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**The B73 maize genome: complexity, diversity, and dynamics**

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#	Paper	IF	Citations
2288	The physical and genetic framework of the maize B73 genome. <b>2009</b> , 5, e1000715		83
2287	A genome-wide characterization of microRNA genes in maize. <b>2009</b> , 5, e1000716		265
2286	Detailed analysis of a contiguous 22-Mb region of the maize genome. <b>2009</b> , 5, e1000728		34
2285	Exceptional diversity, non-random distribution, and rapid evolution of retroelements in the B73 maize genome. <b>2009</b> , 5, e1000732		266
2284	Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. <b>2009</b> , 5, e1000734		389
2283	Loss of RNA-dependent RNA polymerase 2 (RDR2) function causes widespread and unexpected changes in the expression of transposons, genes, and 24-nt small RNAs. <b>2009</b> , 5, e1000737		92
2282	Sequencing, mapping, and analysis of 27,455 maize full-length cDNAs. <b>2009</b> , 5, e1000740		124
2281	Genetic resources for maize cell wall biology. <b>2009</b> , 151, 1703-28		117
2280	Distribution, diversity, evolution, and survival of Helitrons in the maize genome. <b>2009</b> , 106, 19922-7		122
2279	A cornucopia of Helitrons shapes the maize genome. <b>2009</b> , 106, 19747-8		22
2278	Plant science. Solving the maze. <i>Science</i> , <b>2009</b> , 326, 1071-2	33.3	15
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2273	Ancestral grass karyotype reconstruction unravels new mechanisms of genome shuffling as a source of plant evolution. <b>2010</b> , 20, 1545-57		136
2272	Distributed simple sequence repeat markers for efficient mapping from maize public mutagenesis populations. <b>2010</b> , 121, 697-704		6

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2087	Survey of genomics approaches to improve bioenergy traits in maize, sorghum and sugarcane. <b>2011</b> , 53, 105-19	68
2086	The genome of <i>Theobroma cacao</i> . <b>2011</b> , 43, 101-8	502
2085	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <b>2011</b> , 43, 109-16	881
2084	Genome-wide association study of leaf architecture in the maize nested association mapping population. <b>2011</b> , 43, 159-62	746
2083	Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. <b>2011</b> , 43, 163-8	444
2082	Dynamic interactions between transposable elements and their hosts. <b>2011</b> , 12, 615-27	405
2081	Making the most of 'omics' for crop breeding. <b>2011</b> , 29, 33-40	166
2080	DNA sequencing methods contributing to new directions in cereal research. <b>2011</b> , 54, 395-400	17
2079	Transposable element origins of epigenetic gene regulation. <b>2011</b> , 14, 156-61	114
2078	Epigenetic aspects of centromere function in plants. <b>2011</b> , 14, 217-22	30
2077	Transposable elements and plant genome evolution. <b>2011</b> , 1, 565-576	4
2076	Structural characterization of helitrons and their stepwise capturing of gene fragments in the maize genome. <b>2011</b> , 12, 609	11
2075	Comprehensive analysis of tandem amino acid repeats from ten angiosperm genomes. <b>2011</b> , 12, 632	10
2074	Landscape of next-generation sequencing technologies. <b>2011</b> , 83, 4327-41	253

2073	A widespread occurrence of extra open reading frames in plant Ty3/gypsy retrotransposons. <b>2011</b> , 139, 1543-55	19
2072	Adaptive evolution of Xa21 homologs in Gramineae. <b>2011</b> , 139, 1465-75	10
2071	The age of protein kinases. <b>2011</b> , 779, 7-52	38
2070	Mapping resistance gene analogs (RGAs) in cultivated tetraploid cotton using RGA-AFLP analysis. <b>2011</b> , 181, 65-76	13
2069	Molecular characterization of a genomic interval with highly uneven recombination distribution on maize chromosome 10 L. <b>2011</b> , 139, 1109-18	3
2068	Dynamics of Vulmar/VulMITE group of transposable elements in Chenopodiaceae subfamily Betoideae. <b>2011</b> , 139, 1209-16	4
2067	Detection of genetic integrity of conserved maize ( <i>Zea mays</i> L.) germplasm in genebanks using SNP markers. <b>2011</b> , 58, 189-207	17
2066	Genome-wide analysis of the auxin response factor (ARF) gene family in maize ( <i>Zea mays</i> ). <b>2011</b> , 63, 225-234	59
2065	Overexpression of a maize dehydrin gene, ZmDHN2b, in tobacco enhances tolerance to low temperature. <b>2011</b> , 65, 109-118	46
2064	Co-evolution between transposable elements and their hosts: a major factor in genome size evolution?. <b>2011</b> , 19, 777-86	60
2063	Bioinformatics and genomic analysis of transposable elements in eukaryotic genomes. <b>2011</b> , 19, 787-808	40
2062	Exploring giant plant genomes with next-generation sequencing technology. <b>2011</b> , 19, 939-53	45
2061	Phenotypic and gene expression analyses of a ploidy series of maize inbred Oh43. <b>2011</b> , 75, 237-51	46
2060	Evolutionary history of the GH3 family of acyl adenylases in rosids. <b>2011</b> , 76, 489-505	51
2059	Genome-wide analysis of the beta-glucosidase gene family in maize ( <i>Zea mays</i> L. var B73). <b>2011</b> , 77, 159-83	36
2058	Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize. <b>2011</b> , 28, 511-526	217
2057	Genome-wide analysis of BURP domain-containing genes in maize and sorghum. <b>2011</b> , 38, 4553-63	19
2056	Whole-genome survey and characterization of MADS-box gene family in maize and sorghum. <b>2011</b> , 105, 159-173	61

2055	Variation in crossover rates across a 3-Mb contig of bread wheat ( <i>Triticum aestivum</i> ) reveals the presence of a meiotic recombination hotspot. <b>2011</b> , 120, 185-98	44
2054	Identification and characterization of Dicer-like, Argonaute and RNA-dependent RNA polymerase gene families in maize. <b>2011</b> , 30, 1347-63	83
2053	Genome-based prediction of testcross values in maize. <b>2011</b> , 123, 339-50	206
2052	Temporal dynamics in the evolution of the sunflower genome as revealed by sequencing and annotation of three large genomic regions. <b>2011</b> , 123, 779-91	26
2051	QTL for fibre-related traits in grain $\beta$ -glucan in sweet sorghum as a tool for the enhancement of sorghum as a biomass crop. <b>2011</b> , 123, 999-1011	36
2050	Developmental and cell type characterization of bundle sheath and mesophyll chloroplast transcript abundance in maize. <b>2011</b> , 57, 89-102	17
2049	Distinguishing authentic mitochondrial and plastid DNAs from similar DNA sequences in the nucleus using the polymerase chain reaction. <b>2011</b> , 57, 287-95	13
2048	Co-variation among major classes of LRR-encoding genes in two pairs of plant species. <b>2011</b> , 72, 498-509	15
2047	Manipulation of cellular syntheses and the nature of viruses: The virocell concept. <b>2011</b> , 14, 392-399	58
2046	Development of microdissection and chromosome specific genomic library in <i>Lilium tigrinum</i> . <b>2011</b> , 33, 451-455	2
2045	DNA sequencing leads to genomics progress in China. <b>2011</b> , 54, 290-2	8
2044	An introduction to the medicinal plant genome project. <b>2011</b> , 5, 178-84	16
2043	From RNA-seq to large-scale genotyping - genomics resources for rye ( <i>Secale cereale</i> L.). <b>2011</b> , 11, 131	86
2042	Identification of novel maize miRNAs by measuring the precision of precursor processing. <b>2011</b> , 11, 141	37
2041	A highly conserved NB-LRR encoding gene cluster effective against <i>Setosphaeria turcica</i> in sorghum. <b>2011</b> , 11, 151	28
2040	Genetic dissection of maize phenology using an intraspecific introgression library. <b>2011</b> , 11, 4	49
2039	Maize microarray annotation database. <b>2011</b> , 7, 31	9
2038	A pair of new BAC and BIBAC vectors that facilitate BAC/BIBAC library construction and intact large genomic DNA insert exchange. <b>2011</b> , 7, 33	27

2037	Distinct influences of tandem repeats and retrotransposons on CENH3 nucleosome positioning. <b>2011</b> , 4, 3	26
2036	Genome-wide patterns of genetic variation in sweet and grain sorghum ( <i>Sorghum bicolor</i> ). <b>2011</b> , 12, R114	194
2035	A survey of green plant tRNA 3'-end processing enzyme tRNase Zs, homologs of the candidate prostate cancer susceptibility protein ELAC2. <b>2011</b> , 11, 219	13
2034	Back to the sea twice: identifying candidate plant genes for molecular evolution to marine life. <b>2011</b> , 11, 8	61
2033	Genome-wide identification and expression profiling of auxin response factor (ARF) gene family in maize. <b>2011</b> , 12, 178	123
2032	Assessing pooled BAC and whole genome shotgun strategies for assembly of complex genomes. <b>2011</b> , 12, 194	11
2031	Physical mapping and BAC-end sequence analysis provide initial insights into the flax ( <i>Linum usitatissimum</i> L.) genome. <b>2011</b> , 12, 217	57
2030	BAC library resources for map-based cloning and physical map construction in barley ( <i>Hordeum vulgare</i> L.). <b>2011</b> , 12, 247	45
2029	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. <b>2011</b> , 12, 252	47
2028	Sequencing of a QTL-rich region of the <i>Theobroma cacao</i> genome using pooled BACs and the identification of trait specific candidate genes. <b>2011</b> , 12, 379	12
2027	A genetically anchored physical framework for <i>Theobroma cacao</i> cv. Matina 1-6. <b>2011</b> , 12, 413	11
2026	A comparative physical map reveals the pattern of chromosomal evolution between the turkey ( <i>Meleagris gallopavo</i> ) and chicken ( <i>Gallus gallus</i> ) genomes. <b>2011</b> , 12, 447	20
2025	The complete Ac/Ds transposon family of maize. <b>2011</b> , 12, 588	19
2024	Genome-wide identification, classification and analysis of heat shock transcription factor family in maize. <b>2011</b> , 12, 76	136
2023	Proteomic analysis of heterosis during maize seed germination. <b>2011</b> , 11, 1462-72	49
2022	Time to articulate a vision for the future of plant proteomics - A global perspective: An initiative for establishing the International Plant Proteomics Organization (INPPO). <b>2011</b> , 11, 1559-68	24
2021	Rice proteomics: A move toward expanded proteome coverage to comparative and functional proteomics uncovers the mysteries of rice and plant biology. <b>2011</b> , 11, 1630-49	82
2020	<i>Arabidopsis</i> paves the way: genomic and network analyses in crops. <b>2011</b> , 22, 260-70	43



2019	Improvement of resistance to maize dwarf mosaic virus mediated by transgenic RNA interference. <b>2011</b> , 153, 181-7	31
2018	Development and utilisation of conserved-intron scanning marker in sugarcane. <b>2011</b> , 59, 38	12
2017	Genetic dissection of the biotic stress response using a genome-scale gene network for rice. <b>2011</b> , 108, 18548-53	132
2016	Expression of fungal diacylglycerol acyltransferase2 genes to increase kernel oil in maize. <b>2011</b> , 155, 1146-57	44
2015	A 3,000-loci transcription map of chromosome 3B unravels the structural and functional features of gene islands in hexaploid wheat. <b>2011</b> , 157, 1596-608	45
2014	Duplicate maize Wrinkled1 transcription factors activate target genes involved in seed oil biosynthesis. <b>2011</b> , 156, 674-86	123
2013	Comprehensive sequence analysis of 24,783 barley full-length cDNAs derived from 12 clone libraries. <b>2011</b> , 156, 20-8	165
2012	GreenPhylDB v2.0: comparative and functional genomics in plants. <b>2011</b> , 39, D1095-102	95
2011	Selection patterns on restorer-like genes reveal a conflict between nuclear and mitochondrial genomes throughout angiosperm evolution. <b>2011</b> , 108, 1723-8	190
2010	Critical assessment of assembly strategies for non-model species mRNA-Seq data and application of next-generation sequencing to the comparison of C(3) and C(4) species. <b>2011</b> , 62, 3093-102	71
2009	MaizeGDB: curation and outreach go hand-in-hand. <b>2011</b> , 2011, bar022	59
2008	A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. <b>2011</b> , 6, e19379	3791
2007	B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. <b>2011</b> , 156, 1679-90	57
2006	QTL Mapping and Candidate Gene Analysis of Telomere Length Control Factors in Maize ( <i>Zea mays</i> L.). <b>2011</b> , 1, 437-50	7
2005	Phosphate deprivation in maize: genetics and genomics. <b>2011</b> , 156, 1067-77	59
2004	In silico analysis of transcription factor repertoires and prediction of stress-responsive transcription factors from six major gramineae plants. <b>2011</b> , 18, 321-32	38
2003	The maize high-lysine mutant opaque7 is defective in an acyl-CoA synthetase-like protein. <b>2011</b> , 189, 1271-80	31
2002	Improving Nitrogen Use Efficiency in Crops for Sustainable Agriculture. <b>2011</b> , 3, 1452-1485	252

2001	The activator/dissociation transposable elements comprise a two-component gene regulatory switch that controls endogenous gene expression in maize. <b>2011</b> , 187, 749-59	4
2000	Using maize as a model to study pollen tube growth and guidance, cross-incompatibility and sperm delivery in grasses. <b>2011</b> , 108, 727-37	53
1999	Prolyl 4-hydroxylase genes are subjected to alternative splicing in roots of maize seedlings under waterlogging. <b>2011</b> , 108, 1323-35	10
1998	Seventy million years of concerted evolution of a homoeologous chromosome pair, in parallel, in major Poaceae lineages. <b>2011</b> , 23, 27-37	60
1997	<i>Setaria viridis</i> and <i>Setaria italica</i> , model genetic systems for the Panicoid grasses. <b>2011</b> , 62, 3031-7	210
1996	Extensive, clustered parental imprinting of protein-coding and noncoding RNAs in developing maize endosperm. <b>2011</b> , 108, 20042-7	134
1995	Genome-wide association study identifies candidate genes that affect plant height in Chinese elite maize ( <i>Zea mays</i> L.) inbred lines. <b>2011</b> , 6, e29229	78
1994	Strategies for silencing and escape: the ancient struggle between transposable elements and their hosts. <b>2011</b> , 292, 119-52	35
1993	Identification of genes involved in cell wall biogenesis in grasses by differential gene expression profiling of elongating and non-elongating maize internodes. <b>2011</b> , 62, 3545-61	94
1992	The composition and origins of genomic variation among individuals of the soybean reference cultivar Williams 82. <b>2011</b> , 155, 645-55	111
1991	Conserved and divergent rhythms of crassulacean acid metabolism-related and core clock gene expression in the cactus <i>Opuntia ficus-indica</i> . <b>2011</b> , 156, 1978-89	33
1990	Genome-wide characterization of the HD-ZIP IV transcription factor family in maize: preferential expression in the epidermis. <b>2011</b> , 157, 790-803	67
1989	Strategies for engineering a two-celled C(4) photosynthetic pathway into rice. <b>2011</b> , 62, 3001-10	125
1988	SyMAP v3.4: a turnkey synteny system with application to plant genomes. <b>2011</b> , 39, e68	223
1987	Genome rearrangements in maize induced by alternative transposition of reversed ac/ds termini. <b>2011</b> , 188, 59-67	39
1986	Application and comparison of large-scale solution-based DNA capture-enrichment methods on ancient DNA. <b>2011</b> , 1, 74	87
1985	Pack-Mutator-like transposable elements (Pack-MULEs) induce directional modification of genes through biased insertion and DNA acquisition. <b>2011</b> , 108, 1537-42	65
1984	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. <b>2011</b> , 108, 4069-74	462

1983	The ZmASR1 protein influences branched-chain amino acid biosynthesis and maintains kernel yield in maize under water-limited conditions. <b>2011</b> , 157, 917-36	86
1982	Progress towards a reference genome for sunflower. <b>2011</b> , 89, 429-437	62
1981	Next generation sequencing reveals genome downsizing in allotetraploid <i>Nicotiana tabacum</i> , predominantly through the elimination of paternally derived repetitive DNAs. <b>2011</b> , 28, 2843-54	125
1980	BARREN STALK FASTIGIATE1 is an AT-hook protein required for the formation of maize ears. <b>2011</b> , 23, 1756-71	55
1979	Nuclear DNA amounts in angiosperms: targets, trends and tomorrow. <b>2011</b> , 107, 467-590	220
1978	Copy number variation analysis in the great apes reveals species-specific patterns of structural variation. <b>2011</b> , 21, 1626-39	62
1977	High time for a roll call: gene duplication and phylogenetic relationships of TCP-like genes in monocots. <b>2011</b> , 107, 1533-44	31
1976	Molecular Characterization of a Diverse Maize Inbred Line Collection and its Potential Utilization for Stress Tolerance Improvement. <b>2011</b> , 51, 2569-2581	43
1975	Short- and long-term evolutionary dynamics of bacterial insertion sequences: insights from <i>Wolbachia</i> endosymbionts. <b>2011</b> , 3, 1175-86	45
1974	Construction, characterization, and preliminary BAC-end sequence analysis of a bacterial artificial chromosome library of the tea plant ( <i>Camellia sinensis</i> ). <b>2011</b> , 2011, 476723	9
1973	POPcorn: An Online Resource Providing Access to Distributed and Diverse Maize Project Data. <b>2011</b> , 2011, 923035	17
1972	Identification of an active new mutator transposable element in maize. <b>2011</b> , 1, 293-302	33
1971	Allelic Effect Variation at Key Photoperiod Response Quantitative Trait Loci in Maize. <b>2011</b> , 51, 1036-1049	16
1970	A proposed selection criterion for drought resistance across multiple environments in maize. <b>2011</b> , 61, 101-108	25
1969	Endosperm development in <i>Brachypodium distachyon</i> . <b>2011</b> , 62, 735-48	59
1968	Update on chloroplast research: new tools, new topics, and new trends. <b>2011</b> , 4, 1-16	37
1967	Contrasting evolutionary patterns of the Rp1 resistance gene family in different species of Poaceae. <b>2011</b> , 28, 313-25	23
1966	Evolutionary divergence and limits of conserved non-coding sequence detection in plant genomes. <b>2011</b> , 39, 6029-43	30

1965	A public platform for the verification of the phenotypic effect of candidate genes for resistance to aflatoxin accumulation and <i>Aspergillus flavus</i> infection in maize. <b>2011</b> , 3, 754-65	14
1964	Comparative Genomics in Perennial Ryegrass ( <i>Lolium perenne</i> L.): Identification and Characterisation of an Orthologue for the Rice Plant Architecture-Controlling Gene <i>OsABCG5</i> . <b>2011</b> , 2011, 291563	5
1963	Chromosome visualization tool: a whole genome viewer. <b>2011</b> , 2011, 373875	29
1962	The selection and use of sorghum ( <i>Sorghum propinquum</i> ) bacterial artificial chromosomes as cytogenetic FISH probes for maize ( <i>Zea mays</i> L.). <b>2011</b> , 2011, 386862	2
1961	A white spruce gene catalog for conifer genome analyses. <b>2011</b> , 157, 14-28	128
1960	Gramene database in 2010: updates and extensions. <b>2011</b> , 39, D1085-94	145
1959	SplamiR–prediction of spliced miRNAs in plants. <b>2011</b> , 27, 1215-23	13
1958	Heritable epigenetic variation among maize inbreds. <b>2011</b> , 7, e1002372	118
1957	Gene coexpression network alignment and conservation of gene modules between two grass species: maize and rice. <b>2011</b> , 156, 1244-56	106
1956	The MaizeGDB Genome Browser tutorial: one example of database outreach to biologists via video. <b>2011</b> , 2011, bar016	14
1955	Escape from preferential retention following repeated whole genome duplications in plants. <b>2012</b> , 3, 94	52
1954	Evolution and expression of tandem duplicated maize flavonol synthase genes. <b>2012</b> , 3, 101	28
1953	Discolored1 (DSC1) is an ADP-Ribosylation Factor-GTPase Activating Protein Required to Maintain Differentiation of Maize Kernel Structures. <b>2012</b> , 3, 115	8
1952	Co-expression and co-responses: within and beyond transcription. <b>2012</b> , 3, 248	24
1951	OrySPSSP: a comparative platform for small secreted proteins from rice and other plants. <b>2013</b> , 41, D1192-8	12
1950	The Biofuel Feedstock Genomics Resource: a web-based portal and database to enable functional genomics of plant biofuel feedstock species. <b>2012</b> , 2012, bar061	13
1949	Spreading of heterochromatin is limited to specific families of maize retrotransposons. <b>2012</b> , 8, e1003127	124
1948	Rampant horizontal transfer of SPIN transposons in squamate reptiles. <b>2012</b> , 29, 503-15	48

1947	Toward a comprehensive phylogenetic reconstruction of the evolutionary history of mitogen-activated protein kinases in the plant kingdom. <b>2012</b> , 3, 271	26
1946	A gene family derived from transposable elements during early angiosperm evolution has reproductive fitness benefits in <i>Arabidopsis thaliana</i> . <b>2012</b> , 8, e1002931	42
1945	Reshaping of the maize transcriptome by domestication. <b>2012</b> , 109, 11878-83	113
1944	Is behavioral genetics 'too-big-to-know' science?. <b>2012</b> , 35, 360	4
1943	Disruption of a rice pentatricopeptide repeat protein causes a seedling-specific albino phenotype and its utilization to enhance seed purity in hybrid rice production. <b>2012</b> , 159, 227-38	108
1942	Strong epigenetic similarity between maize centromeric and pericentromeric regions at the level of small RNAs, DNA methylation and H3 chromatin modifications. <b>2012</b> , 40, 1550-60	38
1941	Editor's choice: Crop genome plasticity and its relevance to food and feed safety of genetically engineered breeding stacks. <b>2012</b> , 160, 1842-53	58
1940	Dissecting plant genomes with the PLAZA comparative genomics platform. <b>2012</b> , 158, 590-600	212
1939	Comparative analysis of syntenic genes in grass genomes reveals accelerated rates of gene structure and coding sequence evolution in polyploid wheat. <b>2013</b> , 161, 252-65	87
1938	The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. <b>2012</b> , 108, 490-9	96
1937	Identification of positive selection in disease response genes within members of the Poaceae. <b>2012</b> , 7, 1667-75	6
1936	Grass microRNA gene paleohistory unveils new insights into gene dosage balance in subgenome partitioning after whole-genome duplication. <b>2012</b> , 24, 1776-92	42
1935	Maize source leaf adaptation to nitrogen deficiency affects not only nitrogen and carbon metabolism but also control of phosphate homeostasis. <b>2012</b> , 160, 1384-406	116
1934	Statistical significance of optical map alignments. <b>2012</b> , 19, 478-92	15
1933	Next-generation sequencing applications for wheat crop improvement. <b>2012</b> , 99, 365-71	80
1932	Complementation contributes to transcriptome complexity in maize ( <i>Zea mays</i> L.) hybrids relative to their inbred parents. <b>2012</b> , 22, 2445-54	97
1931	Flowering time in maize: linkage and epistasis at a major effect locus. <b>2012</b> , 190, 1547-62	42
1930	The role of PIN auxin efflux carriers in polar auxin transport and accumulation and their effect on shaping maize development. <b>2012</b> , 5, 787-98	48

1929	Repeat associated small RNAs vary among parents and following hybridization in maize. <b>2012</b> , 109, 10444-9	104
1928	Next-generation sequencing reveals the impact of repetitive DNA across phylogenetically closely related genomes of Orobanchaceae. <b>2012</b> , 29, 3601-11	66
1927	Phytozome: a comparative platform for green plant genomics. <b>2012</b> , 40, D1178-86	2713
1926	Genome-wide characterization of nonreference transposons reveals evolutionary propensities of transposons in soybean. <b>2012</b> , 24, 4422-36	42
1925	A genome-wide regulatory framework identifies maize pericarp color1 controlled genes. <b>2012</b> , 24, 2745-64	120
1924	Fine-scale population recombination rates, hotspots, and correlates of recombination in the <i>Medicago truncatula</i> genome. <b>2012</b> , 4, 726-37	56
1923	Megabase-scale inversion polymorphism in the wild ancestor of maize. <b>2012</b> , 191, 883-94	68
1922	Genic and nongenic contributions to natural variation of quantitative traits in maize. <b>2012</b> , 22, 2436-44	96
1921	Selective regulation of maize plasma membrane aquaporin trafficking and activity by the SNARE SYP121. <b>2012</b> , 24, 3463-81	95
1920	Candidate Genes and Political Behavior. <b>2012</b> , 106, 1-34	152
1919	Dynamics and adaptive benefits of protein domain emergence and arrangements during plant genome evolution. <b>2012</b> , 4, 316-29	50
1918	Dynamic gene copy number variation in collinear regions of grass genomes. <b>2012</b> , 29, 861-71	21
1917	Decoding plant and animal genome plasticity from differential paleo-evolutionary patterns and processes. <b>2012</b> , 4, 917-28	46
1916	Genome-wide analysis of syntenic gene deletion in the grasses. <b>2012</b> , 4, 265-77	111
1915	Gene capture by Helitron transposons reshuffles the transcriptome of maize. <b>2012</b> , 190, 965-75	43
1914	Mutator-like elements with multiple long terminal inverted repeats in plants. <b>2012</b> , 2012, 695827	8
1913	Author's response: Humans, fruit flies, and automatons. <b>2012</b> , 35, 381-410	7
1912	Fine mapping and candidate gene prediction of a pleiotropic quantitative trait locus for yield-related trait in <i>Zea mays</i> . <b>2012</b> , 7, e49836	29

1911	From gene activity to behavior (and back again). <b>2012</b> , 35, 369-70	1
1910	Genome-wide analysis of bZIP-encoding genes in maize. <b>2012</b> , 19, 463-76	169
1909	Tackling drought stress: receptor-like kinases present new approaches. <b>2012</b> , 24, 2262-78	118
1908	PPR8522 encodes a chloroplast-targeted pentatricopeptide repeat protein necessary for maize embryogenesis and vegetative development. <b>2012</b> , 63, 5843-57	42
1907	Dynamic nucleotide-binding site and leucine-rich repeat-encoding genes in the grass family. <b>2012</b> , 159, 197-210	79
1906	A comprehensive dataset of genes with a loss-of-function mutant phenotype in Arabidopsis. <b>2012</b> , 158, 1115-29	117
1905	Transcriptional and metabolic analysis of senescence induced by preventing pollination in maize. <b>2012</b> , 159, 1730-44	60
1904	Reliable transient transformation of intact maize leaf cells for functional genomics and experimental study. <b>2012</b> , 159, 1309-18	19
1903	Ontogeny of the maize shoot apical meristem. <b>2012</b> , 24, 3219-34	60
1902	Foodomics: A New Omics for a New Food Era. <b>2012</b> , 94-115	
1901	Cytogenetic characterization and genome size of the medicinal plant <i>Catharanthus roseus</i> (L.) G. Don. <b>2012</b> , 2012, pls002	14
1900	Application of genomic tools in plant breeding. <b>2012</b> , 13, 179-95	175
1899	Lebensmittelchemie 2011. <b>2012</b> , 60, 346-351	
1898	Genotyping-by-Sequencing in Plants. <b>2012</b> , 1, 460-83	208
1897	McClintock's challenge in the 21st century. <b>2012</b> , 109, 20200-3	15
1896	Why size really matters when sequencing plant genomes. <b>2012</b> , 5, 415-425	24
1895	Molecular Biology of Lignification in Grasses. <b>2012</b> , 77-112	7
1894	Active transposition in genomes. <b>2012</b> , 46, 651-75	263

1893	Roadmap for annotating transposable elements in eukaryote genomes. <b>2012</b> , 859, 53-68	12
1892	Teosinte as a model system for population and ecological genomics. <b>2012</b> , 28, 606-15	50
1891	Changes in genome content generated via segregation of non-allelic homologs. <b>2012</b> , 72, 390-9	21
1890	Centromere retention and loss during the descent of maize from a tetraploid ancestor. <b>2012</b> , 109, 21004-9	29
1889	Gene duplication within the Green Lineage: the case of TEL genes. <b>2012</b> , 63, 5061-77	28
1888	Presidential address. Transposable elements, epigenetics, and genome evolution. <i>Science</i> , <b>2012</b> , 338, 758-67	33.3 365
1887	Virus-induced gene complementation reveals a transcription factor network in modulation of tomato fruit ripening. <b>2012</b> , 2, 836	27
1886	Current challenges in de novo plant genome sequencing and assembly. <b>2012</b> , 13, 243	131
1885	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <b>2012</b> , 491, 705-10	821
1884	Genetic and physical fine mapping of the novel brown midrib gene bm6 in maize ( <i>Zea mays</i> L.) to a 180 kb region on chromosome 2. <b>2012</b> , 125, 1223-35	15
1883	A transposable element insertion within ZmGE2 gene is associated with increase in embryo to endosperm ratio in maize. <b>2012</b> , 125, 1463-71	26
1882	Integrating cereal genomics to support innovation in the Triticeae. <b>2012</b> , 12, 573-83	35
1881	An integrated cytogenetic and physical map reveals unevenly distributed recombination spots along the papaya sex chromosomes. <b>2012</b> , 20, 753-67	19
1880	Deletion commonly found in Waxy gene of Japanese and Korean cultivars of Job's tears ( <i>Coix lacryma-jobi</i> L.). <b>2012</b> , 30, 1747-1756	7
1879	Assessment of possible allergenicity of hypothetical ORFs in common food crops using current bioinformatic guidelines and its implications for the safety assessment of GM crops. <b>2012</b> , 50, 3741-51	6
1878	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. <b>2012</b> , 44, 217-20	424
1877	Contrasting patterns of evolution following whole genome versus tandem duplication events in <i>Populus</i> . <b>2012</b> , 22, 95-105	100
1876	Pod corn is caused by rearrangement at the Tunicate1 locus. <b>2012</b> , 24, 2733-44	41



1875	Molecular phylogenetic and expression analysis of the complete WRKY transcription factor family in maize. <b>2012</b> , 19, 153-64	174
1874	Brachypodium distachyon promoters as efficient building blocks for transgenic research in maize. <b>2012</b> , 63, 4263-73	45
1873	A physical, genetic and functional sequence assembly of the barley genome. <b>2012</b> , 491, 711-6	1124
1872	Chromosome organization and dynamics during interphase, mitosis, and meiosis in plants. <b>2012</b> , 158, 26-34	76
1871	Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. <b>2012</b> , 158, 824-34	242
1870	A crop of maize variants. <b>2012</b> , 44, 734-5	9
1869	Modifying crops to increase cell wall digestibility. <b>2012</b> , 185-186, 65-77	95
1868	Grass phenylpropanoids: regulate before using!. <b>2012</b> , 184, 112-20	48
1867	Linking microarray data to QTLs highlights new genes related to AI tolerance in maize. <b>2012</b> , 191-192, 8-15	6
1866	Are we ready for genome-scale modeling in plants?. <b>2012</b> , 191-192, 53-70	49
1865	Epigenetic and epigenomic variation in Arabidopsis thaliana. <b>2012</b> , 17, 149-54	76
1864	Epigenetic neofunctionalisation and regulatory gene evolution in grasses. <b>2012</b> , 17, 389-94	11
1863	Transposable elements: an abundant and natural source of regulatory sequences for host genes. <b>2012</b> , 46, 21-42	354
1862	Evolution of genome content: population dynamics of transposable elements in flies and humans. <b>2012</b> , 855, 361-83	32
1861	Can genetic variability for nitrogen metabolism in the developing ear of maize be exploited to improve yield?. <b>2012</b> , 194, 440-452	20
1860	Using next-generation sequencing approaches to isolate simple sequence repeat (SSR) loci in the plant sciences. <b>2012</b> , 99, 193-208	331
1859	Dicentric chromosome formation and epigenetics of centromere formation in plants. <b>2012</b> , 39, 125-30	22
1858	Mass spectrometry for nutritional peptidomics: How to analyze food bioactives and their health effects. <b>2012</b> , 75, 3546-59	111

1857	Translational plant proteomics: a perspective. <b>2012</b> , 75, 4588-601	56
1856	Interactions between <i>Fusarium verticillioides</i> , <i>Ustilago maydis</i> , and <i>Zea mays</i> : an endophyte, a pathogen, and their shared plant host. <b>2012</b> , 49, 578-87	56
1855	The soybean aldehyde dehydrogenase (ALDH) protein superfamily. <b>2012</b> , 495, 128-33	27
1854	Genome-wide analysis and environmental response profiling of the FK506-binding protein gene family in maize ( <i>Zea mays</i> L.). <b>2012</b> , 498, 212-22	23
1853	An efficient RNA interference screening strategy for gene functional analysis. <b>2012</b> , 13, 491	14
1852	The tomato genome: implications for plant breeding, genomics and evolution. <b>2012</b> , 13, 167	34
1851	FISH using a gag-like fragment probe reveals a common Ty3-gypsy-like retrotransposon in genome of <i>Coffea</i> species. <b>2012</b> , 55, 825-33	8
1850	Paramutation: a trans-homolog interaction affecting heritable gene regulation. <b>2012</b> , 15, 536-43	49
1849	MASIVEdb: the Sirevirus Plant Retrotransposon Database. <b>2012</b> , 13, 158	17
1848	The polyphenol oxidase gene family in land plants: Lineage-specific duplication and expansion. <b>2012</b> , 13, 395	119
1847	Whole Genome Profiling provides a robust framework for physical mapping and sequencing in the highly complex and repetitive wheat genome. <b>2012</b> , 13, 47	20
1846	Identification, characterization and distribution of transposable elements in the flax ( <i>Linum usitatissimum</i> L.) genome. <b>2012</b> , 13, 644	25
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1844	The SLEEPER genes: a transposase-derived angiosperm-specific gene family. <b>2012</b> , 12, 192	27
1843	The plant short-chain dehydrogenase (SDR) superfamily: genome-wide inventory and diversification patterns. <b>2012</b> , 12, 219	64
1842	A spruce gene map infers ancient plant genome reshuffling and subsequent slow evolution in the gymnosperm lineage leading to extant conifers. <b>2012</b> , 10, 84	77
1841	Bioenergy grass feedstock: current options and prospects for trait improvement using emerging genetic, genomic, and systems biology toolkits. <b>2012</b> , 5, 80	42
1840	Noise or Symphony: Comparative Evolutionary Analysis of Sugarcane Transposable Elements with Other Grasses. <b>2012</b> , 169-192	3

1839	DNA methylation in plants: relationship to small RNAs and histone modifications, and functions in transposon inactivation. <b>2012</b> , 53, 766-84	142
1838	Behavior genetics and postgenomics. <b>2012</b> , 35, 331-58	145
1837	Diversity in global maize germplasm: characterization and utilization. <b>2012</b> , 37, 843-55	90
1836	The draft genome of a diploid cotton <i>Gossypium raimondii</i> . <b>2012</b> , 44, 1098-103	673
1835	The repetitive DNA content of eukaryotic genomes. <b>2012</b> , 7, 1-28	125
1834	The evolutionary dynamics of transposable elements in eukaryote genomes. <b>2012</b> , 7, 68-91	32
1833	Identification of drought-responsive genes by cDNA-amplified fragment length polymorphism in maize. <b>2012</b> , 161, 203-213	2
1832	The Parasitic Plant Genome Project: New Tools for Understanding the Biology of Orobanche and Striga. <b>2012</b> , 60, 295-306	76
1831	Next-generation sequencing as a tool for plant ecology and evolution. <b>2012</b> , 5, 411-413	5
1830	The absence of heat shock protein HSP101 affects the proteome of mature and germinating maize embryos. <b>2012</b> , 11, 3246-58	7
1829	Phytotoxicity, accumulation and transport of silver nanoparticles by <i>Arabidopsis thaliana</i> . <b>2013</b> , 7, 323-37	204
1828	Translational Root Genomics for Crop Improvement. <b>2012</b> , 249-264	1
1827	Molecular Markers in Plant Improvement. <b>2012</b> , 67-80	
1826	Genetic Variant Discovery and Its Use in Genome Characterization of Agronomically Important Crop Species. <b>2012</b> , 137-167	0
1825	Advances in identifying and exploiting natural genetic variation. <b>2012</b> , 195-205	
1824	From epigenetics to epigenomics and their implications in plant breeding. <b>2012</b> , 207-226	3
1823	Draft genome sequence of pigeonpea ( <i>Cajanus cajan</i> ), an orphan legume crop of resource-poor farmers. <b>2011</b> , 30, 83-9	587
1822	Comparative Evolutionary Genomics of Land Plants. <b>2012</b> , 227-275	2

1821	So Many Repeats and So Little Time: How to Classify Transposable Elements. <b>2012</b> , 1-15	4
1820	Rider Transposon Insertion and Phenotypic Change in Tomato. <b>2012</b> , 297-312	10
1819	Helitron Proliferation and Gene-Fragment Capture. <b>2012</b> , 193-217	2
1818	Transposable Element Annotation in Completely Sequenced Eukaryote Genomes. <b>2012</b> , 17-39	9
1817	Using Nextgen Sequencing to Investigate Genome Size Variation and Transposable Element Content. <b>2012</b> , 41-58	8
1816	Expression Profiling of Organellar Genes. <b>2012</b> , 323-355	4
1815	The impact of transposable elements on eukaryotic genomes: from genome size increase to genetic adaptation to stressful environments. <b>2012</b> , 509, 7-15	203
1814	Regulation of transposable elements in maize. <b>2012</b> , 15, 511-6	26
1813	Epigenetic control of transposon transcription and mobility in Arabidopsis. <b>2012</b> , 15, 503-10	88
1812	Control of meiotic recombination frequency in plant genomes. <b>2012</b> , 15, 556-61	50
1811	Functional characterization of wheat copalyl diphosphate synthases sheds light on the early evolution of labdane-related diterpenoid metabolism in the cereals. <b>2012</b> , 84, 40-6	49
1810	Genome-wide genetic changes during modern breeding of maize. <b>2012</b> , 44, 812-5	256
1809	Maize HapMap2 identifies extant variation from a genome in flux. <b>2012</b> , 44, 803-7	470
1808	Ancient and Recent Polyploidy in Monocots. <b>2012</b> , 93-108	14
1807	Maize ( <i>Zea Mays</i> ) as a Model for Studying the Impact of Gene and Regulatory Sequence Loss Following Whole-Genome Duplication. <b>2012</b> , 137-145	4
1806	Construction of BIBAC and BAC libraries from a variety of organisms for advanced genomics research. <b>2012</b> , 7, 479-99	21
1805	Nutritionally Enhanced Staple Food Crops. <b>2012</b> , 169-291	35
1804	Evolutionary Biology of Dyneins. <b>2012</b> , 88-121	6

1803	Translational Biology Approaches to Improve Abiotic Stress Tolerance in Crops. <b>2012</b> , 207-239	2
1802	Role of Plant Laccases in Lignin Polymerization. <b>2012</b> , 61, 145-172	46
1801	Maize: Physiological and Molecular Approaches for Improving Drought Tolerance. <b>2012</b> , 751-778	3
1800	Genomics Applications for the Developing World. <b>2012</b> ,	6
1799	RNA Abundance Analysis. <b>2012</b> ,	2
1798	Maize Production in a Changing Climate: Impacts, Adaptation, and Mitigation Strategies. <b>2012</b> , 114, 1-58	139
1797	OPTIMAS-DW: a comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. <b>2012</b> , 12, 245	42
1796	Maize ( <i>Zea mays</i> L.) genome diversity as revealed by RNA-sequencing. <b>2012</b> , 7, e33071	123
1795	Extensive pyrosequencing reveals frequent intra-genomic variations of internal transcribed spacer regions of nuclear ribosomal DNA. <b>2012</b> , 7, e43971	93
1794	A highly conserved, small LTR retrotransposon that preferentially targets genes in grass genomes. <b>2012</b> , 7, e32010	44
1793	The Tnt1 retrotransposon escapes silencing in tobacco, its natural host. <b>2012</b> , 7, e33816	8
1792	Biased gene fractionation and dominant gene expression among the subgenomes of <i>Brassica rapa</i> . <b>2012</b> , 7, e36442	195
1791	Genome-wide association studies identified three independent polymorphisms associated with Tocopherol content in maize kernels. <b>2012</b> , 7, e36807	96
1790	The R2R3-MYB transcription factor gene family in maize. <b>2012</b> , 7, e37463	177
1789	Characterization of miRNAs in response to short-term waterlogging in three inbred lines of <i>Zea mays</i> . <b>2012</b> , 7, e39786	65
1788	CCCH-type zinc finger family in maize: genome-wide identification, classification and expression profiling under abscisic acid and drought treatments. <b>2012</b> , 7, e40120	98
1787	SNP discovery with EST and NextGen sequencing in switchgrass ( <i>Panicum virgatum</i> L.). <b>2012</b> , 7, e44112	16
1786	Choosing the best plant for the job: a cost-effective assay to prescreen ancient plant remains destined for shotgun sequencing. <b>2012</b> , 7, e45644	15

1785	PICARA, an analytical pipeline providing probabilistic inference about a priori candidates genes underlying genome-wide association QTL in plants. <b>2012</b> , 7, e46596	20
1784	A fish-specific transposable element shapes the repertoire of p53 target genes in zebrafish. <b>2012</b> , 7, e46642	16
1783	Integration of two diploid potato linkage maps with the potato genome sequence. <b>2012</b> , 7, e36347	160
1782	Selection-driven extinction dynamics for group II introns in Enterobacteriales. <b>2012</b> , 7, e52268	14
1781	Exploring the genetic characteristics of two recombinant inbred line populations via high-density SNP markers in maize. <b>2012</b> , 7, e52777	23
1780	A novel family of terminal-repeat retrotransposon in miniature (TRIM) in the genome of the red harvester ant, <i>Pogonomyrmex barbatus</i> . <b>2012</b> , 7, e53401	14
1779	TriAnnot: A Versatile and High Performance Pipeline for the Automated Annotation of Plant Genomes. <b>2012</b> , 3, 5	54
1778	TCUP: A Novel hAT Transposon Active in Maize Tissue Culture. <b>2012</b> , 3, 6	19
1777	The Maize PIN Gene Family of Auxin Transporters. <b>2012</b> , 3, 16	78
1776	Genomic Databases for Crop Improvement. <b>2012</b> , 2, 62-73	35
1775	Why assembling plant genome sequences is so challenging. <b>2012</b> , 1, 439-59	84
1774	Transposable elements: from DNA parasites to architects of metazoan evolution. <b>2012</b> , 3, 409-22	19
1773	Sequencing Technologies and Their Use in Plant Biotechnology and Breeding. <b>2012</b> ,	3
1772	Plant Protein Analysis. <b>2012</b> ,	2
1771	Preparation of megabase-sized DNA from a variety of organisms using the nuclei method for advanced genomics research. <b>2012</b> , 7, 467-78	66
1770	The First Ten Years of Plant Genome Sequencing and Prospects for the Next Decade. <b>2012</b> , 1-15	4
1769	Conserved Noncoding Sequences in Plant Genomes. <b>2012</b> , 113-122	1
1768	Total centromere size and genome size are strongly correlated in ten grass species. <b>2012</b> , 20, 403-12	42

1767	The TvPirin gene is necessary for haustorium development in the parasitic plant <i>Triphysaria versicolor</i> . <b>2012</b> , 158, 1046-53	19
1766	Non-coding RNAs in the plant response to abiotic stress. <b>2012</b> , 236, 943-58	38
1765	Tuning gene expression with nucleosome-disfavoring sequences. <b>2012</b> , 44, 735-6	1
1764	A maize cystatin suppresses host immunity by inhibiting apoplastic cysteine proteases. <b>2012</b> , 24, 1285-300	95
1763	Co-evolution of Genes for Specification in Arthropod-Plant Interactions: A Bioinformatic Analysis in Plant and Arthropod Genomes. <b>2012</b> , 1-14	
1762	Parallel domestication of the <i>Shattering1</i> genes in cereals. <b>2012</b> , 44, 720-4	287
1761	Comparative population genomics of maize domestication and improvement. <b>2012</b> , 44, 808-11	600
1760	The Impact of Transposable Elements on Gene and Genome Evolution. <b>2012</b> , 35-58	15
1759	The Variation of Base Composition in Plant Genomes. <b>2012</b> , 209-235	26
1758	Envisioning the transition to a next-generation biofuels industry in the US Midwest. <b>2012</b> , 6, 376-386	18
1757	Genome sequence of foxtail millet ( <i>Setaria italica</i> ) provides insights into grass evolution and biofuel potential. <b>2012</b> , 30, 549-54	447
1756	Reference genome sequence of the model plant <i>Setaria</i> . <b>2012</b> , 30, 555-61	573
1755	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.). <b>2012</b> , 2, 321-9	8
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1753	Computational analysis of RNA-seq. <b>2012</b> , 883, 201-19	9
1752	Evolution and expression analysis of the $\beta$ -glucosidase (GLU) encoding gene subfamily in maize. <b>2012</b> , 34, 179-187	9
1751	Two loci in sorghum with NB-LRR encoding genes confer resistance to <i>Colletotrichum sublineolum</i> . <b>2012</b> , 124, 1005-15	31
1750	Functional markers in wheat: current status and future prospects. <b>2012</b> , 125, 1-10	150

1749	QTLs for agronomic and cell wall traits in a maize RIL progeny derived from a cross between an old Minnesota13 line and a modern Iodent line. <b>2012</b> , 125, 531-49	31
1748	Development of pachytene FISH maps for six maize chromosomes and their integration with other maize maps for insights into genome structure variation. <b>2012</b> , 20, 363-80	9
1747	Genome-wide analysis and identification of HAK potassium transporter gene family in maize ( <i>Zea mays</i> L.). <b>2012</b> , 39, 8465-73	57
1746	Selection of Reference Genes for Normalizing Gene Expression During Seed Priming and Germination Using qPCR in <i>Zea mays</i> and <i>Spinacia oleracea</i> . <b>2012</b> , 30, 478-487	27
1745	Genomics of a phylum distant from flowering plants: conifers. <b>2012</b> , 8, 573-582	16
1744	Analysis of Crystallinity Index and Hydrolysis Rates in the Bioenergy Crop <i>Sorghum bicolor</i> . <b>2012</b> , 5, 387-397	28
1743	Recent progress in the understanding of tissue culture-induced genome level changes in plants and potential applications. <b>2012</b> , 31, 597-620	151
1742	Diversification of hAT transposase paralogues in the sugarcane genome. <b>2012</b> , 287, 205-19	7
1741	Advances in biotechnology and linking outputs to variation in complex traits: Plant and Animal Genome meeting January 2012. <b>2012</b> , 12, 1-9	5
1740	Divergent evolution of oxidosqualene cyclases in plants. <b>2012</b> , 193, 1022-1038	88
1739	Root herbivory: molecular analysis of the maize transcriptome upon infestation by Southern corn rootworm, <i>Diabrotica undecimpunctata howardi</i> . <b>2012</b> , 144, 303-19	17
1738	Molecular, phylogenetic and comparative genomic analysis of the cytokinin oxidase/dehydrogenase gene family in the Poaceae. <b>2012</b> , 10, 67-82	34
1737	Small RNAs and transposon silencing in plants. <b>2012</b> , 54, 100-7	28
1736	Carbonic anhydrase and the molecular evolution of C4 photosynthesis. <b>2012</b> , 35, 22-37	35
1735	Dynamic evolution of herbivore-induced sesquiterpene biosynthesis in sorghum and related grass crops. <b>2012</b> , 69, 70-80	48
1734	The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. <b>2012</b> , 69, 475-88	28
1733	Crop genomics: advances and applications. <b>2011</b> , 13, 85-96	362
1732	Repetitive DNA and next-generation sequencing: computational challenges and solutions. <b>2011</b> , 13, 36-46	1053



1731	Systematic analysis and comparison of nucleotide-binding site disease resistance genes in maize. <b>2012</b> , 279, 2431-43	48
1730	Identification and fine mapping of rhm1 locus for resistance to Southern corn leaf blight in maize. <b>2012</b> , 54, 321-9	10
1729	Recent progress using high-throughput sequencing technologies in plant molecular breeding. <b>2012</b> , 54, 215-27	26
1728	Phenotyping for abiotic stress tolerance in maize. <b>2012</b> , 54, 238-49	84
1727	In silico archeogenomics unveils modern plant genome organisation, regulation and evolution. <b>2012</b> , 15, 122-30	58
1726	Exact and approximate area-proportional circular Venn and Euler diagrams. <b>2012</b> , 18, 321-31	82
1725	Cold stress selectively unsilences tandem repeats in heterochromatin associated with accumulation of H3K9ac. <b>2012</b> , 35, 2130-42	58
1724	Evolution of the large genome in <i>Capsicum annuum</i> occurred through accumulation of single-type long terminal repeat retrotransposons and their derivatives. <b>2012</b> , 69, 1018-29	46
1723	Advances in plant genome sequencing. <b>2012</b> , 70, 177-90	128
1722	Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. <b>2012</b> , 71, 492-502	144
1721	Specific changes in total and mitochondrial proteomes are associated with higher levels of heterosis in maize hybrids. <b>2012</b> , 72, 70-83	33
1720	Gene duplication and an accelerated evolutionary rate in 11S globulin genes are associated with higher protein synthesis in dicots as compared to monocots. <b>2012</b> , 12, 15	12
1719	Emerging knowledge from genome sequencing of crop species. <b>2012</b> , 50, 250-66	30
1718	The first draft of the pigeonpea genome sequence. <b>2012</b> , 21, 98-112	126
1717	Identification of qSOR1, a major rice QTL involved in soil-surface rooting in paddy fields. <b>2012</b> , 124, 75-86	52
1716	Mining and validation of pyrosequenced simple sequence repeats (SSRs) from American cranberry ( <i>Vaccinium macrocarpon</i> Ait.). <b>2012</b> , 124, 87-96	64
1715	Genetic analysis and fine mapping of the Ga1-S gene region conferring cross-incompatibility in maize. <b>2012</b> , 124, 459-65	12
1714	A computational study of the dynamics of LTR retrotransposons in the <i>Populus trichocarpa</i> genome. <b>2012</b> , 8, 61-75	38

1713	Genome-scale identification of resistance gene analogs and the development of their intron length polymorphism markers in maize. <b>2012</b> , 29, 437-447	18
1712	Diversification, phylogeny and evolution of auxin response factor (ARF) family: insights gained from analyzing maize ARF genes. <b>2012</b> , 39, 2401-15	59
1711	Structural characterization of plant defensin protein superfamily. <b>2012</b> , 39, 4461-9	19
1710	Cloning and characterization of a maize bZIP transcription factor, ZmbZIP72, confers drought and salt tolerance in transgenic Arabidopsis. <b>2012</b> , 235, 253-66	138
1709	Matita, a new retroelement from peanut: characterization and evolutionary context in the light of the Arachis A-B genome divergence. <b>2012</b> , 287, 21-38	40
1708	Modulation of auxin-binding protein 1 gene expression in maize and the teosintes by transposon insertions in its promoter. <b>2012</b> , 287, 143-53	3
1707	Genome-wide identification and analysis of microRNA responding to long-term waterlogging in crown roots of maize seedlings. <b>2013</b> , 147, 181-93	54
1706	Dissecting the genetic basis of physiological processes determining maize kernel weight using the IBM (B73Mo17) Syn4 population. <b>2013</b> , 145, 33-43	22
1705	Plant genomics: sowing the seeds of success. <b>2013</b> , 14, 404	5
1704	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <b>2013</b> , 14, R64	39
1703	Comprehensive genotyping of the USA national maize inbred seed bank. <b>2013</b> , 14, R55	337
1702	Conservation and divergence of transcriptomic and epigenomic variation in maize hybrids. <b>2013</b> , 14, R57	74
1701	Comparative analysis of tandem repeats from hundreds of species reveals unique insights into centromere evolution. <b>2013</b> , 14, R10	265
1700	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. <b>2013</b> , 6, 47	9
1699	Utilization of transposable element as a novel genetic tool for modification of the stress response in rice. <b>2013</b> , 32, 505-516	32
1698	Identification of Major QTL for Waterlogging Tolerance Using Genome-Wide Association and Linkage Mapping of Maize Seedlings. <b>2013</b> , 31, 594-606	40
1697	Kinetics and functional diversity among the five members of the NADP-malic enzyme family from Zea mays, a C4 species. <b>2013</b> , 115, 65-80	20
1696	Diagnostics in Plant Breeding. <b>2013</b> ,	1

1695	Biofuels as a sustainable energy source: an update of the applications of proteomics in bioenergy crops and algae. <b>2013</b> , 93, 234-44	57
1694	Breeding aflatoxin-resistant maize lines using recent advances in technologies - a review. <b>2013</b> , 30, 1382-91	30
1693	Genomics and Breeding for Climate-Resilient Crops. <b>2013</b> ,	3
1692	Proteomics of model and crop plant species: status, current limitations and strategic advances for crop improvement. <b>2013</b> , 93, 5-19	68
1691	Plant Transposable Elements. <b>2013</b> ,	2
1690	Discovery of structural alterations in solid tumor oligodendroglioma by single molecule analysis. <b>2013</b> , 14, 505	25
1689	Genome-wide identification and expression analysis of calcium-dependent protein kinase in maize. <b>2013</b> , 14, 433	125
1688	Genome-wide identification, classification and expression profiling of nicotianamine synthase (NAS) gene family in maize. <b>2013</b> , 14, 238	30
1687	Integration of mate pair sequences to improve shotgun assemblies of flow-sorted chromosome arms of hexaploid wheat. <b>2013</b> , 14, 222	13
1686	Pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.] consensus linkage map constructed using four RIL mapping populations and newly developed EST-SSRs. <b>2013</b> , 14, 159	76
1685	Tandem repeats derived from centromeric retrotransposons. <b>2013</b> , 14, 142	66
1684	De novo assembly and characterization of transcriptome using Illumina paired-end sequencing and identification of <i>CesA</i> gene in ramie ( <i>Boehmeria nivea</i> L. Gaud). <b>2013</b> , 14, 125	97
1683	Draft genome sequence of the rubber tree <i>Hevea brasiliensis</i> . <b>2013</b> , 14, 75	181
1682	Comparison of class 2 transposable elements at superfamily resolution reveals conserved and distinct features in cereal grass genomes. <b>2013</b> , 14, 71	44
1681	Extensive genomic characterization of a set of near-isogenic lines for heterotic QTL in maize ( <i>Zea mays</i> L.). <b>2013</b> , 14, 61	11
1680	Genome-wide expression profiling of maize in response to individual and combined water and nitrogen stresses. <b>2013</b> , 14, 3	89
1679	Two recently duplicated maize NAC transcription factor paralogs are induced in response to <i>Colletotrichum graminicola</i> infection. <b>2013</b> , 13, 85	35
1678	PLANEX: the plant co-expression database. <b>2013</b> , 13, 83	43

1677	Characterization of a new high copy Stowaway family MITE, BRAMI-1 in Brassica genome. <b>2013</b> , 13, 56	26
1676	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. <b>2013</b> , 13, 42	19
1675	Crop Improvement. <b>2013</b> ,	5
1674	Overview of repeat annotation and de novo repeat identification. <b>2013</b> , 1057, 275-87	12
1673	Computational methods for identification of DNA transposons. <b>2013</b> , 1057, 289-304	2
1672	Genome-wide identification of the maize calcium-dependent protein kinase gene family. <b>2013</b> , 169, 2111-25	34
1671	Nucleotide Composition of the Nelumbo nucifera Genome. <b>2013</b> , 6, 85-97	2
1670	Floral transition in maize infected with <i>Sporisorium reilianum</i> disrupts compatibility with this biotrophic fungal pathogen. <b>2013</b> , 237, 1251-66	8
1669	Genome-wide identification and expression profiling of ankyrin-repeat gene family in maize. <b>2013</b> , 223, 303-18	17
1668	Genetic and Morphometric Analysis of Cob Architecture and Biomass-Related Traits in the Interbred B73 × Mo17 Recombinant Inbred Lines of Maize. <b>2013</b> , 6, 903-916	5
1667	Radiation hybrid QTL mapping of <i>Tdes2</i> involved in the first meiotic division of wheat. <b>2013</b> , 126, 1977-90	8
1666	Targeted linkage map densification to improve cell wall related QTL detection and interpretation in maize. <b>2013</b> , 126, 1151-65	15
1665	Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. <b>2013</b> , 126, 1103-19	17
1664	ZmWRKY33, a WRKY maize transcription factor conferring enhanced salt stress tolerances in Arabidopsis. <b>2013</b> , 70, 207-216	87
1663	DcSto: carrot Stowaway-like elements are abundant, diverse, and polymorphic. <b>2013</b> , 141, 255-67	13
1662	TEnest 2.0: computational annotation and visualization of nested transposable elements. <b>2013</b> , 1057, 305-19	3
1661	Copy number variation of transposable elements in <i>Triticum-Aegilops</i> genus suggests evolutionary and revolutionary dynamics following allopolyploidization. <b>2013</b> , 32, 1615-24	22
1660	Maize proteomics: an insight into the biology of an important cereal crop. <b>2013</b> , 13, 637-62	52

1659	Mechanism for full-length RNA processing of Arabidopsis genes containing intragenic heterochromatin. <b>2013</b> , 4, 2301	63
1658	Dispersion and domestication shaped the genome of bread wheat. <b>2013</b> , 11, 564-71	55
1657	Conservation and functional element discovery in 20 angiosperm plant genomes. <b>2013</b> , 30, 1729-44	30
1656	New insights into the dynamics of plant cell nuclei and chromosomes. <b>2013</b> , 305, 253-301	25
1655	Comparative molecular cytogenetic analyses of a major tandemly repeated DNA family and retrotransposon sequences in cultivated jute <i>Corchorus</i> species (Malvaceae). <b>2013</b> , 112, 123-34	22
1654	Molecular biology of maize <i>Ac/Ds</i> elements: an overview. <b>2013</b> , 1057, 59-82	26
1653	Integrated genomics and molecular breeding approaches for dissecting the complex quantitative traits in crop plants. <b>2013</b> , 38, 971-87	12
1652	Transferability of rice SSR markers to <i>Miscanthus sinensis</i> , a potential biofuel crop. <b>2013</b> , 191, 455-468	9
1651	Distribution, evolution, and diversity of retrotransposons at the flamenco locus reflect the regulatory properties of piRNA clusters. <b>2013</b> , 110, 19842-7	72
1650	Small RNAs, big impact: small RNA pathways in transposon control and their effect on the host stress response. <b>2013</b> , 21, 587-600	39
1649	Comparative transcriptomics as a tool for the identification of root branching genes in maize. <b>2013</b> , 11, 1092-102	34
1648	Genome-wide identification and characterisation of F-box family in maize. <b>2013</b> , 288, 559-77	44
1647	Genome-wide identification and analysis of membrane-bound O-acyltransferase (MBOAT) gene family in plants. <b>2013</b> , 238, 907-22	8
1646	Intraspecific variation of recombination rate in maize. <b>2013</b> , 14, R103	134
1645	Identification and fine-mapping of a QTL, <i>qMrdd1</i> , that confers recessive resistance to maize rough dwarf disease. <b>2013</b> , 13, 145	35
1644	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <b>2013</b> , 14, R41	241
1643	<i>gff2sequence</i> , a new user friendly tool for the generation of genomic sequences. <b>2013</b> , 6, 15	15
1642	A novel RNA binding protein affects <i>rbCL</i> gene expression and is specific to bundle sheath chloroplasts in C4 plants. <b>2013</b> , 13, 138	24

1641	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <b>2013</b> , 2, 10	461
1640	Ups and downs of a transcriptional landscape shape iron deficiency associated chlorosis of the maize inbreds B73 and Mo17. <b>2013</b> , 13, 213	9
1639	Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). <b>2013</b> , 14, 335	68
1638	Identification and characterization of a repertoire of genes differentially expressed in developing top ear shoots between a superior hybrid and its parental inbreds in <i>Zea mays</i> L. <b>2013</b> , 288, 691-705	8
1637	Retrotransposon replication in plants. <b>2013</b> , 3, 604-14	42
1636	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <b>2013</b> , 76, 718-27	219
1635	Tana1, a new putatively active Tc1-like transposable element in the genome of sturgeons. <b>2013</b> , 66, 223-32	11
1634	Genetic and epigenetic changes involving (retro)transposons in animal hybrids and polyploids. <b>2013</b> , 140, 295-311	23
1633	Whole-genome sequencing of <i>Oryza brachyantha</i> reveals mechanisms underlying <i>Oryza</i> genome evolution. <b>2013</b> , 4, 1595	132
1632	Early transcriptomic adaptation to NaCl stress altered the expression of a quarter of the total genes in the maize genome and exhibited shared and distinctive profiles with NaCl and high pH stresses. <b>2013</b> , 55, 1147-65	19
1631	Genomics reveals new landscapes for crop improvement. <b>2013</b> , 14, 206	79
1630	Transposing from the laboratory to the classroom to generate authentic research experiences for undergraduates. <b>2013</b> , 193, 367-75	19
1629	Parallel proteomic and phosphoproteomic analyses of successive stages of maize leaf development. <b>2013</b> , 25, 2798-812	74
1628	Divergent evolutionary mechanisms of co-located <i>Tak/Lrk</i> and <i>Glu-D3</i> loci revealed by comparative analysis of grass genomes. <b>2013</b> , 56, 195-204	2
1627	LBD18 acts as a transcriptional activator that directly binds to the <i>EXPANSIN14</i> promoter in promoting lateral root emergence of <i>Arabidopsis</i> . <b>2013</b> , 73, 212-24	96
1626	Sorghum and Sugarcane Proteomics. <b>2013</b> , 141-168	1
1625	Association Genetics Strategies and Resources. <b>2013</b> , 187-203	6
1624	Genetic Enhancement of Sorghum for Biomass Utilization. <b>2013</b> , 391-425	9

1623	Bringing the Benefits of Sorghum Genomics to Africa. <b>2013</b> , 519-540	
1622	CHH islands: de novo DNA methylation in near-gene chromatin regulation in maize. <b>2013</b> , 23, 628-37	211
1621	Accessing complex crop genomes with next-generation sequencing. <b>2013</b> , 126, 1-11	210
1620	The draft genome of watermelon ( <i>Citrullus lanatus</i> ) and resequencing of 20 diverse accessions. <b>2013</b> , 45, 51-8	503
1619	Plastidial NADP-malic enzymes from grasses: unraveling the way to the C4 specific isoforms. <b>2013</b> , 63, 39-48	13
1618	Chitinase modifying proteins from phylogenetically distinct lineages of Brassica pathogens. <b>2013</b> , 82, 1-9	17
1617	A computational workflow to identify allele-specific expression and epigenetic modification in maize. <b>2013</b> , 11, 247-52	7
1616	A post-genomic view of behavioral development and adaptation to the environment. <b>2013</b> , 33, 89-109	72
1615	Genomic parasites or symbionts? Modeling the effects of environmental pressure on transposition activity in asexual populations. <b>2013</b> , 90, 145-51	21
1614	Significance and Biological Consequences of Polyploidization in Land Plant Evolution. <b>2013</b> , 277-293	28
1613	High bioavailability iron maize ( <i>Zea mays</i> L.) developed through molecular breeding provides more absorbable iron in vitro (Caco-2 model) and in vivo ( <i>Gallus gallus</i> ). <b>2013</b> , 12, 3	40
1612	A bountiful harvest: genomic insights into crop domestication phenotypes. <b>2013</b> , 64, 47-70	244
1611	A Field Guide to Transposable Elements. <b>2013</b> , 15-40	15
1610	Transposons in Plant Gene Regulation. <b>2013</b> , 93-116	3
1609	Transposons, Genomic Shock, and Genome Evolution. <b>2013</b> , 181-201	12
1608	Methylome of DNase I sensitive chromatin in <i>Populus trichocarpa</i> shoot apical meristematic cells: a simplified approach revealing characteristics of gene-body DNA methylation in open chromatin state. <b>2013</b> , 197, 416-430	39
1607	Comparative Genomic Analysis of C4 Photosynthesis Pathway Evolution in Grasses. <b>2013</b> , 447-477	4
1606	Mutation identification by direct comparison of whole-genome sequencing data from mutant and wild-type individuals using k-mers. <b>2013</b> , 31, 325-30	111

1605	Genomic distribution of maize facultative heterochromatin marked by trimethylation of H3K27. <b>2013</b> , 25, 780-93	77
1604	Miniature inverted-repeat transposable elements: discovery, distribution, and activity. <b>2013</b> , 56, 475-86	54
1603	Distinguishing ecological from evolutionary approaches to transposable elements. <b>2013</b> , 88, 573-84	16
1602	Draft genome of the wheat A-genome progenitor <i>Triticum urartu</i> . <b>2013</b> , 496, 87-90	589
1601	Allopolyploidy has a moderate impact on restructuring at three contrasting transposable element insertion sites in resynthesized <i>Brassica napus</i> allotetraploids. <b>2013</b> , 198, 593-604	46
1600	The dynamics of LTR retrotransposon accumulation across 25 million years of panicoid grass evolution. <b>2013</b> , 110, 194-204	66
1599	A decade of plant proteomics and mass spectrometry: translation of technical advancements to food security and safety issues. <b>2013</b> , 32, 335-65	59
1598	Progress toward understanding heterosis in crop plants. <b>2013</b> , 64, 71-88	267
1597	Future Cereal Starch Bioengineering: Cereal Ancestors Encounter Gene Technology and Designer Enzymes. <b>2013</b> , 90, 274-287	45
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1594	The draft genome of the fast-growing non-timber forest species moso bamboo ( <i>Phyllostachys heterocycla</i> ). <b>2013</b> , 45, 456-61, 461e1-2	340
1593	Prospects and Limitations for Development and Application of Functional Markers in Plants. <b>2013</b> , 329-346	4
1592	Sustainable Food Production. <b>2013</b> , 1182-1200	3
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1589	Integrating Omics Data and Expression QTL to Understand Maize Heterosis. <b>2013</b> , 85-103	
1588	Genetic Rules of Heterosis in Plants. <b>2013</b> , 313-321	5



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1586	<i>Arabidopsis thaliana</i> : A Useful but Limited Model to Investigate Stress Impacts on Rhizosphere Community Composition and Function. <b>2013</b> , 265-270	3
1585	Wheat Zapper: a flexible online tool for colinearity studies in grass genomes. <b>2013</b> , 13, 11-7	8
1584	Epigenetic characterization of chromatin in cycling cells of pedunculate oak, <i>Quercus robur</i> L.. <b>2013</b> , 9, 1247-1256	1
1583	Cereal Genomics: Excitements, Challenges and Opportunities. <b>2013</b> , 1-9	
1582	Application of Next-Generation Sequencing Technologies for Genetic Diversity Analysis in Cereals. <b>2013</b> , 77-99	1
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1580	Transposons in Cereals: Shaping Genomes and Driving Their Evolution. <b>2013</b> , 127-154	1
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1576	High-Throughput and Precision Phenotyping for Cereal Breeding Programs. <b>2013</b> , 341-374	13
1575	Genetics and consequences of crop domestication. <b>2013</b> , 61, 8267-76	83
1574	Co-evolution of plant LTR-retrotransposons and their host genomes. <b>2013</b> , 4, 493-501	34
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1572	What contemporary viruses tell us about evolution: a personal view. <b>2013</b> , 158, 1833-48	22
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1570	C <sub>4</sub> photosynthesis: from evolutionary analyses to strategies for synthetic reconstruction of the trait. <b>2013</b> , 16, 315-21	12

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1562	RNA sequencing reveals the complex regulatory network in the maize kernel. <b>2013</b> , 4, 2832	167
1561	A genome-wide analysis of simple sequence repeats in maize and the development of polymorphism markers from next-generation sequence data. <b>2013</b> , 6, 403	25
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1551	Generation of tandem direct duplications by reversed-ends transposition of maize ac elements. <b>2013</b> , 9, e1003691	31
1550	Genome-Wide Analysis of Polyphenol Oxidase Genes and Their Transcriptional Patterns during Grain Development in Sorghum. <b>2013</b> , 174, 710-721	4
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1537	Evolutionary dynamics of retrotransposons assessed by high-throughput sequencing in wild relatives of wheat. <b>2013</b> , 5, 1010-20	25
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1527	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. <b>2013</b> , 23, 1651-62	199
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1525	Natural variation in maize aphid resistance is associated with 2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one glucoside methyltransferase activity. <b>2013</b> , 25, 2341-55	171
1524	dbWFA: a web-based database for functional annotation of <i>Triticum aestivum</i> transcripts. <b>2013</b> , 2013, bat014	9
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1521	The potential of C4 grasses for cellulosic biofuel production. <b>2013</b> , 4, 107	140
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1518	Seed shattering in a wild sorghum is conferred by a locus unrelated to domestication. <b>2013</b> , 110, 15824-9	44
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1514	A developmental transcriptional network for maize defines coexpression modules. <b>2013</b> , 161, 1830-43	63
1513	Horizontal transfer and evolution of prokaryote transposable elements in eukaryotes. <b>2013</b> , 5, 822-32	30
1512	The perennial ryegrass GenomeZipper: targeted use of genome resources for comparative grass genomics. <b>2013</b> , 161, 571-82	63
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1504	Ionic Characterization of Maize Kernels in the Intermated B73 [Mo17 Population. <b>2013</b> , 53, 208-220	48
1503	Breeding Potential of Elite Maize Landraces to Improve Forage Yield and Quality of Two Heterotic Patterns. <b>2013</b> , 53, 121-131	2
1502	Genetic improvement of biofuel plants: recent progress and patents. <b>2013</b> , 7, 2-12	7
1501	The Orphan Legume Genome Whose Time Has Come: Symposium Highlights from the American Peanut Research & Education Society Annual Meeting. <b>2013</b> , 40, 66-69	5
1500	Maize Metabolic Network Construction and Transcriptome Analysis. <b>2013</b> , 6, plantgenome2012.09.0025	50
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1498	Phenotypic and Genetic Characterization of a Maize Association Mapping Panel Developed for the Identification of New Sources of Resistance to Aspergillus flavus and Aflatoxin Accumulation. <b>2013</b> , 53, 2374-2383	42

1497	Deep sequencing of RNA from ancient maize kernels. <b>2013</b> , 8, e50961	29
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1495	Genome-wide identification and analysis of expression profiles of maize mitogen-activated protein kinase kinase kinase. <b>2013</b> , 8, e57714	51
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1493	The requirement of WHIRLY1 for embryogenesis is dependent on genetic background in maize. <b>2013</b> , 8, e67369	22
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1490	Proteomic and phytohormone analysis of the response of maize ( <i>Zea mays</i> L.) seedlings to sugarcane mosaic virus. <b>2013</b> , 8, e70295	26
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1488	Insights into the loblolly pine genome: characterization of BAC and fosmid sequences. <b>2013</b> , 8, e72439	41
1487	Characterisation and analysis of the <i>Aegilops sharonensis</i> transcriptome, a wild relative of wheat in the <i>Sitopsis</i> section. <b>2013</b> , 8, e72782	10
1486	Identification of <i>Pyrus</i> single nucleotide polymorphisms (SNPs) and evaluation for genetic mapping in European pear and interspecific <i>Pyrus</i> hybrids. <b>2013</b> , 8, e77022	50
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1483	Long-range genomic enrichment, sequencing, and assembly to determine unknown sequences flanking a known microRNA. <b>2013</b> , 8, e83721	4
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1480	Resistance to sap-sucking insects in modern-day agriculture. <b>2013</b> , 4, 222	17

1479	Phylogenomics of MADS-Box Genes in Plants - Two Opposing Life Styles in One Gene Family. <b>2013</b> , 2, 1150-64	37
1478	First insights into the large genome of <i>Epimedium sagittatum</i> (Sieb. et Zucc) Maxim, a Chinese Ttraditional medicinal plant. <b>2013</b> , 14, 13559-76	3
1477	The Metabolic Interplay between Plants and Phytopathogens. <b>2013</b> , 3, 1-23	30
1476	Dynamic evolution of <i>rht-1</i> homologous regions in grass genomes. <b>2013</b> , 8, e75544	3
1475	Genomewide Association Mapping of Flowering Time, Kernel Composition, and Disease Resistance in Historical Minnesota Maize Inbreds. <b>2013</b> , 53, 2518-2529	18
1474	Variation in DNA Methylation Patterns is More Common among Maize Inbreds than among Tissues. <b>2013</b> , 6, plantgenome2012.06.0009	24
1473	Whole transcriptome profiling of maize during early somatic embryogenesis reveals altered expression of stress factors and embryogenesis-related genes. <b>2014</b> , 9, e111407	62
1472	Transposable element <i>rbg</i> induces the differential expression of opaque-2 mutant gene in two maize o2 NILs derived from the same inbred line. <b>2014</b> , 9, e85159	5
1471	Scanning of transposable elements and analyzing expression of transposase genes of sweet potato [ <i>Ipomoea batatas</i> ]. <b>2014</b> , 9, e90895	5
1470	Sequence and ionomic analysis of divergent strains of maize inbred line B73 with an altered growth phenotype. <b>2014</b> , 9, e96782	8
1469	The use of massive sequencing to detect differences between immature embryos of MON810 and a comparable non-GM maize variety. <b>2014</b> , 9, e100895	6
1468	Identification and characterization of microRNAs in small brown planthopper ( <i>Laodephax striatellus</i> ) by next-generation sequencing. <b>2014</b> , 9, e103041	8
1467	Genomic distribution of H3K9me2 and DNA methylation in a maize genome. <b>2014</b> , 9, e105267	108
1466	Molecular evolution and expansion analysis of the NAC transcription factor in <i>Zea mays</i> . <b>2014</b> , 9, e111837	39
1465	Heterosis in Plants. <b>2014</b> , 539-543	
1464	Computational and Statistical Analyses of Insertional Polymorphic Endogenous Retroviruses in a Non-Model Organism. <b>2014</b> , 2, 221-245	5
1463	Red card for pathogens: phytoalexins in sorghum and maize. <b>2014</b> , 19, 9114-33	30
1462	Alterations in Soluble Class III Peroxidases of Maize Shoots by Flooding Stress. <b>2014</b> , 2, 303-322	14

1461	A Genome-Wide Analysis of the AAAP Gene Family in Maize. <b>2014</b> , 07,	5
1460	. <b>2014</b> ,	12
1459	. <b>2014</b> ,	3
1458	Phenotypic and Transcriptional Analysis of Divergently Selected Maize Populations Reveals the Role of Developmental Timing in Seed Size Determination. <b>2014</b> , 165, 658-669	33
1457	Physiological and protein profiling response to drought stress in KS141, a Korean maize inbred line. <b>2014</b> , 17, 273-280	6
1456	Application of iPBS in high-throughput sequencing for the development of retrotransposon-based molecular markers. <b>2014</b> , 1, 40-44	12
1455	The Use of Association Genetics Approaches in Plant Breeding. <b>2014</b> , 17-68	2
1454	Sorghum biomass: a novel renewable carbon source for industrial bioproducts. <b>2014</b> , 5, 159-174	32
1453	The peculiar landscape of repetitive sequences in the olive ( <i>Olea europaea</i> L.) genome. <b>2014</b> , 6, 776-91	51
1452	Plant protein peptidase inhibitors: an evolutionary overview based on comparative genomics. <b>2014</b> , 15, 812	25
1451	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. <b>2014</b> , 15, 823	168
1450	A computational platform to maintain and migrate manual functional annotations for BioCyc databases. <b>2014</b> , 8, 115	3
1449	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. <b>2014</b> , 15, 512	334
1448	Identification and characterization of the RCI2 gene family in maize ( <i>Zea mays</i> ). <b>2014</b> , 93, 655-66	10
1447	Evolutionary history of Methyltransferase 1 genes in hexaploid wheat. <b>2014</b> , 15, 922	8
1446	Evolutionary convergence of cell-specific gene expression in independent lineages of C4 grasses. <b>2014</b> , 165, 62-75	72
1445	Evolution of centromeric retrotransposons in grasses. <b>2014</b> , 6, 1335-52	21
1444	Comparative genomic analysis reveals multiple long terminal repeats, lineage-specific amplification, and frequent interelement recombination for Cassandra retrotransposon in pear ( <i>Pyrus bretschneideri</i> Rehd.). <b>2014</b> , 6, 1423-36	20



1443	The plasticity of NBS resistance genes in sorghum is driven by multiple evolutionary processes. <b>2014</b> , 14, 253	38
1442	Transcriptomic complexity in young maize primary roots in response to low water potentials. <b>2014</b> , 15, 741	54
1441	Shared subgenome dominance following polyploidization explains grass genome evolutionary plasticity from a seven protochromosome ancestor with 16K protogenes. <b>2014</b> , 6, 12-33	56
1440	The State Agricultural Experiment Station System Meets Biotechnology:A Perspective. <b>2014</b> , 10, 323-327	
1439	P element temperature-specific transposition: a model for possible regulation of mobile elements activity by pre-mRNA secondary structure. <b>2014</b> , 48, 378-382	
1438	Transcriptional responses indicate maintenance of photosynthetic proteins as key to the exceptional chilling tolerance of C4 photosynthesis in <i>Miscanthus giganteus</i> . <b>2014</b> , 65, 3737-47	18
1437	Automated update, revision, and quality control of the maize genome annotations using MAKER-P improves the B73 RefGen_v3 gene models and identifies new genes. <b>2015</b> , 167, 25-39	43
1436	Meiotic chromosome structure and function in plants. <b>2014</b> , 143, 6-17	9
1435	The First Plant Genome Sequence <i>Arabidopsis thaliana</i> . <b>2014</b> , 91-117	4
1434	Overexpression of the maize GRF10, an endogenous truncated growth-regulating factor protein, leads to reduction in leaf size and plant height. <b>2014</b> , 56, 1053-63	49
1433	A MITE transposon insertion is associated with differential methylation at the maize flowering time QTL Vgt1. <b>2014</b> , 4, 805-12	59
1432	Sequencing-based large-scale genomics approaches with small numbers of isolated maize meiocytes. <b>2014</b> , 5, 57	12
1431	Diversification of the plant-specific hybrid glycine-rich protein (HyGRP) genes in cereals. <b>2014</b> , 5, 489	5
1430	Karyotype variability in tropical maize sister inbred lines and hybrids compared with KYS standard line. <b>2014</b> , 5, 544	10
1429	The Evolution of Plant Gene and Genome Sequencing. <b>2014</b> , 47-90	5
1428	Insights into the Common Ancestor of Cereals. <b>2014</b> , 69, 175-194	
1427	A genome-wide association study of the maize hypersensitive defense response identifies genes that cluster in related pathways. <b>2014</b> , 10, e1004562	43
1426	Three groups of transposable elements with contrasting copy number dynamics and host responses in the maize ( <i>Zea mays</i> ssp. <i>mays</i> ) genome. <b>2014</b> , 10, e1004298	32

1425	WHIRLY1 is a major organizer of chloroplast nucleoids. <b>2014</b> , 5, 432	31
1424	Predicting the function of 4-coumarate:CoA ligase (LJ4CL1) in <i>Lonicera japonica</i> . <b>2014</b> , 15, 2386-99	8
1423	Early embryogenesis-specific expression of the rice transposon Ping enhances amplification of the MITE mPing. <b>2014</b> , 10, e1004396	8
1422	Climate Change: New Breeding Pressures and Goals. <b>2014</b> , 284-293	2
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1420	Retrotransposon-based molecular markers for analysis of genetic diversity within the Genus <i>Linum</i> . <b>2014</b> , 2014, 231589	19
1419	Sequence-Based Analysis of Structural Organization and Composition of the Cultivated Sunflower ( <i>Helianthus annuus</i> L.) Genome. <b>2014</b> , 3, 295-319	12
1418	Recurrent loss of specific introns during angiosperm evolution. <b>2014</b> , 10, e1004843	17
1417	Assessing the metabolic impact of nitrogen availability using a compartmentalized maize leaf genome-scale model. <b>2014</b> , 166, 1659-74	63
1416	Genome-wide identification, phylogenetic analysis, expression profiling, and protein-protein interaction properties of TOPLESS gene family members in tomato. <b>2014</b> , 65, 1013-23	18
1415	The landscape of transposable elements in the finished genome of the fungal wheat pathogen <i>Mycosphaerella graminicola</i> . <b>2014</b> , 15, 1132	49
1414	Genetic Determinants for Enzymatic Digestion of Lignocellulosic Biomass Are Independent of Those for Lignin Abundance in a Maize Recombinant Inbred Population. <b>2014</b> , 165, 1475-1487	39
1413	Insights into the maize pan-genome and pan-transcriptome. <b>2014</b> , 26, 121-35	336
1412	Dynamic transcriptome landscape of maize embryo and endosperm development. <b>2014</b> , 166, 252-64	177
1411	Whole-genome sequencing of cultivated and wild peppers provides insights into <i>Capsicum</i> domestication and specialization. <b>2014</b> , 111, 5135-40	466
1410	Maize centromeres expand and adopt a uniform size in the genetic background of oat. <b>2014</b> , 24, 107-16	66
1409	Genetic perturbation of the maize methylome. <b>2014</b> , 26, 4602-16	126
1408	Nonsyntenic genes drive highly dynamic complementation of gene expression in maize hybrids. <b>2014</b> , 26, 3939-48	43

1407	Differential nuclease sensitivity profiling of chromatin reveals biochemical footprints coupled to gene expression and functional DNA elements in maize. <b>2014</b> , 26, 3883-93	58
1406	Quantitative trait loci mapping of metal concentrations in leaves of the maize IBM population. <b>2014</b> , 151, 55-60	18
1405	Development of an <i>Arabidopsis thaliana</i> genomic contig sequence data set and application to single nucleotide polymorphisms discovery. <b>2014</b> , 14, 411-8	9
1404	Genetic diversity of maize germplasm assessed by retrotransposon-based markers. <b>2014</b> , 35, 1921-7	7
1403	A barley PHD finger transcription factor that confers male sterility by affecting tapetal development. <b>2014</b> , 12, 765-77	39
1402	G-quadruplex (G4) motifs in the maize ( <i>Zea mays</i> L.) genome are enriched at specific locations in thousands of genes coupled to energy status, hypoxia, low sugar, and nutrient deprivation. <b>2014</b> , 41, 627-47	33
1401	The low-recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. <b>2014</b> , 79, 981-92	22
1400	The maize DWARF1 encodes a gibberellin 3-oxidase and is dual localized to the nucleus and cytosol. <b>2014</b> , 166, 2028-39	59
1399	The <i>Spirodela polyrhiza</i> genome reveals insights into its neotenus reduction fast growth and aquatic lifestyle. <b>2014</b> , 5, 3311	180
1398	Genome-wide identification and characterization of maize expansin genes expressed in endosperm. <b>2014</b> , 289, 1061-74	50
1397	Small kernel 1 encodes a pentatricopeptide repeat protein required for mitochondrial nad7 transcript editing and seed development in maize ( <i>Zea mays</i> ) and rice ( <i>Oryza sativa</i> ). <b>2014</b> , 79, 797-809	94
1396	11 Application of Genomics to the Study of Pathogenicity and Development in <i>Fusarium</i> . <b>2014</b> , 267-300	2
1395	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes. <b>2014</b> , 615-649	17
1394	Genomics of plant genetic resources: a gateway to a new era of global food security. <b>2014</b> , 12, S2-S5	2
1393	Genome-wide identification, splicing, and expression analysis of the myosin gene family in maize ( <i>Zea mays</i> ). <b>2014</b> , 65, 923-38	7
1392	Conversion steps in bioenergy production Analysis of the energy flow from photon to biofuel. <b>2014</b> , 5, 385-404	8
1391	Differential genome evolution and speciation of <i>Coix lacryma-jobi</i> L. and <i>Coix aquatica</i> Roxb. hybrid guangxi revealed by repetitive sequence analysis and fine karyotyping. <b>2014</b> , 15, 1025	34
1390	Genome-wide identification of microRNA and siRNA responsive to endophytic beneficial diazotrophic bacteria in maize. <b>2014</b> , 15, 766	40

1389	Maize and millet transcription factors annotated using comparative genomic and transcriptomic data. <b>2014</b> , 15, 818	16
1388	Flexible and scalable genotyping-by-sequencing strategies for population studies. <b>2014</b> , 15, 979	35
1387	Molecular characterization of the piggyBac-like element, a candidate marker for phylogenetic research of <i>Chilo suppressalis</i> (Walker) in China. <b>2014</b> , 15, 28	6
1386	High-resolution mapping and characterization of qRgls2, a major quantitative trait locus involved in maize resistance to gray leaf spot. <b>2014</b> , 14, 230	15
1385	Insights into the evolution and diversification of the AT-hook Motif Nuclear Localized gene family in land plants. <b>2014</b> , 14, 266	39
1384	Non-specific lipid transfer proteins in maize. <b>2014</b> , 14, 281	47
1383	Genome-wide association study of Fusarium ear rot disease in the U.S.A. maize inbred line collection. <b>2014</b> , 14, 372	62
1382	Mapping mutations in plant genomes with the user-friendly web application CandiSNP. <b>2014</b> , 10, 41	8
1381	Organization and evolution of transposable elements along the bread wheat chromosome 3B. <b>2014</b> , 15, 546	69
1380	Chromatin structure and gene expression changes associated with loss of MOP1 activity in <i>Zea mays</i> . <b>2014</b> , 9, 1047-59	16
1379	Transposable element dynamics among asymbiotic and ectomycorrhizal <i>Amanita</i> fungi. <b>2014</b> , 6, 1564-78	35
1378	Developmental dynamics of Kranz cell transcriptional specificity in maize leaf reveals early onset of C4-related processes. <b>2014</b> , 65, 3543-55	54
1377	Tetris is a foldback transposon that provided the building blocks for an emerging satellite DNA of <i>Drosophila virilis</i> . <b>2014</b> , 6, 1302-13	29
1376	Evolutionary history of trihelix family and their functional diversification. <b>2014</b> , 21, 499-510	26
1375	A new genome-wide method to track horizontally transferred sequences: application to <i>Drosophila</i> . <b>2014</b> , 6, 416-32	10
1374	The pattern and distribution of deleterious mutations in maize. <b>2014</b> , 4, 163-71	56
1373	Next Generation Sequencing and Germplasm Resources. <b>2014</b> , 369-390	
1372	Differential methylation during maize leaf growth targets developmentally regulated genes. <b>2014</b> , 164, 1350-64	58

1371	A high-resolution genetic map of yellow monkeyflower identifies chemical defense QTLs and recombination rate variation. <b>2014</b> , 4, 813-21	26
1370	The Aux/IAA gene <i>rum1</i> involved in seminal and lateral root formation controls vascular patterning in maize ( <i>Zea mays</i> L.) primary roots. <b>2014</b> , 65, 4919-30	44
1369	MAGIC: access portal to a cross-platform gene expression compendium for maize. <b>2014</b> , 30, 1316-8	2
1368	An assay to monitor the activity of DNA transposition complexes yields a general quality control measure for transpositional recombination reactions. <b>2014</b> , 4, 1-8	1
1367	Heterosis in early maize ear inflorescence development: a genome-wide transcription analysis for two maize inbred lines and their hybrid. <b>2014</b> , 15, 13892-915	20
1366	The Wheat Black Jack: Advances Towards Sequencing the 21 Chromosomes of Bread Wheat. <b>2014</b> , 405-438	7
1365	BambooGDB: a bamboo genome database with functional annotation and an analysis platform. <b>2014</b> , 2014, bau006	53
1364	Characterization of Rubisco activase genes in maize: an $\beta$ isoform gene functions alongside a $\beta$ isoform gene. <b>2014</b> , 164, 2096-106	31
1363	Genome-wide discovery and characterization of maize long non-coding RNAs. <b>2014</b> , 15, R40	308
1362	Plant genome sequencing - applications for crop improvement. <b>2014</b> , 26, 31-7	128
1361	Responses of highly resistant and susceptible maize to vascular puncture inoculation with Maize dwarf mosaic virus. <b>2014</b> , 86, 19-27	8
1360	Emerging technologies advancing forage and turf grass genomics. <b>2014</b> , 32, 190-9	18
1359	Getting the most out of natural variation in C4 photosynthesis. <b>2014</b> , 119, 157-67	16
1358	Genomics and bioinformatics resources for translational science in Rosaceae. <b>2014</b> , 8, 49-64	16
1357	Colocalizations Between Several QTLs for Cell Wall Degradability and Composition in the F288 F271 Early Maize RIL Progeny Raise the Question of the Nature of the Possible Underlying Determinants and Breeding Targets for Biofuel Capacity. <b>2014</b> , 7, 142-156	20
1356	Sequencing and Assembly of the Transgenic Papaya Genome. <b>2014</b> , 187-203	2
1355	Copy number polymorphism in plant genomes. <b>2014</b> , 127, 1-18	122
1354	A segmental duplication encompassing $\beta$ -haplotype triggers pollen-part self-compatibility in Japanese pear ( <i>Pyrus pyrifolia</i> ). <b>2014</b> , 33, 117-128	12

1353	Identification of RNA silencing components in soybean and sorghum. <b>2014</b> , 15, 4	30
1352	In silico analysis of PHB gene family in maize. <b>2014</b> , 73, 181-191	5
1351	Plant genome size variation: bloating and purging DNA. <b>2014</b> , 13, 308-17	91
1350	Transposon variation by order during allopolyploidisation between Brassica oleracea and Brassica rapa. <b>2014</b> , 16, 825-35	11
1349	High-throughput SNP Profiling of Genetic Resources in Crop Plants Using Genotyping Arrays. <b>2014</b> , 113-130	9
1348	Analysis of retrotransposon activity in plants. <b>2014</b> , 1112, 195-210	13
1347	Early History of the Angiosperms. <b>2014</b> , 69, 195-222	4
1346	Levels of selection and the formal Darwinism project. <b>2014</b> , 29, 217-224	3
1345	Genetic analysis and major QTL detection for maize kernel size and weight in multi-environments. <b>2014</b> , 127, 1019-37	75
1344	Genetic analysis of resistance to six virus diseases in a multiple virus-resistant maize inbred line. <b>2014</b> , 127, 867-80	31
1343	Identification of miRNAs and their target genes in developing maize ears by combined small RNA and degradome sequencing. <b>2014</b> , 15, 25	75
1342	Miscanthus Genetics and Agronomy for Bioenergy Feedstock. <b>2014</b> , 43-73	3
1341	Crystallographic structure of ChitA, a glycoside hydrolase family 19, plant class IV chitinase from Zea mays. <b>2014</b> , 23, 586-93	16
1340	Low-Oxygen Stress in Plants. <b>2014</b> ,	9
1339	The Tvv1 retrotransposon family is conserved between plant genomes separated by over 100 million years. <b>2014</b> , 127, 1223-35	18
1338	Genome-wide identification and phylogenetic analysis of Family-1 UDP glycosyltransferases in maize (Zea mays). <b>2014</b> , 239, 1265-79	51
1337	Correlation of mRNA and protein abundance in the developing maize leaf. <b>2014</b> , 78, 424-40	76
1336	Revisiting Plant-Herbivore Co-Evolution in the Molecular Biology Era. <b>2014</b> , 361-384	11

1335	Comparative transcriptomics of early meiosis in Arabidopsis and maize. <b>2014</b> , 41, 139-52		32
1334	Caterpillar attack triggers accumulation of the toxic maize protein RIP2. <b>2014</b> , 201, 928-939		37
1333	Natural variation of TaGASR7-A1 affects grain length in common wheat under multiple cultivation conditions. <b>2014</b> , 34, 937-947		53
1332	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. <b>2014</b> , 5, 3722		138
1331	Understanding the complex nature of salinity and drought-stress response in cereals using proteomics technologies. <b>2014</b> , 14, 611-21		36
1330	Genomic signatures of specialized metabolism in plants. <i>Science</i> , <b>2014</b> , 344, 510-3	33.3	177
1329	Reduced representation approaches to interrogate genome diversity in large repetitive plant genomes. <b>2014</b> , 13, 257-67		30
1328	Ostertagia ostertagi macrophage migration inhibitory factor is present in all developmental stages and may cross-regulate host functions through interaction with the host receptor. <b>2014</b> , 44, 355-67		19
1327	In silico analysis of plant and animal transposable elements. <b>2014</b> , 10, 297-306		
1326	Increased understanding of the cereal phytase complement for better mineral bio-availability and resource management. <b>2014</b> , 59, 373-381		35
1325	Nitrate induction triggers different transcriptional changes in a high and a low nitrogen use efficiency maize inbred line. <b>2014</b> , 56, 1080-94		43
1324	Transposable elements, a treasure trove to decipher epigenetic variation: insights from Arabidopsis and crop epigenomes. <b>2014</b> , 65, 2801-12		46
1323	Profiling of extensively diversified plant LINEs reveals distinct plant-specific subclades. <b>2014</b> , 79, 385-97		25
1322	Entering the second century of maize quantitative genetics. <b>2014</b> , 112, 30-8		107
1321	Regulatory motifs identified from a maize developmental coexpression network. <b>2014</b> , 57, 181-4		3
1320	Major repeat components covering one-third of the ginseng ( <i>Panax ginseng</i> C.A. Meyer) genome and evidence for allotetraploidy. <b>2014</b> , 77, 906-16		45
1319	Plant Epigenetics and Epigenomics. <b>2014</b> ,		4
1318	Genome assembly and annotation for red clover ( <i>Trifolium pratense</i> ; Fabaceae). <b>2014</b> , 101, 327-37		40

1317	An introduction to the vast world of transposable elements – what about the diatoms?. <b>2014</b> , 29, 91-104	5
1316	Epigenetics and plant genome evolution. <b>2014</b> , 18, 1-8	74
1315	Calcium-dependent protein kinases in plants: evolution, expression and function. <b>2014</b> , 55, 551-69	111
1314	Identification and characterization of the SET domain gene family in maize. <b>2014</b> , 41, 1341-54	15
1313	Small RNAs and heritable epigenetic variation in plants. <b>2014</b> , 24, 100-7	84
1312	Genomics of Plant Genetic Resources. <b>2014</b> ,	13
1311	Natural variations and genome-wide association studies in crop plants. <b>2014</b> , 65, 531-51	401
1310	Comparative analyses of C <sub>3</sub> and C <sub>4</sub> photosynthesis in developing leaves of maize and rice. <b>2014</b> , 32, 1158-65	160
1309	An automated proteogenomic method uses mass spectrometry to reveal novel genes in Zea mays. <b>2014</b> , 13, 157-67	69
1308	MAKER-P: a tool kit for the rapid creation, management, and quality control of plant genome annotations. <b>2014</b> , 164, 513-24	260
1307	De novo genome assembly of the economically important weed horseweed using integrated data from multiple sequencing platforms. <b>2014</b> , 166, 1241-54	60
1306	HelitronScanner uncovers a large overlooked cache of Helitron transposons in many plant genomes. <b>2014</b> , 111, 10263-8	106
1305	Genome-wide high resolution parental-specific DNA and histone methylation maps uncover patterns of imprinting regulation in maize. <b>2014</b> , 24, 167-76	98
1304	The impact of widespread regulatory neofunctionalization on homeolog gene evolution following whole-genome duplication in maize. <b>2014</b> , 24, 1348-55	60
1303	Allopolyploidy, diversification, and the Miocene grassland expansion. <b>2014</b> , 111, 15149-54	130
1302	The Maize TFome--development of a transcription factor open reading frame collection for functional genomics. <b>2014</b> , 80, 356-66	49
1301	The maize brown midrib2 (bm2) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <b>2014</b> , 77, 380-92	67
1300	Variation in allelic expression associated with a recombination hotspot in Zea mays. <b>2014</b> , 79, 375-84	7



1299	"Omics" of maize stress response for sustainable food production: opportunities and challenges. <b>2014</b> , 18, 714-32	53
1298	Genome sequence of the hot pepper provides insights into the evolution of pungency in Capsicum species. <b>2014</b> , 46, 270-8	594
1297	Natural variation at sympathy for the ligule controls penetrance of the semidominant Liguleless narrow-R mutation in Zea mays. <b>2014</b> , 4, 2297-306	10
1296	Insights into the effects of long-term artificial selection on seed size in maize. <b>2014</b> , 198, 409-21	25
1295	QTL mapping and phenotypic variation for root architectural traits in maize (Zea mays L.). <b>2014</b> , 127, 2293-311	66
1294	Unraveling genomic complexity at a quantitative disease resistance locus in maize. <b>2014</b> , 198, 333-44	35
1293	Genetic dissection of a genomic region with pleiotropic effects on domestication traits in maize reveals multiple linked QTL. <b>2014</b> , 198, 345-53	24
1292	First evidence of mariner-like transposons in the genome of the marine microalga Amphora acutiuscula (Bacillariophyta). <b>2014</b> , 165, 730-44	5
1291	Patterns of genomic integration of nuclear chloroplast DNA fragments in plant species. <b>2014</b> , 21, 127-40	34
1290	Nucleotide polymorphism and copy number variant detection using exome capture and next-generation sequencing in the polyploid grass Panicum virgatum. <b>2014</b> , 79, 993-1008	32
1289	Genome-wide identification of housekeeping genes in maize. <b>2014</b> , 86, 543-54	54
1288	A rapid and enhanced DNA detection method for crop cultivar discrimination. <b>2014</b> , 185, 57-62	24
1287	Epigenetic regulation and functional exaptation of transposable elements in higher plants. <b>2014</b> , 21, 83-88	44
1286	Structural basis of hAT transposon end recognition by Hermes, an octameric DNA transposase from Musca domestica. <b>2014</b> , 158, 353-367	51
1285	Identification of small secreted peptides (SSPs) in maize and expression analysis of partial SSP genes in reproductive tissues. <b>2014</b> , 240, 713-28	14
1284	Expansion of banana (Musa acuminata) gene families involved in ethylene biosynthesis and signalling after lineage-specific whole-genome duplications. <b>2014</b> , 202, 986-1000	32
1283	Young but not relatively old retrotransposons are preferentially located in gene-rich euchromatic regions in tomato (Solanum lycopersicum) plants. <b>2014</b> , 80, 582-91	27
1282	Antagonistic roles of abscisic acid and cytokinin during response to nitrogen depletion in oleaginous microalga Nannochloropsis oceanica expand the evolutionary breadth of phytohormone function. <b>2014</b> , 80, 52-68	75

1281	Differential analysis of proteomes and metabolomes reveals additively balanced networking for metabolism in maize heterosis. <b>2014</b> , 13, 3987-4001	12
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1279	Influence of amount of starting material for DNA extraction on detection of low-level presence of genetically engineered traits. <b>2014</b> , 62, 4349-58	4
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1277	Integrated syntenic and phylogenomic analyses reveal an ancient genome duplication in monocots. <b>2014</b> , 26, 2792-802	140
1276	A pair of homoeolog ClpP5 genes underlies a virescent yellow-like mutant and its modifier in maize. <b>2014</b> , 79, 192-205	23
1275	Quantitative genetic analysis of chlorophyll a fluorescence parameters in maize in the field environments. <b>2014</b> , 56, 695-708	12
1274	Genetic mechanisms of allopolyploid speciation through hybrid genome doubling: novel insights from wheat ( <i>Triticum</i> and <i>Aegilops</i> ) studies. <b>2014</b> , 309, 199-258	11
1273	Assessment and refinement of eukaryotic gene structure prediction with gene-structure-aware multiple protein sequence alignment. <b>2014</b> , 15, 189	21
1272	Paleo-evolutionary plasticity of plant disease resistance genes. <b>2014</b> , 15, 187	38
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1270	Genome and transcriptome sequencing identifies breeding targets in the orphan crop tef ( <i>Eragrostis tef</i> ). <b>2014</b> , 15, 581	98
1269	Mating system shifts and transposable element evolution in the plant genus <i>Capsella</i> . <b>2014</b> , 15, 602	41
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1267	Comparative mapping in the Poaceae family reveals translocations in the complex polyploid genome of sugarcane. <b>2014</b> , 14, 190	25
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1262	Maize early endosperm growth and development: from fertilization through cell type differentiation. <b>2014</b> , 101, 1259-74		51
1261	Transposon-mediated mutation of CYP76AD3 affects betalain synthesis and produces variegated flowers in four o'clock ( <i>Mirabilis jalapa</i> ). <b>2014</b> , 171, 1586-90		18
1260	Plant systems biology: insights, advances and challenges. <b>2014</b> , 240, 33-54		55
1259	Analysis of DNA methylation of perennial ryegrass under drought using the methylation-sensitive amplification polymorphism (MSAP) technique. <b>2014</b> , 289, 1075-84		45
1258	Diversity and evolution of transposable elements in <i>Arabidopsis</i> . <b>2014</b> , 22, 203-16		23
1257	Quantitative trait loci for resistance to Maize rayado fino virus. <b>2014</b> , 34, 989-996		7
1256	A transposable element insertion disturbed starch synthase gene SSIIb in maize. <b>2014</b> , 34, 1159-1171		2
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1254	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , <b>2014</b> , 345, 1251788	33.3	1129
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1252	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , <b>2014</b> , 345, 1250091	33.3	225
1251	One code to find them all: a perl tool to conveniently parse RepeatMasker output files. <b>2014</b> , 5, 13		80
1250	Blood from 'junk': the LTR chimeric transcript Pu.2 promotes erythropoiesis. <b>2014</b> , 5, 15		0
1249	Small auxin upregulated RNA (SAUR) gene family in maize: identification, evolution, and its phylogenetic comparison with <i>Arabidopsis</i> , rice, and sorghum. <b>2014</b> , 56, 133-50		68
1248	Genome sequence of the cultivated cotton <i>Gossypium arboreum</i> . <b>2014</b> , 46, 567-72		613
1247	Genomewide analysis of LATERAL ORGAN BOUNDARIES Domain gene family in <i>Zea mays</i> . <b>2014</b> , 93, 79-91		33
1246	A Survey Sequence Comparison of <i>Saccharum</i> Genotypes Reveals Allelic Diversity Differences. <b>2014</b> , 7, 71-83		13

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1243	Identification and functional characterization of bidirectional gene pairs and their intergenic regions in maize. <b>2014</b> , 15, 338	9
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1237	Genetic architecture of rind penetrometer resistance in two maize recombinant inbred line populations. <b>2014</b> , 14, 152	23
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1234	eQTL mapping of transposon silencing reveals a position-dependent stable escape from epigenetic silencing and transposition of AtMu1 in the Arabidopsis lineage. <b>2014</b> , 26, 3261-71	8
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1231	Identification and characterization of MOR-CP, a cysteine protease induced by ozone and developmental senescence in maize ( <i>Zea mays</i> L.) leaves. <b>2014</b> , 108, 245-50	1
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1227	Efficient screening of long terminal repeat retrotransposons that show high insertion polymorphism via high-throughput sequencing of the primer binding site. <b>2014</b> , 57, 245-52	17
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1099	Expression analysis of genes encoding mitogen-activated protein kinases in maize provides a key link between abiotic stress signaling and plant reproduction. <b>2015</b> , 15, 107-20	18
1098	Persistence of subgenomes in paleopolyploid cotton after 60 my of evolution. <b>2015</b> , 32, 1063-71	57
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1077	Discovery of novel genes derived from transposable elements using integrative genomic analysis. <b>2015</b> , 32, 1487-506	38
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1026	Next-generation sequencing (NGS) transcriptomes reveal association of multiple genes and pathways contributing to secondary metabolites accumulation in tuberous roots of <i>Aconitum heterophyllum</i> Wall. <b>2015</b> , 242, 239-58	27
1025	Comprehensive analysis of CCCH-type zinc finger family genes facilitates functional gene discovery and reflects recent allopolyploidization event in tetraploid switchgrass. <b>2015</b> , 16, 129	28
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98	Calibration of a crop growth model in APSIM for 15 publicly available corn hybrids in North America.	0
97	Comprehensive collection of genes and comparative analysis of full-length transcriptome sequences from Japanese larch ( <i>Larix kaempferi</i> ) and Kuril larch ( <i>Larix gmelinii</i> var. <i>japonica</i> ). <b>2022</b> , 22,	0
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