> (Pall.) Maxim. <i>Plant Cell Reports</i> , 2011, 30, 955-964.	2.8	20

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1095	Mapping 49 quantitative trait loci at high resolution through sequencing-based genotyping of rice recombinant inbred lines. <i>Theoretical and Applied Genetics</i> , 2011, 122, 327-340.	1.8	134
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1097	High-resolution genetic mapping and candidate gene identification of the SLP1 locus that controls glume development in rice. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1489-1496.	1.8	14
1098	Comparison of a high-density genetic linkage map to genome features in the model grass <i>Brachypodium distachyon</i> . <i>Theoretical and Applied Genetics</i> , 2011, 123, 455-464.	1.8	70
1099	Temporal dynamics in the evolution of the sunflower genome as revealed by sequencing and annotation of three large genomic regions. <i>Theoretical and Applied Genetics</i> , 2011, 123, 779-791.	1.8	30
1100	Development and application of a set of breeder-friendly SNP markers for genetic analyses and molecular breeding of rice (<i>Oryza sativa</i> L.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 869-879.	1.8	93
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1103	Selection-Driven Divergence After Gene Duplication in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2011, 73, 153-165.	0.8	16
1104	Proteomic analysis of secreted proteins from aseptically grown rice. <i>Phytochemistry</i> , 2011, 72, 312-320.	1.4	22
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1106	Chromosomal Location of HWA1 and HWA2, Complementary Hybrid Weakness Genes in Rice. <i>Rice</i> , 2011, 4, 29-38.	1.7	25
1107	Isolation and characterization of Ty1-copia group of LTRs in genome of three species of <i>Datura</i> : <i>D. innoxia</i> , <i>D. stramonium</i> and <i>D. metel</i> . <i>Physiology and Molecular Biology of Plants</i> , 2011, 17, 255-261.	1.4	2
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1116	The impact of Ty3-gypsy group LTR retrotransposons Fatima on B-genome specificity of polyploid wheats. <i>BMC Plant Biology</i> , 2011, 11, 99.	1.6	26
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1131	A genetically anchored physical framework for <i>Theobroma cacao</i> cv. Matina 1-6. <i>BMC Genomics</i> , 2011, 12, 413.	1.2	13
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1135	Plant organelle proteomics: Collaborating for optimal cell function. <i>Mass Spectrometry Reviews</i> , 2011, 30, 772-853.	2.8	89
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1147	The Biotron Breeding System: A Rapid and Reliable Procedure for Genetic Studies and Breeding in Rice. <i>Plant and Cell Physiology</i> , 2011, 52, 1249-1257.	1.5	51
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1174	Endosperm development in <i>Brachypodium distachyon</i> . <i>Journal of Experimental Botany</i> , 2011, 62, 735-748.	2.4	68
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1178	Detection of a QTL for accumulating Cd in rice that enables efficient Cd phytoextraction from soil. <i>Breeding Science</i> , 2011, 61, 43-51.	0.9	45
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1184	Expressed sequence tags from organ-specific cDNA libraries of tea (<i>Camellia sinensis</i>) and polymorphisms and transferability of EST-SSRs across <i>Camellia</i> species. <i>Breeding Science</i> , 2012, 62, 186-195.	0.9	23

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1190	SNP Discovery through Next-Generation Sequencing and Its Applications. <i>International Journal of Plant Genomics</i> , 2012, 2012, 1-15.	2.2	237
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1194	Softening-up mannan-rich cell walls. <i>Journal of Experimental Botany</i> , 2012, 63, 3976-3988.	2.4	98
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1198	Molecular Spectrum of Somaclonal Variation in Regenerated Rice Revealed by Whole-Genome Sequencing. <i>Plant and Cell Physiology</i> , 2012, 53, 256-264.	1.5	114
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1204	Genome-Wide Characterization of Nonreference Transposons Reveals Evolutionary Propensities of Transposons in Soybean. <i>Plant Cell</i> , 2012, 24, 4422-4436.	3.1	51
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1206	Rice Carotenoid β -Ring Hydroxylase CYP97A4 is Involved in Lutein Biosynthesis. <i>Plant and Cell Physiology</i> , 2012, 53, 987-1002.	1.5	58
1207	Dynamic Gene Copy Number Variation in Collinear Regions of Grass Genomes. <i>Molecular Biology and Evolution</i> , 2012, 29, 861-871.	3.5	24
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1209	Gene Content and Gene Transfer from Mitochondria to the Nucleus During Evolution. <i>Advances in Botanical Research</i> , 2012, 63, 21-40.	0.5	6
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1218	Genome-wide transcriptome analysis of rice genes responsive to chilling stress. <i>Canadian Journal of Plant Science</i> , 2012, 92, 447-460.	0.3	13
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1223	Proteomics and its application in plant biotechnology. , 2012, , 55-65.		0
1224	Deciphering and Prediction of Transcriptome Dynamics under Fluctuating Field Conditions. <i>Cell</i> , 2012, 151, 1358-1369.	13.5	219
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1228	Current challenges in de novo plant genome sequencing and assembly. <i>Genome Biology</i> , 2012, 13, 243.	13.9	157
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1233	Rice choline monooxygenase (OsCMO) protein functions in enhancing glycine betaine biosynthesis in transgenic tobacco but does not accumulate in rice (<i>Oryza sativa</i> L. ssp. japonica). <i>Plant Cell Reports</i> , 2012, 31, 1625-1635.	2.8	44
1234	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	1.4	39
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1241	Genomics of gene banks: A case study in rice. <i>American Journal of Botany</i> , 2012, 99, 407-423.	0.8	152
1242	Genetic, Molecular and Genomic Basis of Rice Defense against Insects. <i>Critical Reviews in Plant Sciences</i> , 2012, 31, 74-91.	2.7	28
1243	Application of large-scale sequencing to marker discovery in plants. <i>Journal of Biosciences</i> , 2012, 37, 829-841.	0.5	35
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1247	Abnormal endosperm development causes female sterility in rice insertional mutant OsAPC6. <i>Plant Science</i> , 2012, 183, 167-174.	1.7	26
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1250	An efficient RNA interference screening strategy for gene functional analysis. <i>BMC Genomics</i> , 2012, 13, 491.	1.2	16
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1253	Evolutionary force of AT-rich repeats to trap genomic and episomal DNAs into the rice genome: lessons from endogenous pararetrovirus. <i>Plant Journal</i> , 2012, 72, 817-828.	2.8	26
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1260	FSTVAL: a new web tool to validate bulk flanking sequence tags. <i>Plant Methods</i> , 2012, 8, 19.	1.9	15
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1262	The Rice Oligonucleotide Array Database: an atlas of rice gene expression. <i>Rice</i> , 2012, 5, 17.	1.7	192
1263	OGRO: The Overview of functionally characterized Genes in Rice online database. <i>Rice</i> , 2012, 5, 26.	1.7	152
1264	Nomenclature report on rice WRKY's - Conflict regarding gene names and its solution. <i>Rice</i> , 2012, 5, 3.	1.7	51
1265	Noise or Symphony: Comparative Evolutionary Analysis of Sugarcane Transposable Elements with Other Grasses. <i>Topics in Current Genetics</i> , 2012, , 169-192.	0.7	4
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1267	The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <i>Nature Genetics</i> , 2012, 44, 1098-1103.	9.4	935
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1272	Relevance of Proteomic Investigations in Plant Abiotic Stress Physiology. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 621-635.	1.0	50
1273	So Many Repeats and So Little Time: How to Classify Transposable Elements. <i>Topics in Current Genetics</i> , 2012, , 1-15.	0.7	5
1274	Genome-Wide Analysis of Transposition Using Next Generation Sequencing Technologies. <i>Topics in Current Genetics</i> , 2012, , 59-70.	0.7	3
1275	Whole genome sequencing and future breeding of rice. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2012, 21, 10-14.	0.9	2
1276	Genetic Diversity and Genetic Changes in the Introgression Lines Derived from <i>Oryza sativa</i> L. Mating with <i>O. rufipogon</i> Griff.. <i>Journal of Integrative Agriculture</i> , 2012, 11, 1059-1066.	1.7	6

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1278	Rice functional genomics research: Progress and implications for crop genetic improvement. <i>Biotechnology Advances</i> , 2012, 30, 1059-1070.	6.0	100
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1282	Genome sequencing reveals agronomically important loci in rice using MutMap. <i>Nature Biotechnology</i> , 2012, 30, 174-178.	9.4	1,087
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1285	Development of a molecular marker for assessment of intraspecific polymorphism by the Rc gene that determines the red color of pericarp in rice <i>Oryza sativa</i> L.. <i>Russian Journal of Genetics: Applied Research</i> , 2012, 2, 357-366.	0.4	0
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1287	Proteomic Markers for Oxidative Stress: New Tools for Reactive Oxygen Species and Photosynthesis Research. , 2012, , 181-196.		5
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1298	A Highly Conserved, Small LTR Retrotransposon that Preferentially Targets Genes in Grass Genomes. <i>PLoS ONE</i> , 2012, 7, e32010.	1.1	54
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1306	An Efficient Genome Fragment Assembling Using GA with Neighborhood Aware Fitness Function. Applied Computational Intelligence and Soft Computing, 2012, 2012, 1-11.	1.6	3
1307	Genetic Diversity of Upland Rice Germplasm in Malaysia Based on Quantitative Traits. Scientific World Journal, The, 2012, 2012, 1-9.	0.8	48
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1309	Why Assembling Plant Genome Sequences Is So Challenging. Biology, 2012, 1, 439-459.	1.3	123
1310	Progression of DNA Marker and the Next Generation of Crop Development. , 0, , .		1
1311	Sequencing Technologies and Their Use in Plant Biotechnology and Breeding. , 2012, , .		5
1312	Plant Protein Analysis. , 0, , .		2
1313	Fruit Germplasm Characterization: Genomics Approaches for the Valorisation of Genetic Diversity. , 2012, , .		2
1314	Functional characterization of sugarcane mustang domesticated transposases and comparative diversity in sugarcane, rice, maize and sorghum. Genetics and Molecular Biology, 2012, 35, 632-639.	0.6	9
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1316	Plant Transposable Elements: Biology and Evolution. , 2012, , 17-34.		61
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1319	Genome size and DNA base composition of geophytes: the mirror of phenology and ecology?. Annals of Botany, 2012, 109, 65-75.	1.4	141
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1321	Protein-Protein Interactions in Plants. Plant and Cell Physiology, 2012, 53, 617-625.	1.5	47
1322	Sequence polymorphisms in wild, weedy, and cultivated rice suggest seed-shattering locus <i>sh4</i> played a minor role in Asian rice domestication. Ecology and Evolution, 2012, 2, 2106-2113.	0.8	54
1323	The Impact of Transposable Elements on Gene and Genome Evolution. , 2012, , 35-58.		19
1324	Concerted Evolution of Multigene Families and Homoeologous Recombination. , 2012, , 171-193.		58
1325	The Variation of Base Composition in Plant Genomes. , 2012, , 209-235.		32
1326	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. Nature Biotechnology, 2012, 30, 549-554.	9.4	636
1327	Genome-Enabled Insights into Legume Biology. Annual Review of Plant Biology, 2012, 63, 283-305.	8.6	79
1328	Plant Chromosomal Deletions, Insertions, and Rearrangements. , 2012, , 3-36.		10
1329	Characterization of Imcrop, a Mutator-like MITE family in the rice genome. Genes and Genomics, 2012, 34, 189-198.	0.5	6
1330	Fine mapping of grain length QTLs on chromosomes 1 and 7 in Basmati rice (<i>Oryza sativa</i> L.). Journal of Plant Biochemistry and Biotechnology, 2012, 21, 157-166.	0.9	43
1331	Characterization of active miniature inverted-repeat transposable elements in the peanut genome. Theoretical and Applied Genetics, 2012, 124, 1429-1438.	1.8	76
1332	Fine mapping of QTLs for rice grain yield under drought reveals sub-QTLs conferring a response to variable drought severities. Theoretical and Applied Genetics, 2012, 125, 155-169.	1.8	99
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1334	A multiple gene complex on rice chromosome 4 is involved in durable resistance to rice blast. Theoretical and Applied Genetics, 2012, 125, 551-559.	1.8	31
1335	A large-effect QTL for rice grain yield under upland drought stress on chromosome 1. Molecular Breeding, 2012, 30, 535-547.	1.0	85

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1336	Detection of allelic variation at the Wx locus with single-segment substitution lines in rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	65
1337	Analysis of expressed sequence tags from grapevine flower and fruit and development of simple sequence repeat markers. <i>Molecular Biology Reports</i> , 2012, 39, 6825-6834.	1.0	11
1338	Large-scale collection and annotation of gene models for date palm (<i>Phoenix dactylifera</i> , L.). <i>Plant Molecular Biology</i> , 2012, 79, 521-536.	2.0	26
1339	Analysis of transcriptional and upstream regulatory sequence activity of two environmental stress-inducible genes, NBS-Str1 and BLEC-Str8, of rice. <i>Transgenic Research</i> , 2012, 21, 351-366.	1.3	14
1340	High synteny and colinearity among Eucalyptus genomes revealed by high-density comparative genetic mapping. <i>Tree Genetics and Genomes</i> , 2012, 8, 339-352.	0.6	49
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1342	Structural and expression analysis of prolamin genes in <i>Oryza sativa</i> L. <i>Plant Biotechnology Reports</i> , 2012, 6, 251-262.	0.9	3
1343	Random BAC FISH of monocot plants reveals differential distribution of repetitive DNA elements in small and large chromosome species. <i>Plant Cell Reports</i> , 2012, 31, 621-628.	2.8	16
1344	Diversification of hAT transposase paralogues in the sugarcane genome. <i>Molecular Genetics and Genomics</i> , 2012, 287, 205-219.	1.0	9
1345	Identification of an active Mutator-like element (MULE) in rice (<i>Oryza sativa</i>). <i>Molecular Genetics and Genomics</i> , 2012, 287, 261-271.	1.0	13
1346	Genome change in wheat observed through the structure and expression of $\hat{1}\pm/\hat{1}^2$ -gliadin genes. <i>Functional and Integrative Genomics</i> , 2012, 12, 341-355.	1.4	17
1347	A novel blast resistance gene, Pi54rh cloned from wild species of rice, <i>Oryza rhizomatis</i> confers broad spectrum resistance to <i>Magnaporthe oryzae</i> . <i>Functional and Integrative Genomics</i> , 2012, 12, 215-228.	1.4	130
1348	Phylogenetic, structure and expression analysis of ABC1Ps gene family in rice. <i>Biologia Plantarum</i> , 2012, 56, 667-674.	1.9	7
1349	Measurements of genomic GC content in plant genomes with flow cytometry: a test for reliability. <i>New Phytologist</i> , 2012, 193, 513-521.	3.5	38
1350	Mapping QTL for heat tolerance at flowering stage in rice using SNP markers. <i>Plant Breeding</i> , 2012, 131, 33-41.	1.0	170
1351	Dynamic evolution of herbivore-induced sesquiterpene biosynthesis in sorghum and related grass crops. <i>Plant Journal</i> , 2012, 69, 70-80.	2.8	64
1352	The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. <i>Plant Journal</i> , 2012, 69, 475-488.	2.8	36
1353	Next-generation sequencing and syntenic integration of flow-sorted arms of wheat chromosome 4A exposes the chromosome structure and gene content. <i>Plant Journal</i> , 2012, 69, 377-386.	2.8	137

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1355	Bulk segregant analysis: An effective approach for mapping consistent-effect drought grain yield QTLs in rice. <i>Field Crops Research</i> , 2012, 134, 185-192.	2.3	63
1356	Mass spectrum sequential subtraction speeds up searching large peptide <sc>MS</sc>/<sc>MS</sc> spectra datasets against large nucleotide databases for proteogenomics. <i>Genes To Cells</i> , 2012, 17, 633-644.	0.5	26
1357	In silico archeogenomics unveils modern plant genome organisation, regulation and evolution. <i>Current Opinion in Plant Biology</i> , 2012, 15, 122-130.	3.5	68
1358	Biosynthesis and emission of insect herbivory-induced volatile indole in rice. <i>Phytochemistry</i> , 2012, 73, 15-22.	1.4	31
1359	Advances in plant genome sequencing. <i>Plant Journal</i> , 2012, 70, 177-190.	2.8	156
1360	Dissection of genotype-phenotype associations in rice grains using metabolome quantitative trait loci analysis. <i>Plant Journal</i> , 2012, 70, 624-636.	2.8	173
1361	Targeted disruption of an orthologue of <i>DOMAINS REARRANGED METHYLASE2</i> , <i>OsDRM2</i> , impairs the growth of rice plants by abnormal DNA methylation. <i>Plant Journal</i> , 2012, 71, 85-98.	2.8	110
1362	Rice LGD1 containing RNA binding activity affects growth and development through alternative promoters. <i>Plant Journal</i> , 2012, 71, 288-302.	2.8	21
1363	Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. <i>Plant Journal</i> , 2012, 71, 492-502.	2.8	209
1364	Genome-wide DNA polymorphisms in elite <i>indica</i> rice inbreds discovered by whole-genome sequencing. <i>Plant Biotechnology Journal</i> , 2012, 10, 623-634.	4.1	175
1365	In-depth molecular and phenotypic characterization in a rice insertion line library facilitates gene identification through reverse and forward genetics approaches. <i>Plant Biotechnology Journal</i> , 2012, 10, 555-568.	4.1	20
1366	Genetic Advances in Adapting Rice to a Rapidly Changing Climate. <i>Journal of Agronomy and Crop Science</i> , 2012, 198, 360-373.	1.7	84
1367	Toward understanding transcriptional regulatory networks in abiotic stress responses and tolerance in rice. <i>Rice</i> , 2012, 5, 6.	1.7	183
1368	Recent advances of metabolomics in plant biotechnology. <i>Plant Biotechnology Reports</i> , 2012, 6, 1-15.	0.9	125
1369	Emerging Knowledge from Genome Sequencing of Crop Species. <i>Molecular Biotechnology</i> , 2012, 50, 250-266.	1.3	35
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1371	Analysis of ESTs from a Normalized cDNA Library of the Rhizome Tip of <i>Oryza longistaminata</i> . <i>Journal of Plant Biology</i> , 2012, 55, 33-42.	0.9	5

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1373	A QTL for rice grain yield in aerobic environments with large effects in three genetic backgrounds. <i>Theoretical and Applied Genetics</i> , 2012, 124, 323-332.	1.8	62
1374	Mapping and characterization of seed dormancy QTLs using chromosome segment substitution lines in rice. <i>Theoretical and Applied Genetics</i> , 2012, 124, 893-902.	1.8	58
1375	Delimitation of a QTL region controlling cold tolerance at booting stage of a cultivar, "Lijiangxintuanheigu"™, in rice, <i>Oryza sativa</i> L.. <i>Theoretical and Applied Genetics</i> , 2012, 124, 937-946.	1.8	70
1376	A computational study of the dynamics of LTR retrotransposons in the <i>Populus trichocarpa</i> genome. <i>Tree Genetics and Genomes</i> , 2012, 8, 61-75.	0.6	43
1377	The β -conglycinin deficiency in wild soybean is associated with the tail-to-tail inverted repeat of the β -subunit genes. <i>Plant Molecular Biology</i> , 2012, 78, 301-309.	2.0	15
1378	Turning over a new leaf in plant genomics. <i>Genome Biology</i> , 2013, 14, 403.	3.8	4
1379	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <i>Genome Biology</i> , 2013, 14, R64.	3.8	45
1380	Exploiting EST databases for the development and characterisation of 3425 gene-tagged CISP markers in biofuel crop sugarcane and their transferability in cereals and orphan tropical grasses. <i>BMC Research Notes</i> , 2013, 6, 47.	0.6	12
1381	Next-Generation Sequencing as a Tool for Detailed Molecular Characterisation of Genomic Insertions and Flanking Regions in Genetically Modified Plants: a Pilot Study Using a Rice Event Unauthorised in the EU. <i>Food Analytical Methods</i> , 2013, 6, 1718-1727.	1.3	65
1382	Gene identification using rice genome sequences. <i>Genes and Genomics</i> , 2013, 35, 415-424.	0.5	3
1383	Exploring the genome of the salt-marsh <i>Spartina maritima</i> (Poaceae, Chloridoideae) through BAC end sequence analysis. <i>Plant Molecular Biology</i> , 2013, 83, 591-606.	2.0	11
1384	Sequencing-based genome-wide association study in rice. <i>Current Opinion in Plant Biology</i> , 2013, 16, 133-138.	3.5	107
1385	Recent emergence of the wheat Lr34 multi-pathogen resistance: insights from haplotype analysis in wheat, rice, sorghum and <i>Aegilops tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2013, 126, 663-672.	1.8	79
1386	Rapid establishment of introgression lines using cytoplasmic male sterility and a restorer gene in <i>Oryza sativa</i> cv. Nipponbare. <i>Molecular Breeding</i> , 2013, 32, 831-839.	1.0	2
1387	Genome-wide InDel marker system for application in rice breeding and mapping studies. <i>Euphytica</i> , 2013, 192, 131-143.	0.6	48
1388	Proteomics of model and crop plant species: Status, current limitations and strategic advances for crop improvement. <i>Journal of Proteomics</i> , 2013, 93, 5-19.	1.2	81
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1391	Molecular diversity in rice blast resistance gene Pi-ta makes it highly effective against dynamic population of Magnaporthe oryzae. Functional and Integrative Genomics, 2013, 13, 309-322.	1.4	22
1393	qDTY12.1: a locus with a consistent effect on grain yield under drought in rice. BMC Genetics, 2013, 14, 12.	2.7	124
1394	Comparison of class 2 transposable elements at superfamily resolution reveals conserved and distinct features in cereal grass genomes. BMC Genomics, 2013, 14, 71.	1.2	63
1395	Saturated linkage map construction in Rubus idaeus using genotyping by sequencing and genome-independent imputation. BMC Genomics, 2013, 14, 2.	1.2	171
1396	Characterization of a new high copy Stowaway family MITE, BRAMI-1 in Brassica genome. BMC Plant Biology, 2013, 13, 56.	1.6	32
1397	Promzea: a pipeline for discovery of co-regulatory motifs in maize and other plant species and its application to the anthocyanin and phlobaphene biosynthetic pathways and the Maize Development Atlas. BMC Plant Biology, 2013, 13, 42.	1.6	19
1398	Characterization of the basal angiosperm Aristolochia fimbriata: a potential experimental system for genetic studies. BMC Plant Biology, 2013, 13, 13.	1.6	22
1399	Gene body methylation shows distinct patterns associated with different gene origins and duplication modes and has a heterogeneous relationship with gene expression in <i>Oryza sativa</i> (rice). New Phytologist, 2013, 198, 274-283.	3.5	57
1400	Differential expression of heat shock proteins and heat stress transcription factor genes in rice exposed to different levels of heat stress. Journal of Plant Biochemistry and Biotechnology, 2013, 22, 277-285.	0.9	17
1401	Computational Methods for Identification of DNA Transposons. Methods in Molecular Biology, 2013, 1057, 289-304.	0.4	2
1402	Whole genome resequencing of mutant F2 progeny bulk combined with <i>de novo</i> assembly of gap regions identifies the rice blast resistance gene <i>Pii</i> . New Phytologist, 2013, 200, 276-283.	3.5	196
1403	Genetics and Genomics of Rice. , 2013, , .		8
1404	Identification of rice <i>Allene Oxide Cyclase</i> mutants and the function of jasmonate for defence against <i>Magnaporthe oryzae</i> . Plant Journal, 2013, 74, 226-238.	2.8	204
1405	Identification of qRBS1, a QTL involved in resistance to bacterial seedling rot in rice. Theoretical and Applied Genetics, 2013, 126, 2417-2425.	1.8	19
1406	Radiation hybrid QTL mapping of Tdes2 involved in the first meiotic division of wheat. Theoretical and Applied Genetics, 2013, 126, 1977-1990.	1.8	12
1407	Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. Theoretical and Applied Genetics, 2013, 126, 1103-1119.	1.8	21
1408	SNP-based analysis of genetic diversity in anther-derived rice by whole genome sequencing. Rice, 2013, 6, 6.	1.7	41

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1409	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <i>Rice</i> , 2013, 6, 4.	1.7	1,777
1410	Re-sequencing of mitochondrial genes in a standard rice cultivar Nipponbare. <i>Rice</i> , 2013, 6, 2.	1.7	3
1411	Molecular mapping of four blast resistance genes using recombinant inbred lines of 93-11 and nipponbare. <i>Journal of Plant Biology</i> , 2013, 56, 91-97.	0.9	6
1412	TEnest 2.0: Computational Annotation and Visualization of Nested Transposable Elements. <i>Methods in Molecular Biology</i> , 2013, 1057, 305-319.	0.4	4
1413	Molecular Cytogenetics of Rice and Its Wild Relatives. , 2013, , 71-79.		0
1414	A Recessive Resistance to <i>Rice yellow mottle virus</i> Is Associated with a Rice Homolog of the <i>CPR5</i> Gene, a Regulator of Active Defense Mechanisms. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 1455-1463.	1.4	49
1415	Rice transglutaminase gene: Identification, protein expression, functionality, light dependence and specific cell location. <i>Plant Science</i> , 2013, 205-206, 97-110.	1.7	19
1416	Dispersion and domestication shaped the genome of bread wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 564-571.	4.1	79
1417	Varietal differences in sink production and grain-filling ability in recently developed high-yielding rice (<i>Oryza sativa</i> L.) varieties in Japan. <i>Field Crops Research</i> , 2013, 150, 74-82.	2.3	103
1418	Analysis of the early-flowering mechanisms and generation of T-DNA tagging lines in Kitaake, a model rice cultivar. <i>Journal of Experimental Botany</i> , 2013, 64, 4169-4182.	2.4	48
1419	Genetic and Physiological Analysis of a Novel Type of Interspecific Hybrid Weakness in Rice. <i>Molecular Plant</i> , 2013, 6, 716-728.	3.9	32
1420	Genome Structure of <i>Jatropha curcas</i> L. , 2013, , 563-576.		4
1421	New Insights into the Dynamics of Plant Cell Nuclei and Chromosomes. <i>International Review of Cell and Molecular Biology</i> , 2013, 305, 253-301.	1.6	29
1422	Rice Resistance to Planthoppers and Leafhoppers. <i>Critical Reviews in Plant Sciences</i> , 2013, 32, 162-191.	2.7	179
1423	A knockdown mutation of YELLOW-GREEN LEAF2 blocks chlorophyll biosynthesis in rice. <i>Plant Cell Reports</i> , 2013, 32, 1855-1867.	2.8	64
1424	Integrated genomics and molecular breeding approaches for dissecting the complex quantitative traits in crop plants. <i>Journal of Biosciences</i> , 2013, 38, 971-987.	0.5	13
1425	The Wild Relative of Rice: Genomes and Genomics. , 2013, , 9-25.		94
1426	The repetitive component of the sunflower genome as shown by different procedures for assembling next generation sequencing reads. <i>BMC Genomics</i> , 2013, 14, 686.	1.2	52

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1428	Genome-wide identification and characterisation of F-box family in maize. <i>Molecular Genetics and Genomics</i> , 2013, 288, 559-577.	1.0	63
1429	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	13.9	329
1430	Analysing complex Triticeae genomes – concepts and strategies. <i>Plant Methods</i> , 2013, 9, 35.	1.9	19
1431	Genome-wide copy number variations in <i>Oryza sativa</i> L. <i>BMC Genomics</i> , 2013, 14, 649.	1.2	26
1432	Transcriptome analysis of leaf and root of rice seedling to acute dehydration. <i>Rice</i> , 2013, 6, 38.	1.7	42
1433	Diversity and genetics of nitrogen-induced susceptibility to the blast fungus in rice and wheat. <i>Rice</i> , 2013, 6, 32.	1.7	79
1434	Biosynthesis and Catabolism of Purine Alkaloids. <i>Advances in Botanical Research</i> , 2013, , 111-138.	0.5	26
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1436	Producing more with less: Strategies and novel technologies for plant-based food biofortification. <i>Food Research International</i> , 2013, 54, 961-971.	2.9	153
1437	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
1438	A BAC physical map of <i>aus</i> rice cultivar <i>asalath</i> TM , and the map-based genomic sequence of <i>asalath</i> TM chromosome 1. <i>Plant Journal</i> , 2013, 76, 699-708.	2.8	13
1439	Proteomics of nonmodel plant species. <i>Proteomics</i> , 2013, 13, 663-673.	1.3	50
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1441	Genomics reveals new landscapes for crop improvement. <i>Genome Biology</i> , 2013, 14, 206.	3.8	99
1442	Divergent evolutionary mechanisms of co-located <i>Tak/Lrk</i> and <i>Glu-D3</i> loci revealed by comparative analysis of grass genomes. <i>Genome</i> , 2013, 56, 195-204.	0.9	2
1443	Differential subcellular localization, enzymatic properties and expression patterns of ¹³ C-aminobutyric acid transaminases (GABA-Ts) in rice (<i>Oryza sativa</i>). <i>Journal of Plant Physiology</i> , 2013, 170, 196-201.	1.6	23
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1447	Rice Proteomic Analysis: Sample Preparation for Protein Identification. Methods in Molecular Biology, 2013, 956, 151-184.	0.4	6
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1450	Spatial and temporal activity of upstream regulatory regions of rice anther-specific genes in transgenic rice and Arabidopsis. Transgenic Research, 2013, 22, 31-46.	1.3	21
1451	A QTL for high grain yield under lowland drought in the background of popular rice variety Sabitri from Nepal. Field Crops Research, 2013, 144, 281-287.	2.3	82
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1453	Identification and fine mapping of two blast resistance genes in rice cultivar 93-11. Crop Journal, 2013, 1, 2-14.	2.3	32
1455	A Bountiful Harvest: Genomic Insights into Crop Domestication Phenotypes. Annual Review of Plant Biology, 2013, 64, 47-70.	8.6	326
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1462	Salt Stress and MAPK Signaling in Plants. , 2013, , 157-173.		5
1463	Draft genome of the wheat A-genome progenitor Triticum urartu. Nature, 2013, 496, 87-90.	13.7	700
1464	Virus-Induced Gene Silencing for Rice Using Agroinoculation. Methods in Molecular Biology, 2013, 975, 33-45.	0.4	9

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1467	Arguments for standardizing transposable element annotation in plant genomes. <i>Trends in Plant Science</i> , 2013, 18, 367-376.	4.3	26
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1473	Application of Next-Generation Sequencing Technologies for Genetic Diversity Analysis in Cereals. , 2013, , 77-99.		1
1474	Genome Sequencing and Comparative Genomics in Cereals. , 2013, , 101-126.		0
1475	Transposons in Cereals: Shaping Genomes and Driving Their Evolution. , 2013, , 127-154.		1
1476	Functional Annotation of Plant Genomes. , 2013, , 155-176.		0
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1478	Genome-wide analysis of the CCCH zinc finger gene family in <i>Medicago truncatula</i> . <i>Plant Cell Reports</i> , 2013, 32, 1543-1555.	2.8	58
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1480	Validation of yield-enhancing quantitative trait loci from a low-yielding wild ancestor of rice. <i>Molecular Breeding</i> , 2013, 32, 101-120.	1.0	34
1481	Isolation and characterization of rice (<i>Oryza sativa</i> L.) E3-ubiquitin ligase OsHOS1 gene in the modulation of cold stress response. <i>Plant Molecular Biology</i> , 2013, 83, 351-363.	2.0	36
1482	Co-evolution of plant LTR-retrotransposons and their host genomes. <i>Protein and Cell</i> , 2013, 4, 493-501.	4.8	42
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1491	Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleo- and neoduplicated subgenomes. <i>Plant Journal</i> , 2013, 76, 1030-1044.	2.8	99
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1499	The Repertoires of Ubiquitinating and Deubiquitinating Enzymes in Eukaryotic Genomes. <i>Molecular Biology and Evolution</i> , 2013, 30, 1172-1187.	3.5	70
1500	Genetic and Physiological Characterization of Two Clusters of Quantitative Trait Loci Associated With Seed Dormancy and Plant Height in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 323-331.	0.8	21
1501	Detection and verification of QTLs associated with heat-induced quality decline of rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T 339-346.	0.9	42
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1512	Fine-Mapping and Identification of a Candidate Gene Underlying the <i>d2</i> Dwarfing Phenotype in Pearl Millet, <i>Cenchrus americanus</i> (L.) Morrone. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 563-572.	0.8	20
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1529	Rice Annotation Project Database (RAP-DB): An Integrative and Interactive Database for Rice Genomics. <i>Plant and Cell Physiology</i> , 2013, 54, e6-e6.	1.5	614
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1562	First Insights into the Large Genome of <i>Epimedium sagittatum</i> (Sieb. et Zucc) Maxim, a Chinese Traditional Medicinal Plant. <i>International Journal of Molecular Sciences</i> , 2013, 14, 13559-13576.	1.8	6
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1581	Paleogenomics in Triticeae for translational research. <i>Current Plant Biology</i> , 2014, 1, 34-39.	2.3	14
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1684	Natural Variations and Genome-Wide Association Studies in Crop Plants. <i>Annual Review of Plant Biology</i> , 2014, 65, 531-551.	8.6	567
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1688	<i>Klebsormidium flaccidum</i> genome reveals primary factors for plant terrestrial adaptation. <i>Nature Communications</i> , 2014, 5, 3978.	5.8	532
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1701	Global Genomic Diversity of <i>Oryza sativa</i> Varieties Revealed by Comparative Physical Mapping. <i>Genetics</i> , 2014, 196, 937-949.	1.2	10
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1730	A High-Density SNP Genotyping Array for Rice Biology and Molecular Breeding. <i>Molecular Plant</i> , 2014, 7, 541-553.	3.9	251
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1829	The Sol Genomics Network (SGN)â€”from genotype to phenotype to breeding. <i>Nucleic Acids Research</i> , 2015, 43, D1036-D1041.	6.5	520
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1838	Single-copy gene based 50â€”K SNP chip for genetic studies and molecular breeding in rice. <i>Scientific Reports</i> , 2015, 5, 11600.	1.6	124
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1870	RiceNet v2: an improved network prioritization server for rice genes. <i>Nucleic Acids Research</i> , 2015, 43, W122-W127.	6.5	95
1871	Widely distributed hot and cold spots in meiotic recombination as shown by the sequencing of rice F_2 plants. <i>New Phytologist</i> , 2015, 206, 1491-1502.	3.5	86
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1875	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	1.2	86
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1879	Fine mapping of qGW1, a major QTL for grain weight in sorghum. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1813-1825.	1.8	40
1881	Epigenetic Mutation of <i>RAV6</i> Affects Leaf Angle and Seed Size in Rice. <i>Plant Physiology</i> , 2015, 169, 2118-2128.	2.3	94
1882	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5411-9.	3.3	165
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1884	Multiplex SSR-PCR approaches for semi-automated genotyping and characterization of loci linked to blast disease resistance genes in rice. <i>Comptes Rendus - Biologies</i> , 2015, 338, 709-722.	0.1	6
1885	Genomics of Wild Relatives and Alien Introgressions. , 2015, , 347-381.		8
1886	Unraveling the light-specific metabolic and regulatory signatures of rice through combined in silico modeling and multi-omics analysis. <i>Plant Physiology</i> , 2015, 169, pp.01379.2015.	2.3	68
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1898	Map-based Cloning and Characterization of a Brown Planthopper Resistance Gene BPH26 from <i>Oryza sativa</i> L. ssp. indica Cultivar ADR52. <i>Scientific Reports</i> , 2014, 4, 5872.	1.6	158
1899	Floral traits to enhance outcrossing for higher hybrid seed production in rice: present status and future prospects. <i>Euphytica</i> , 2015, 201, 1-14.	0.6	37
1900	Simple Sequence Repeat Markers in Genetic Divergence and Marker-Assisted Selection of Rice Cultivars: A Review. <i>Critical Reviews in Food Science and Nutrition</i> , 2015, 55, 41-49.	5.4	61
1901	Novel Transgenic Rice-Based Vaccines. <i>Archivum Immunologiae Et Therapiae Experimentalis</i> , 2015, 63, 87-99.	1.0	25
1902	Telomereâ€™centric genome repatterning determines recurring chromosome number reductions during the evolution of eukaryotes. <i>New Phytologist</i> , 2015, 205, 378-389.	3.5	64
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1904	Population transcriptomics reveals a potentially positive role of expression diversity in adaptation. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 284-299.	4.1	26
1905	QTL analysis of Na ⁺ and K ⁺ concentrations in shoots and roots under NaCl stress based on linkage and association analysis in japonica rice. <i>Euphytica</i> , 2015, 201, 109-121.	0.6	41
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1910	Detection of Genetic Factors Responsible for Grain Quality and Cooking Characteristics of Japanese Rice Cultivars. <i>Journal of the Japanese Society for Food Science and Technology</i> , 2016, 63, 484-487.	0.1	2
1911	Reverse Genetics and High Throughput Sequencing Methodologies for Plant Functional Genomics. <i>Current Genomics</i> , 2016, 17, 460-475.	0.7	27
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1913	Genome-wide characterization of non-reference transposons in crops suggests non-random insertion. <i>BMC Genomics</i> , 2016, 17, 536.	1.2	13
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1929	Improvement of Rice Biomass Yield through QTL-Based Selection. PLoS ONE, 2016, 11, e0151830.	1.1	25
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1936	Association Analysis in Rice: From Application to Utilization. <i>Frontiers in Plant Science</i> , 2016, 7, 1202.	1.7	37
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1938	Moving through the Stressed Genome: Emerging Regulatory Roles for Transposons in Plant Stress Response. <i>Frontiers in Plant Science</i> , 2016, 7, 1448.	1.7	117
1939	An Efficient Strategy Combining SSR Markers- and Advanced QTL-seq-driven QTL Mapping Unravels Candidate Genes Regulating Grain Weight in Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 1535.	1.7	21
1940	QTL Analysis of Spike Morphological Traits and Plant Height in Winter Wheat (<i>Triticum aestivum</i> L.) Using a High-Density SNP and SSR-Based Linkage Map. <i>Frontiers in Plant Science</i> , 2016, 7, 1617.	1.7	179
1941	Modeling Rice Metabolism: From Elucidating Environmental Effects on Cellular Phenotype to Guiding Crop Improvement. <i>Frontiers in Plant Science</i> , 2016, 7, 1795.	1.7	18
1942	Characterization and Genetic Analysis of Rice Mutant <i>crr1</i> Exhibiting Compromised Non-host Resistance to <i>Puccinia striiformis</i> f. sp. <i>tritici</i> (Pst). <i>Frontiers in Plant Science</i> , 2016, 7, 1822.	1.7	8
1943	Genetic resources offer efficient tools for rice functional genomics research. <i>Plant, Cell and Environment</i> , 2016, 39, 998-1013.	2.8	42
1944	Combining mapping of physiological quantitative trait loci and transcriptome for cold tolerance for counteracting male sterility induced by low temperatures during reproductive stage in rice. <i>Physiologia Plantarum</i> , 2016, 157, 175-192.	2.6	23
1945	The genome of black raspberry (<i>Rubus occidentalis</i>). <i>Plant Journal</i> , 2016, 87, 535-547.	2.8	111
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1947	Phenylalanine ammonia-lyase gene families in cucurbit species: Structure, evolution, and expression. <i>Journal of Integrative Agriculture</i> , 2016, 15, 1239-1255.	1.7	16
1948	Transcriptome shock in an interspecific F1 triploid hybrid of <i>Oryza</i> revealed by RNA sequencing. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 150-164.	4.1	38
1949	A genetic delineation of Patchouli (<i>Pogostemon cablin</i>) revealed by specific locus amplified fragment sequencing. <i>Journal of Systematics and Evolution</i> , 2016, 54, 491-501.	1.6	16
1950	Somaclonal variation does not preclude the use of rice transformants for genetic screening. <i>Plant Journal</i> , 2016, 85, 648-659.	2.8	34
1951	A Collection of Conserved Noncoding Sequences to Study Gene Regulation in Flowering Plants. <i>Plant Physiology</i> , 2016, 171, 2586-2598.	2.3	39

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1953	Landscape of genomic diversity and trait discovery in soybean. <i>Scientific Reports</i> , 2016, 6, 23598.	1.6	151
1954	Long Terminal Repeat Retrotransposon Content in Eight Diploid Sunflower Species Inferred from Next-Generation Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2299-2308.	0.8	11
1955	Coevolutionary Dynamics of Rice Blast Resistance Gene <i>Pi-ta</i> and <i>Magnaporthe oryzae</i> Avirulence Gene <i>AVR-Pita 1</i> . <i>Phytopathology</i> , 2016, 106, 676-683.	1.1	30
1956	Analysis of representative organ-specific genes and promoters of rice using a 3' ORF-oriented long oligomer microarray. <i>Journal of Plant Biology</i> , 2016, 59, 579-593.	0.9	8
1957	Robust phenotyping strategies for evaluation of stem non-structural carbohydrates (NSC) in rice. <i>Journal of Experimental Botany</i> , 2016, 67, 6125-6138.	2.4	31
1958	The Melon Genome. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 173-181.	0.3	3
1959	CRISPR/Cas9 in rice can induce new mutations in later generations, leading to chimerism and unpredicted segregation of the targeted mutation. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	25
1960	Open access resources for genome-wide association mapping in rice. <i>Nature Communications</i> , 2016, 7, 10532.	5.8	371
1961	Comprehensive analysis of multi-tissue transcriptome data and the genome-wide investigation of GRAS family in <i>Phyllostachys edulis</i> . <i>Scientific Reports</i> , 2016, 6, 27640.	1.6	11
1962	Genome-wide identification and analysis of rice genes to elucidate morphological agronomic traits. <i>Journal of Plant Biology</i> , 2016, 59, 639-647.	0.9	5
1963	<i>de novo</i> assemblies of three <i>Oryza glaberrima</i> accessions provide first insights about pan-genome of African rices. <i>Genome Biology and Evolution</i> , 2017, 9, evw253.	1.1	18
1964	Development of a universal and simplified ddRAD library preparation approach for SNP discovery and genotyping in angiosperm plants. <i>Plant Methods</i> , 2016, 12, 39.	1.9	86
1965	Breeding vis-à-vis Genomics of Tropical Tree Crops. , 2016, , 203-255.		1
1966	Analysis of <i>Hopi</i> / <i>Osr27</i> and <i>Houba</i> / <i>Tos5</i> / <i>Osr13</i> retrotransposons in rice. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 213-218.	0.5	10
1967	Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1511-1522.	4.1	20
1968	Marker imputation efficiency for genotyping-by-sequencing data in rice (<i>Oryza sativa</i>) and alfalfa (<i>Medicago sativa</i>). <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	57
1969	High throughput transformation of a <i>Sorghum</i> cDNA library for rice improvement. <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 125, 471-478.	1.2	2

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1972	Genome-Wide Comparative Analysis of Microsatellites in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 117-135.	1.0	13
1973	Repetitive Sequences. <i>Compendium of Plant Genomes</i> , 2016, , 115-123.	0.3	0
1974	Genetics, Transcriptional Profiles, and Catalytic Properties of the UDP-Arabinose Mutase Family from Barley. <i>Biochemistry</i> , 2016, 55, 322-334.	1.2	13
1975	A high-quality carrot genome assembly provides new insights into carotenoid accumulation and asterid genome evolution. <i>Nature Genetics</i> , 2016, 48, 657-666.	9.4	432
1976	Application of whole genome shotgun sequencing for detection and characterization of genetically modified organisms and derived products. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 4595-4614.	1.9	43
1977	The draft genome of MD-2 pineapple using hybrid error correction of long reads. <i>DNA Research</i> , 2016, 23, 427-439.	1.5	35
1978	Exploiting genotyping by sequencing to characterize the genomic structure of the American cranberry through high-density linkage mapping. <i>BMC Genomics</i> , 2016, 17, 451.	1.2	45
1979	Field Guide to Plant Model Systems. <i>Cell</i> , 2016, 167, 325-339.	13.5	99
1980	Markers associated with heading and aftermath heading in perennial ryegrass full-sib families. <i>BMC Plant Biology</i> , 2016, 16, 160.	1.6	16
1981	Global identification and expression analysis of stress-responsive genes of the Argonaute family in apple. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2015-2030.	1.0	4
1982	Elucidating and mining the Tulipa and Lilium transcriptomes. <i>Plant Molecular Biology</i> , 2016, 92, 249-261.	2.0	16
1983	India's Computational Biology Growth and Challenges. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2016, 8, 263-276.	2.2	2
1984	Identification of Candidate Genes for Drought Stress Tolerance. , 2016, , 385-414.		3
1985	Genomics Resources for Plants. , 2016, , 29-57.		2
1986	Dissimilar manifestation of heterosis under nutrient-deficient and nutrient-sufficient condition. <i>Plant Physiology</i> , 2016, 172, pp.00579.2016.	2.3	4
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1989	SNP-based discovery of salinity-tolerant QTLs in a bi-parental population of rice (<i>Oryza sativa</i>). Molecular Genetics and Genomics, 2016, 291, 2081-2099.	1.0	36
1990	Repeat Sequences in the Tomato Genome. Compendium of Plant Genomes, 2016, , 173-199.	0.3	1
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1992	A flow cytometric method for estimating S-phase duration in plants. Journal of Experimental Botany, 2016, 67, 6077-6087.	2.4	24
1993	REL2, A Gene Encoding An Unknown Function Protein which Contains DUF630 and DUF632 Domains Controls Leaf Rolling in Rice. Rice, 2016, 9, 37.	1.7	70
1994	Draft genome of the living fossil Ginkgo biloba. GigaScience, 2016, 5, 49.	3.3	232
1996	Comparison of molecular genetic utilities of TD, AFLP, and MSAP among the accessions of japonica, indica, and Tongil of <i>Oryza sativa</i> L.. Genes and Genomics, 2016, 38, 819-830.	0.5	8
1997	Deciphering the evolutionary interplay between subgenomes following polyploidy: A paleogenomics approach in grasses. American Journal of Botany, 2016, 103, 1167-1174.	0.8	20
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1999	Unraveling the molecular basis of oxidative stress management in a drought tolerant rice genotype Nagina 22. BMC Genomics, 2016, 17, 774.	1.2	25
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2003	Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. Plant Cell, 2016, 28, 2700-2714.	3.1	183
2004	A GIS-based Upscaling Estimation of Nutrient Runoff Losses from Rice Paddy Fields to a Regional Level. Journal of Environmental Quality, 2016, 45, 1865-1873.	1.0	14
2005	NABIC: A New Access Portal to Search, Visualize, and Share Agricultural Genomics Data. Evolutionary Bioinformatics, 2016, 12, EBO.S34493.	0.6	10
2006	Structural Diversity of a Novel LTR Retrotransposon, RTPOSON, in the Genus <i>Oryza</i> . Evolutionary Bioinformatics, 2016, 12, EBO.S35158.	0.6	1

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2009	Ricebase: a breeding and genetics platform for rice, integrating individual molecular markers, pedigrees and whole-genome-based data. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw107.	1.4	30
2010	Pollen Killer Gene S35 Function Requires Interaction with an Activator That Maps Close to S24, Another Pollen Killer Gene in Rice. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1459-1468.	0.8	14
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2015	Identification and characterization of abundant repetitive sequences in <i>Eragrostis tef</i> cv. Enatite genome. <i>BMC Plant Biology</i> , 2016, 16, 39.	1.6	16
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2019	Rice: The First Crop Genome. <i>Rice</i> , 2016, 9, 14.	1.7	66
2020	<i>OsSIDP366</i> , a DUF1644 gene, positively regulates responses to drought and salt stresses in rice. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 492-502.	4.1	54
2021	Comparative analysis of nine different small heat shock protein gene promoters in <i>Oryza sativa</i> L. subsp. indica. <i>Plant Systematics and Evolution</i> , 2016, 302, 1195-1206.	0.3	1
2022	Evolutionary Dynamics of the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) Subfamily in Angiosperms. <i>Plant Physiology</i> , 2016, 170, 1595-1610.	2.3	114
2023	A Toolbox of Potato Genetic and Genomic Resources. <i>American Journal of Potato Research</i> , 2016, 93, 21-32.	0.5	3
2024	<i>Oryza</i> Genome: Genome Diversity Database of Wild <i>Oryza</i> Species. <i>Plant and Cell Physiology</i> , 2016, 57, e1-e1.	1.5	34

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2026	Ancestors of modern plant crops. <i>Current Opinion in Plant Biology</i> , 2016, 30, 134-142.	3.5	54
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2028	Introgression and Exploitation of QTL for Yield and Yield Components from Related Wild Species in Rice Cultivars. <i>Sustainable Development and Biodiversity</i> , 2016, , 171-202.	1.4	2
2029	Genetics and Genomics of Brachypodium. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , .	0.3	22
2030	Rice Improvement Through Genome-Based Functional Analysis and Molecular Breeding in India. <i>Rice</i> , 2016, 9, 1.	1.7	111
2031	The big five of the monocot genomes. <i>Current Opinion in Plant Biology</i> , 2016, 30, 33-40.	3.5	10
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2035	Natural variation in the glucose content of dilute sulfuric acid-pretreated rice straw liquid hydrolysates: implications for bioethanol production. <i>Bioscience, Biotechnology and Biochemistry</i> , 2016, 80, 863-869.	0.6	4
2036	What makes up plant genomes: The vanishing line between transposable elements and genes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 366-380.	0.9	67
2037	Melon Genome Sequence. <i>Biotechnology in Agriculture and Forestry</i> , 2016, , 15-29.	0.2	0
2038	Repetitive sequences in <i>Eragrostis curvula</i> cDNA EST libraries obtained from genotypes with different ploidy. <i>Biologia Plantarum</i> , 2016, 60, 55-67.	1.9	7
2039	Molecular Marker-Based Assessment of Genetic Diversity and Quality Trait Specific Marker Validation. , 2016, , 107-137.		1
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2041	Emerging tools, concepts and ideas to track the modulator genes underlying plant drought adaptive traits: An overview. <i>Plant Signaling and Behavior</i> , 2016, 11, e1074370.	1.2	6
2042	Finding the Subcellular Location of Barley, Wheat, Rice and Maize Proteins: The Compendium of Crop Proteins with Annotated Locations (cropPAL). <i>Plant and Cell Physiology</i> , 2016, 57, e9-e9.	1.5	51

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2044	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomics Data. <i>Methods in Molecular Biology</i> , 2016, 1374, 115-140.	0.4	216
2045	Gramene: A Resource for Comparative Analysis of Plants Genomes and Pathways. <i>Methods in Molecular Biology</i> , 2016, 1374, 141-163.	0.4	15
2046	PGSB/MIPS Plant Genome Information Resources and Concepts for the Analysis of Complex Grass Genomes. <i>Methods in Molecular Biology</i> , 2016, 1374, 165-186.	0.4	2
2047	Plant Bioinformatics. <i>Methods in Molecular Biology</i> , 2016, . .	0.4	11
2048	Construction of a versatile SNP array for pyramiding useful genes of rice. <i>Plant Science</i> , 2016, 242, 131-139.	1.7	33
2049	The Omics Revolution in Agricultural Research. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 36-44.	2.4	104
2050	The phenome analysis of mutant alleles in Leucine-Rich Repeat Receptor-Like Kinase genes in rice reveals new potential targets for stress tolerant cereals. <i>Plant Science</i> , 2016, 242, 240-249.	1.7	27
2051	Forest tree genomics: 10 achievements from the past 10 years and future prospects. <i>Annals of Forest Science</i> , 2016, 73, 77-103.	0.8	91
2052	Removal of decabromodiphenyl ether (BDE-209) using a combined system involving TiO ₂ photocatalysis and wetland plants. <i>Journal of Hazardous Materials</i> , 2017, 322, 263-269.	6.5	27
2053	Beyond Genomics: Studying Evolution with Gene Coexpression Networks. <i>Trends in Plant Science</i> , 2017, 22, 298-307.	4.3	96
2054	Tandem duplications of receptor-like kinase genes reshaped the homologous chromosome 1 regions in <i>Oryza sativa</i> ssp. <i>indica</i> and <i>japonica</i> and their possible ancestral genomes. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	0
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2056	Phylogenomic analysis of gene co-expression networks reveals the evolution of functional modules. <i>Plant Journal</i> , 2017, 90, 447-465.	2.8	97
2057	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	3.5	68
2058	The rice paradox: Multiple origins but single domestication in Asian rice. <i>Molecular Biology and Evolution</i> , 2017, 34, msx049.	3.5	178
2059	Xanthine Alkaloids: Occurrence, Biosynthesis, and Function in Plants. <i>Progress in the Chemistry of Organic Natural Products</i> , 2017, 105, 1-88.	0.8	50
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2062	Genome-wide characterization and evolution analysis of long terminal repeat retroelements in moso bamboo (<i>Phyllostachys edulis</i>). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	14
2063	Transposon-mediated epigenetic regulation contributes to phenotypic diversity and environmental adaptation in rice. <i>Current Opinion in Plant Biology</i> , 2017, 36, 111-118.	3.5	61
2064	Analysis of Ribosome-Associated mRNAs in Rice Reveals the Importance of Transcript Size and GC Content in Translation. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 203-219.	0.8	43
2065	BioNano Genome Map Resource for <i>Oryza sativa</i> ssp. japonica and indica and Its Application in Rice Genome Sequence Correction and Gap Filling. <i>Molecular Plant</i> , 2017, 10, 895-898.	3.9	11
2066	Phylogenetic analysis of 25 plant species representing 19 angiosperm families and one gymnosperm family based on 390 orthologous genes. <i>Plant Systematics and Evolution</i> , 2017, 303, 413-417.	0.3	9
2067	Genome Engineering and Agriculture: Opportunities and Challenges. <i>Progress in Molecular Biology and Translational Science</i> , 2017, 149, 1-26.	0.9	88
2068	Rice Expression Database (RED): An integrated RNA-Seq-derived gene expression database for rice. <i>Journal of Genetics and Genomics</i> , 2017, 44, 235-241.	1.7	114
2069	Sequencing and de novo assembly of a near complete indica rice genome. <i>Nature Communications</i> , 2017, 8, 15324.	5.8	246
2070	An Evolutionary View of the Biogenesis and Function of Rice Small RNAs. <i>RNA Technologies</i> , 2017, , 69-88.	0.2	0
2071	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
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2073	Host range, mating type and population structure of <i>Magnaporthe</i> sp. of a single barley field in São Paulo state, Brazil. <i>Journal of Phytopathology</i> , 2017, 165, 414-424.	0.5	13
2074	Horizontal Transfer Can Drive a Greater Transposable Element Load in Large Populations. <i>Journal of Heredity</i> , 2017, 108, 36-44.	1.0	11
2075	Rice Epigenomics: How Does Epigenetic Manipulation of Crops Contribute to Agriculture?. <i>RNA Technologies</i> , 2017, , 427-443.	0.2	0
2076	Auxin transport and response requirements for root hydrotropism differ between plant species. <i>Journal of Experimental Botany</i> , 2017, 68, 3441-3456.	2.4	19
2077	Comparative Mapping of Seed Dormancy Loci Between Tropical and Temperate Ecotypes of Weedy Rice (<i>Oryza sativa</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2605-2614.	0.8	11
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2080	Genome-wide association mapping for phenotypic plasticity in rice. <i>Plant, Cell and Environment</i> , 2017, 40, 1565-1575.	2.8	45
2081	Fine mapping of powdery mildew resistance gene PmTm4 in wheat using comparative genomics. <i>Journal of Integrative Agriculture</i> , 2017, 16, 540-550.	1.7	17
2082	QTL mapping revealed TaVp-1A conferred pre-harvest sprouting resistance in wheat population Yanda 1817A-Beinong 6. <i>Journal of Integrative Agriculture</i> , 2017, 16, 435-444.	1.7	7
2083	Estimation of outcrossing rates in intraspecific (<i>Oryza sativa</i>) and interspecific (<i>Oryza sativa</i> × <i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	3
2084	The Peach v2.0 release: high-resolution linkage mapping and deep resequencing improve chromosome-scale assembly and contiguity. <i>BMC Genomics</i> , 2017, 18, 225.	1.2	342
2085	Quantitative trait loci from identification to exploitation for crop improvement. <i>Plant Cell Reports</i> , 2017, 36, 1187-1213.	2.8	81
2086	Natural Variation in the Promoter of GSE5 Contributes to Grain Size Diversity in Rice. <i>Molecular Plant</i> , 2017, 10, 685-694.	3.9	253
2087	Reconstructing the genome of the most recent common ancestor of flowering plants. <i>Nature Genetics</i> , 2017, 49, 490-496.	9.4	203
2088	Distribution of Divo in <i>Coffea</i> genomes, a poorly described family of angiosperm LTR-Retrotransposons. <i>Molecular Genetics and Genomics</i> , 2017, 292, 741-754.	1.0	7
2089	Co-evolution of methods and thoughts in cereal domestication studies: a tale of barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	42
2090	Evolution of genome size and genomic GC content in carnivorous holokinetics (<i>Droseraceae</i>). <i>Annals of Botany</i> , 2017, 119, 409-416.	1.4	25
2091	Genome-wide identification, cloning and characterization of SNARE genes in bread wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.9	1
2092	An innovative SNP genotyping method adapting to multiple platforms and throughputs. <i>Theoretical and Applied Genetics</i> , 2017, 130, 597-607.	1.8	124
2093	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. <i>Methods in Molecular Biology</i> , 2017, 1533, 1-31.	0.4	189
2094	PlaNet: Comparative Co-Expression Network Analyses for Plants. <i>Methods in Molecular Biology</i> , 2017, 1533, 213-227.	0.4	42
2095	Single-cell transcriptome analysis reveals widespread monoallelic gene expression in individual rice mesophyll cells. <i>Science Bulletin</i> , 2017, 62, 1304-1314.	4.3	21
2096	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

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2098	Transcriptionally active LTR retroelement-related sequences and their relationship with small RNA in moso bamboo (<i>Phyllostachys edulis</i>). <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	8
2099	DNA sequencing at 40: past, present and future. <i>Nature</i> , 2017, 550, 345-353.	13.7	729
2100	Improving Crop Adaptations to Climate Change: Contextualizing the Strategy. , 2017, , 277-298.		2
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2102	Sequencing, Assembly, and Annotation of the Soybean Genome. <i>Compendium of Plant Genomes</i> , 2017, , 73-82.	0.3	5
2103	Genetic variation for domestication-related traits revealed in a cultivated rice, Nipponbare (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	5
2104	<i>Panax ginseng</i> genome examination for ginsenoside biosynthesis. <i>GigaScience</i> , 2017, 6, 1-15.	3.3	150
2105	Evolutionary modes of emergence of short interspersed nuclear element (<scp>SINE</scp>) families in grasses. <i>Plant Journal</i> , 2017, 92, 676-695.	2.8	6
2106	Arbuscular Mycorrhizal Technology Based on Ecosystem Services Rendered by Native Flora for Improving Phosphorus Nutrition of Upland Rice: Status and Prospect. , 2017, , 87-105.		1
2107	Physical Map of the Short Arm of Bread Wheat Chromosome 3D. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0021.	1.6	11
2108	Allelic variation of the rice blast resistance gene <i>Pid3</i> in cultivated rice worldwide. <i>Scientific Reports</i> , 2017, 7, 10362.	1.6	19
2109	In silico Analysis of <i>osr40c1</i> Promoter Sequence Isolated from Indica Variety Pokkali. <i>Rice Science</i> , 2017, 24, 228-234.	1.7	9
2110	Construction and characterization of a bacterial artificial chromosome library for <i>Camellia sinensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	6
2111	The Rice Phytochrome Genes, <i>PHYA</i> and <i>PHYB</i> , Have Synergistic Effects on Anther Development and Pollen Viability. <i>Scientific Reports</i> , 2017, 7, 6439.	1.6	24
2112	A bioinformatics approach for identifying transgene insertion sites using whole genome sequencing data. <i>BMC Biotechnology</i> , 2017, 17, 67.	1.7	42
2113	PlantExpress: A Database Integrating <i>OryzaExpress</i> and <i>ArthaExpress</i> for Single-species and Cross-species Gene Expression Network Analyses with Microarray-Based Transcriptome Data. <i>Plant and Cell Physiology</i> , 2017, 58, e1-e1.	1.5	23
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2116	The <i>Aegilops tauschii</i> genome reveals multiple impacts of transposons. <i>Nature Plants</i> , 2017, 3, 946-955.	4.7	164
2117	Plant Bioinformatics: Next Generation Sequencing Approaches. , 2017, , 1-106.		1
2118	Tracking the genome-wide outcomes of a transposable element burst over decades of amplification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10550-E10559.	3.3	41
2119	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
2120	Phylogenetic, structural, and functional characterization of AMT3;1, an ammonium transporter induced by mycorrhization among model grasses. <i>Mycorrhiza</i> , 2017, 27, 695-708.	1.3	28
2121	Development of gene-based identification markers for <i>Phalaenopsis</i> 'KS Little Gem'™ based on comparative genome analysis. <i>Horticulture Environment and Biotechnology</i> , 2017, 58, 162-169.	0.7	2
2122	EpiTEome: Simultaneous detection of transposable element insertion sites and their DNA methylation levels. <i>Genome Biology</i> , 2017, 18, 91.	3.8	21
2123	Genes Sufficient for Synthesizing Peptidoglycan are Retained in Gymnosperm Genomes, and MurE from <i>Larix gmelinii</i> can Rescue the Albino Phenotype of <i>Arabidopsis</i> MurE Mutation. <i>Plant and Cell Physiology</i> , 2017, 58, 587-597.	1.5	18
2124	Genomic skimming for identification of medium/highly abundant transposable elements in <i>Arundo donax</i> and <i>Arundo plinii</i> . <i>Molecular Genetics and Genomics</i> , 2017, 292, 157-171.	1.0	4
2125	Temperature and drought impacts on rice production: An agronomic perspective regarding short- and long-term adaptation measures. <i>Water Resources and Rural Development</i> , 2017, 9, 12-27.	1.1	98
2126	The <i>in silico</i> identification and characterization of a bread wheat (<i>Triticum militinae</i>) introgression line. <i>Plant Biotechnology Journal</i> , 2017, 15, 249-256.	4.1	10
2127	Reconciling the evolutionary origin of bread wheat (<i>Triticum aestivum</i>). <i>New Phytologist</i> , 2017, 213, 1477-1486.	3.5	119
2128	Sequencing and comparative analyses of <i>Aegilops tauschii</i> chromosome arm 3DS reveal rapid evolution of Triticeae genomes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 51-61.	1.7	25
2129	LTR Retrotransposons Show Low Levels of Unequal Recombination and High Rates of Intraelement Gene Conversion in Large Plant Genomes. <i>Genome Biology and Evolution</i> , 2017, 9, 3449-3462.	1.1	45
2130	Genome Sequence-Based Marker Development and Genotyping in Potato. <i>Compendium of Plant Genomes</i> , 2017, , 307-326.	0.3	3
2131	Biotoxicity of Cry1Ab protein on wolf spider <i>Pardosa pseudoannulata</i> . <i>Ecotoxicology</i> , 2017, 26, 1336-1343.	1.1	4
2132	Assembly of an early-matured japonica (Geng) rice genome, Sujing18, based on PacBio and Illumina sequencing. <i>Scientific Data</i> , 2017, 4, 170195.	2.4	9

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2133	DNA fingerprinting in rice (<i>Oryza sativa</i> L.) with transposon markers. <i>Acta Horticulturae</i> , 2017, , 251-260.	0.1	0
2134	Analysis of nuclear mitochondrial DNAs and factors affecting patterns of integration in plant species. <i>Genes and Genetic Systems</i> , 2017, 92, 27-33.	0.2	11
2135	QTL mapping and candidate gene analysis of ferrous iron and zinc toxicity tolerance at seedling stage in rice by genome-wide association study. <i>BMC Genomics</i> , 2017, 18, 828.	1.2	58
2136	Generation of expressed sequence tags for discovery of genes responsible for floral traits of <i>Chrysanthemum morifolium</i> by next-generation sequencing technology. <i>BMC Genomics</i> , 2017, 18, 683.	1.2	29
2137	Development of a Technique for Callus Induction and Plant Regeneration in <i>Oryza sativa</i> L. var. MRQ74 and MR269. <i>Advance Journal of Food Science and Technology</i> , 2017, 13, 128-137.	0.1	1
2138	Identification of A Major Quantitative Trait Locus for Grain Weight In Rice Using Microsatellite Marker. <i>Makara Journal of Science</i> , 2017, 21, .	1.1	2
2139	Rice Crop Responses to Global Warming: An Overview. , 2017, , .		4
2140	Improvement of seed shattering and dormancy in <i>Oryza sativa</i> L. "Hokuriku 193"™ based on genetic information. <i>Breeding Science</i> , 2017, 67, 173-180.	0.9	1
2141	Fine Mapping of Carbon Assimilation Rate 8, a Quantitative Trait Locus for Flag Leaf Nitrogen Content, Stomatal Conductance and Photosynthesis in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 60.	1.7	53
2142	Understanding Host-Pathogen Interactions with Expression Profiling of NILs Carrying Rice-Blast Resistance Pi9 Gene. <i>Frontiers in Plant Science</i> , 2017, 8, 93.	1.7	48
2143	Evolutionary Analyses of GRAS Transcription Factors in Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 8, 273.	1.7	89
2144	New Insights on Leucine-Rich Repeats Receptor-Like Kinase Orthologous Relationships in Angiosperms. <i>Frontiers in Plant Science</i> , 2017, 08, 381.	1.7	54
2145	Cereal Crop Proteomics: Systemic Analysis of Crop Drought Stress Responses Towards Marker-Assisted Selection Breeding. <i>Frontiers in Plant Science</i> , 2017, 8, 757.	1.7	131
2146	Poaceae vs. Abiotic Stress: Focus on Drought and Salt Stress, Recent Insights and Perspectives. <i>Frontiers in Plant Science</i> , 2017, 8, 1214.	1.7	99
2147	Overexpression of Golgi Protein CYP21-4s Improves Crop Productivity in Potato and Rice by Increasing the Abundance of Mannosidic Glycoproteins. <i>Frontiers in Plant Science</i> , 2017, 8, 1250.	1.7	15
2148	A Chemical-Induced, Seed-Soaking Activation Procedure for Regulated Gene Expression in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1447.	1.7	8
2149	Alignment of Common Wheat and Other Grass Genomes Establishes a Comparative Genomics Research Platform. <i>Frontiers in Plant Science</i> , 2017, 8, 1480.	1.7	11
2150	Functional Characterization of a Syntxin Involved in Tomato (<i>Solanum lycopersicum</i>) Resistance against Powdery Mildew. <i>Frontiers in Plant Science</i> , 2017, 8, 1573.	1.7	6

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2152	A High-Density Genetic Map of Wild Emmer Wheat from the Karaca Dağ Region Provides New Evidence on the Structure and Evolution of Wheat Chromosomes. <i>Frontiers in Plant Science</i> , 2017, 8, 1798.	1.7	33
2153	Combined Genomic and Genetic Data Integration of Major Agronomical Traits in Bread Wheat (<i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1843.	1.7	55
2154	An Integrated "Multi-Omics" Comparison of Embryo and Endosperm Tissue-Specific Features and Their Impact on Rice Seed Quality. <i>Frontiers in Plant Science</i> , 2017, 8, 1984.	1.7	48
2155	Potential Uses of Wild Germplasms of Grain Legumes for Crop Improvement. <i>International Journal of Molecular Sciences</i> , 2017, 18, 328.	1.8	58
2156	Quantitative trait loci analysis of blast resistance in <i>Oryza sativa</i> L. "Hokuriku 193". <i>Breeding Science</i> , 2017, 67, 159-164.	0.9	5
2157	Whole-Genome Characteristics and Polymorphic Analysis of Vietnamese Rice Landraces as a Comprehensive Information Resource for Marker-Assisted Selection. <i>International Journal of Genomics</i> , 2017, 2017, 1-11.	0.8	6
2158	Identify QTLs for grain size and weight in common wild rice using chromosome segment substitution lines across six environments. <i>Breeding Science</i> , 2017, 67, 472-482.	0.9	23
2159	Rice "t", 2017, , .		0
2160	Hybrid assembly with long and short reads improves discovery of gene family expansions. <i>BMC Genomics</i> , 2017, 18, 541.	1.2	51
2161	Plant secondary metabolites and its dynamical systems of induction in response to environmental factors: A review. <i>African Journal of Agricultural Research</i> Vol Pp, 2017, 12, 71-84.	0.2	61
2162	Construction of a genetic map using EST-SSR markers and QTL analysis of major agronomic characters in hexaploid sweet potato (<i>Ipomoea batatas</i> (L.) Lam). <i>PLoS ONE</i> , 2017, 12, e0185073.	1.1	13
2163	Genetic dissection of agronomically important traits in closely related temperate & japonica rice cultivars. <i>Breeding Science</i> , 2017, 67, 427-434.	0.9	15
2164	Updating the elite rice variety Kongyu 131 by improving the Gn1a locus. <i>Rice</i> , 2017, 10, 35.	1.7	28
2165	Identification and validation of a novel major QTL for harvest index in rice (<i>Oryza sativa</i> L.). <i>Rice</i> , 2017, 10, 44.	1.7	8
2166	Plant-RRBS, a bisulfite and next-generation sequencing-based methylome profiling method enriching for coverage of cytosine positions. <i>BMC Plant Biology</i> , 2017, 17, 115.	1.6	13
2167	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. <i>BMC Biology</i> , 2017, 15, 86.	1.7	114
2168	DNA fingerprinting and genetic diversities in some Bangladeshi aus rice (<i>Oryza sativa</i> L.) genotypes. <i>SAARC Journal of Agriculture</i> , 2017, 15, 123-137.	0.2	5

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2170	Dealing with iron metabolism in rice: from breeding for stress tolerance to biofortification. <i>Genetics and Molecular Biology</i> , 2017, 40, 312-325.	0.6	39
2171	Sequencing flow-sorted short arm of <i>Haynaldia villosa</i> chromosome 4V provides insights into its molecular structure and virtual gene order. <i>BMC Genomics</i> , 2017, 18, 791.	1.2	10
2172	Cytonuclear Variation of Rubisco in Synthesized Rice Hybrids and Allotetraploids. <i>Plant Genome</i> , 2017, 10, plantgenome2017.05.0041.	1.6	20
2173	Markers Associated with Culm Length and Elongated Internode Length in <i>Japonica</i> Rice. <i>Crop Science</i> , 2017, 57, 2329-2344.	0.8	4
2174	Marker assisted introgression of bacterial blight resistant gene into submergence tolerance rice variety BRRI dhan52. <i>Bangladesh Journal of Agricultural Research</i> , 2017, 42, 403-411.	0.0	2
2175	Molecular function of florigen. <i>Breeding Science</i> , 2017, 67, 327-332.	0.9	26
2176	Validation of house-keeping genes for normalization of gene expression data during diurnal/circadian studies in rice by RT-qPCR. <i>Scientific Reports</i> , 2018, 8, 3203.	1.6	35
2177	High-resolution genetic mapping of a novel brown planthopper resistance locus, Bph34 in <i>Oryza sativa</i> L. X <i>Oryza nivara</i> (Sharma & Shastry) derived interspecific F2 population. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1163-1171.	1.8	65
2178	Aneuploidization under segmental allotetraploidy in rice and its phenotypic manifestation. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1273-1285.	1.8	21
2179	Discovery of Lineage-Specific Genome Change in Rice Through Analysis of Resequencing Data. <i>Genetics</i> , 2018, 209, 617-626.	1.2	4
2180	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.	2.8	119
2181	Transcriptome characterization and screening of molecular markers in ecologically important Himalayan species (<i>Rhododendron arboreum</i>). <i>Genome</i> , 2018, 61, 417-428.	0.9	18
2182	Temperature-dependent QTLs in indica alleles for improving grain quality in rice: increased prominence of QTLs responsible for reduced chalkiness under high-temperature conditions. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	3
2183	Genome-wide Hi-C analysis reveals extensive hierarchical chromatin interactions in rice. <i>Plant Journal</i> , 2018, 94, 1141-1156.	2.8	114
2184	Fine mapping and identification of a novel locus qGL12.2 control grain length in wild rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT / Overlook 22	1.8	22
2185	<i>Oryza nivara</i> Sharma et Shastry. <i>Compendium of Plant Genomes</i> , 2018, , 207-238.	0.3	10
2186	Informatics of Wild Relatives of Rice. <i>Compendium of Plant Genomes</i> , 2018, , 27-40.	0.3	2

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2188	Evolutionary Relationships Among the Oryza Species. Compendium of Plant Genomes, 2018, , 41-54.	0.3	7
2189	Oryza brachyantha A. Chev. et Roehr. Compendium of Plant Genomes, 2018, , 75-85.	0.3	2
2190	The Wild Oryza Genomes. Compendium of Plant Genomes, 2018, , .	0.3	14
2191	The phytotoxicities of decabromodiphenyl ether (BDE-209) to different rice cultivars (Oryza sativa L.). Environmental Pollution, 2018, 235, 692-699.	3.7	39
2192	Multi-Omics Driven Assembly and Annotation of the Sandalwood (<i>Santalum album</i>) Genome. Plant Physiology, 2018, 176, 2772-2788.	2.3	45
2193	Genome Sequences of Oryza Species. , 2018, , 1-20.		2
2194	Marker-Assisted Gene Pyramiding for Durable Resistance to Blast. , 2018, , 393-415.		3
2195	Genes Affecting Eating and Processing Qualities. , 2018, , 417-434.		4
2196	Genome-Wide Association Mapping of Complex Traits in Rice. , 2018, , 497-510.		3
2197	Next-Generation Breeding of Rice by Whole-Genome Approaches. , 2018, , 511-522.		4
2198	Composition and Structure of Rice Centromeres and Telomeres. , 2018, , 37-52.		6
2199	Rice Organelle Genomics: Approaches to Genetic Engineering and Breeding. , 2018, , 53-67.		2
2201	Centromeric <sc>DNA</sc> characterization in the model grass <i>Brachypodium distachyon</i> provides insights on the evolution of the genus. Plant Journal, 2018, 93, 1088-1101.	2.8	28
2202	Evolutionary Epigenomics of Retrotransposon-Mediated Methylation Spreading in Rice. Molecular Biology and Evolution, 2018, 35, 365-382.	3.5	44
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2204	Single-molecule sequencing and optical mapping yields an improved genome of woodland strawberry (Fragaria vesca) with chromosome-scale contiguity. GigaScience, 2018, 7, 1-7.	3.3	209
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2519	The Genomes of the Allohexaploid <i>Echinochloa crus-galli</i> and Its Progenitors Provide Insights into Polyploidization-Driven Adaptation. <i>Molecular Plant</i> , 2020, 13, 1298-1310.	3.9	47
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2529	Regulation of Rice Tillering by RNA-Directed DNA Methylation at Miniature Inverted-Repeat Transposable Elements. <i>Molecular Plant</i> , 2020, 13, 851-863.	3.9	63
2530	Fluorescent reporters for functional analysis in rice leaves. <i>Plant Direct</i> , 2020, 4, e00188.	0.8	8
2531	Construction of three half-sib SSR linkage maps derived from overwintering cultivated rice and segregation distortion loci mapping. <i>Genome</i> , 2020, 63, 239-251.	0.9	1
2532	Evolutionary dynamics and impacts of chromosome regions carrying R-gene clusters in rice. <i>Scientific Reports</i> , 2020, 10, 872.	1.6	22
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2548	Designing future crops: challenges and strategies for sustainable agriculture. <i>Plant Journal</i> , 2021, 105, 1165-1178.	2.8	110
2549	Deployment of wild relatives for genetic improvement in rice (<i>Oryza sativa</i>). <i>Plant Breeding</i> , 2021, 140, 23-52.	1.0	18
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2569	Genetic Engineering for Biotic Stress Management in Rice. <i>Concepts and Strategies in Plant Sciences</i> , 2021, , 117-139.	0.6	0
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2573	Chromosome-level “de novo“ genome assemblies of over 100 plant species. <i>Breeding Science</i> , 2021, 71, 117-124.	0.9	19
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2581	The <i>mop1</i> mutation affects the recombination landscape in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	17
2582	Development and Field Evaluation of Near-Isogenic Lines of GR2-EBRRI dhan29 Golden Rice. <i>Frontiers in Plant Science</i> , 2021, 12, 619739.	1.7	14
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2590	Genome-wide association study to identify chromosomal regions related to panicle architecture in rice (<i>Oryza sativa</i>). <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2849-2865.	0.8	2
2591	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	3.1	180
2592	Phytohormone signaling and crosstalk in regulating drought stress response in plants. <i>Plant Cell Reports</i> , 2021, 40, 1305-1329.	2.8	113
2594	Genetic Mapping by Sequencing More Precisely Detects Loci Responsible for Anaerobic Germination Tolerance in Rice. <i>Plants</i> , 2021, 10, 705.	1.6	7
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2597	Improving rice salt tolerance by precision breeding in a new era. <i>Current Opinion in Plant Biology</i> , 2021, 60, 101996.	3.5	61
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2602	Marker-Assisted Introgression and Stacking of Major QTLs Controlling Grain Number (Gn1a) and Number of Primary Branching (WFP) to NERICA Cultivars. <i>Plants</i> , 2021, 10, 844.	1.6	31
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2604	First set of microsatellite markers for immortal (Helichrysum italicum (Roth) G. Don): A step towards the selection of the most promising genotypes for cultivation. <i>Industrial Crops and Products</i> , 2021, 162, 113298.	2.5	12
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2606	Phospholipases C and D and Their Role in Biotic and Abiotic Stresses. <i>Plants</i> , 2021, 10, 921.	1.6	10
2607	Vigorous growth and high yielding of rice (<i>Oryza sativa</i>) introgression lines and transformants carrying a <i>PRR37</i> allele from wild rice <i>O. longistaminata</i> . <i>Plant Breeding</i> , 2021, 140, 409-418.	1.0	0
2608	Amplification dynamics of miniature inverted repeat transposable elements and their impact on rice trait variability. <i>Plant Journal</i> , 2021, 107, 118-135.	2.8	16
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2610	Knockdown of OsSAE1a affects acquisition and mobilization of nitrogen, and growth and development of rice. <i>Plant Growth Regulation</i> , 2021, 94, 221-231.	1.8	0
2611	Distribution of adenylyl cyclase/cAMP phosphodiesterase gene, CAPE, in streptophytes reproducing via motile sperm. <i>Scientific Reports</i> , 2021, 11, 10054.	1.6	5
2613	Elevated atmospheric CO ₂ concentration triggers redistribution of nitrogen to promote tillering in rice. <i>Plant-Environment Interactions</i> , 2021, 2, 125-136.	0.7	3
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2615	Advances in Cereal Crop Genomics for Resilience under Climate Change. <i>Life</i> , 2021, 11, 502.	1.1	26
2616	Identification and expression analysis of chloroplast ribonucleoproteins (cpRNPs) in Arabidopsis and rice. <i>Genome</i> , 2021, 64, 515-524.	0.9	4
2617	Genetic Variability through Induced Mutation. , 0, , .		1

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2620	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
2621	Skim sequencing: an advanced NGS technology for crop improvement. <i>Journal of Genetics</i> , 2021, 100, 1.	0.4	10
2622	Genome-Wide Identification and Evolutionary Analysis of Argonaute Genes in Hexaploid Bread Wheat. <i>BioMed Research International</i> , 2021, 2021, 1-9.	0.9	3
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2624	Combining QTL-seq and linkage mapping to fine map a candidate gene in <i>qCTS6</i> for cold tolerance at the seedling stage in rice. <i>BMC Plant Biology</i> , 2021, 21, 278.	1.6	18
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2626	<i>Oryza</i> pan-genomics: A new foundation for future rice research and improvement. <i>Crop Journal</i> , 2021, 9, 622-632.	2.3	7
2627	Apache Spark based kernelized fuzzy clustering framework for single nucleotide polymorphism sequence analysis. <i>Computational Biology and Chemistry</i> , 2021, 92, 107454.	1.1	21
2628	Spatio-Temporal Estimation of Biomass Growth in Rice Using Canopy Surface Model from Unmanned Aerial Vehicle Images. <i>Remote Sensing</i> , 2021, 13, 2388.	1.8	11
2629	Identification of genomic locations associated with grain micronutrients (iron and zinc) in rice (<i>Oryza sativa</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 221-230.	0.8	3
2630	Combined gene family characterization and RNA-Seq to study the response of $\hat{\Gamma}^2$ -ketoacyl-CoA synthase to abiotic stress in rice (<i>Oryza sativa</i> L.). <i>Plant Growth Regulation</i> , 2021, 95, 97-110.	1.8	1
2631	CHH Methylation Islands: A Nonconserved Feature of Grass Genomes That Is Positively Associated with Transposable Elements but Negatively Associated with Gene-Body Methylation. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	25
2632	«ñçnh hÆ°á»Ýng cá»Ša vÃ1ng sinh thÃj; Ä'áº;n tÃnh tráº;ng cháº;yt lÆ°á»Æng cá»Ša 20 giá'ng lÃªa ráº«y. <i>Tap Chi Khoa Hoc = Journal of Science</i> , 2021, 57, 147-156.	0.1	0
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2635	Recent advances and emerging trends in antiviral defense networking in rice. <i>Crop Journal</i> , 2021, 9, 553-563.	2.3	6
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2643	Unfolding molecular switches in plant heat stress resistance: A comprehensive review. <i>Plant Cell Reports</i> , 2022, 41, 775-798.	2.8	21
2644	RetroScan: An Easy-to-Use Pipeline for Retrocopy Annotation and Visualization. <i>Frontiers in Genetics</i> , 2021, 12, 719204.	1.1	4
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2646	Key Roles of De-Domestication and Novel Mutation in Origin and Diversification of Global Weedy Rice. <i>Biology</i> , 2021, 10, 828.	1.3	4
2647	Potential of rice landraces with strong culms as genetic resources for improving lodging resistance against super typhoons. <i>Scientific Reports</i> , 2021, 11, 15780.	1.6	7
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2649	Identification of four functional component content QTLs of brown rice in the Yunnan mini-core collection and its near-isogenic lines using association mapping. <i>Cereal Research Communications</i> , 2022, 50, 357-366.	0.8	2
2650	Genotypic Variation of Endophytic Nitrogen-Fixing Activity and Bacterial Flora in Rice Stem Based on Sugar Content. <i>Frontiers in Plant Science</i> , 2021, 12, 719259.	1.7	11
2651	Genome-Wide Association Mapping of Mixed Linkage (1,3;1,4)- β -D-Glucan and Starch Contents in Rice Whole Grain. <i>Frontiers in Plant Science</i> , 2021, 12, 665745.	1.7	6
2652	<i>Os</i> ZIP62/ <i>Os</i> FD7, a functional ortholog of FLOWERING LOCUS D, regulates floral transition and panicle development in rice. <i>Journal of Experimental Botany</i> , 2021, 72, 7826-7845.	2.4	11
2653	Recent progress on rice resistance to blast disease. <i>Scientia Sinica Vitae</i> , 2021, , .	0.1	0
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2659	The rice <i>EP3</i> and <i>OsFBK1</i> E3 ligases alter plant architecture and flower development, and affect transcript accumulation of microRNA pathway genes and their targets. <i>Plant Biotechnology Journal</i> , 2022, 20, 297-309.	4.1	5
2660	Papaya (<i>Carica papaya</i> L.) Flavour Profiling. <i>Genes</i> , 2021, 12, 1416.	1.0	13
2661	Utilization of Whole Genome Re-Sequencing for Large-InDel Markers Development in Malting Barley. <i>Han'guk Yukchong Hakhoe Chi</i> , 2021, 53, 266-276.	0.2	0
2662	K ϵ mer counting and curated libraries drive efficient annotation of repeats in plant genomes. <i>Plant Genome</i> , 2021, 14, e20143.	1.6	5
2664	Hyperspectral Image Classification Using Deep Genome Graph-Based Approach. <i>Sensors</i> , 2021, 21, 6467.	2.1	4
2665	Loss of Function of <i>OsFBX267</i> and <i>OsGA20ox2</i> in Rice Promotes Early Maturing and Semi-Dwarfism in β -Irradiated IWP and Genome-Edited Pusa Basmati-1. <i>Frontiers in Plant Science</i> , 2021, 12, 714066.	1.7	4
2666	Epigenetic remodeling by DNA glycosylases during rice reproduction. <i>Molecular Plant</i> , 2021, 14, 1433-1435.	3.9	0
2667	Development of Genome-Wide Functional Markers Using Draft Genome Assembly of Guava (<i>Psidium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 708332.	1.7	8
2669	Wild relatives of plants as sources for the development of abiotic stress tolerance in plants. , 2022, , 471-518.		13
2670	Genomics-based approaches to improve abiotic stress tolerance in plants: Present status and future prospects. , 2022, , 195-219.		0
2671	Cr-Prom: A Convolutional Neural Network-Based Model for the Prediction of Rice Promoters. <i>IEEE Access</i> , 2021, 9, 81485-81491.	2.6	15
2672	Genetic mapping in crop plants. <i>Open Journal of Plant Science</i> , 0, , 019-026.	0.2	2
2673	Building pan-genome infrastructures for crop plants and their use in association genetics. <i>DNA Research</i> , 2021, 28, .	1.5	57
2674	Bioinformatics Approaches for High-Density Linkage Mapping in Rice Research. , 2021, , 29-54.		0
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2677	Diversity analysis of the rice cultivars (<i>Oryza sativa</i> L.) by utilizing SSRs rice diversity by SSRs. Journal of Food Processing and Preservation, 2021, 45, e15232.	0.9	0
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