

Joachim Messing

List of Publications by Year in descending order

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220
papers

65,262
citations

9786

73
h-index

1900

208
g-index

253
all docs

253
docs citations

253
times ranked

24598
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mpl8 and pUC19 vectors. <i>Gene</i> , 1985, 33, 103-119.	2.2	16,607
2	The pUC plasmids, an M13mp7-derived system for insertion mutagenesis and sequencing with synthetic universal primers. <i>Gene</i> , 1982, 19, 259-268.	2.2	6,753
3	[2] New M13 vectors for cloning. <i>Methods in Enzymology</i> , 1983, 101, 20-78.	1.0	5,560
4	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	27.8	3,365
5	A new pair of M13 vectors for selecting either DNA strand of double-digest restriction fragments. <i>Gene</i> , 1982, 19, 269-276.	2.2	3,300
6	A system for shotgun DNA sequencing. <i>Nucleic Acids Research</i> , 1981, 9, 309-321.	14.5	2,907
7	[1] Production of single-stranded plasmid DNA. <i>Methods in Enzymology</i> , 1987, 153, 3-11.	1.0	2,717
8	Construction of improved M13 vectors using oligodeoxynucleotide-directed mutagenesis. <i>Gene</i> , 1983, 26, 101-106.	2.2	2,690
9	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642
10	Genome sequencing and analysis of the model grass Brachypodium distachyon. <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
11	CARPEL FACTORY, a Dicer Homolog, and HEN1, a Novel Protein, Act in microRNA Metabolism in Arabidopsis thaliana. <i>Current Biology</i> , 2002, 12, 1484-1495.	3.9	1,125
12	Filamentous coliphage M13 as a cloning vehicle: insertion of a HindII fragment of the lac regulatory region in M13 replicative form in vitro.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1977, 74, 3642-3646.	7.1	724
13	The making of strand-specific M13 probes. <i>Gene</i> , 1982, 17, 271-277.	2.2	721
14	New pUC-derived cloning vectors with different selectable markers and DNA replication origins. <i>Gene</i> , 1991, 100, 189-194.	2.2	498
15	Close Split of Sorghum and Maize Genome Progenitors. <i>Genome Research</i> , 2004, 14, 1916-1923.	5.5	443
16	The complete nucleotide sequence of an infectious clone of cauliflower mosaic virus by M13mp7 shotgun sequencing. <i>Nucleic Acids Research</i> , 1981, 9, 2871-2888.	14.5	437
17	The nucleotide sequence of the maize controlling element Activator. <i>Cell</i> , 1984, 37, 635-643.	28.9	330
18	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	14.5	295

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19	Pattern of diversity in the genomic region near the maize domestication gene <i>tb1</i> . Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 700-707.	7.1	294
20	Sequence composition and genome organization of maize. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14349-14354.	7.1	290
21	Methylation of single-stranded DNA in vitro introduces new restriction endonuclease cleavage sites. Nature, 1978, 272, 375-377.	27.8	284
22	Physical and Genetic Structure of the Maize Genome Reflects Its Complex Evolutionary History. PLoS Genetics, 2007, 3, e123.	3.5	270
23	The <i>Spirodela polyrhiza</i> genome reveals insights into its neotenus reduction fast growth and aquatic lifestyle. Nature Communications, 2014, 5, 3311.	12.8	262
24	A versatile primer for DNA sequencing in the M13mp2 cloning system. Gene, 1980, 10, 69-73.	2.2	254
25	Gene expression of a gene family in maize based on noncollinear haplotypes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9055-9060.	7.1	248
26	In-Depth View of Structure, Activity, and Evolution of Rice Chromosome 10. Science, 2003, 300, 1566-1569.	12.6	245
27	Gene movement by Helitron transposons contributes to the haplotype variability of maize. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9068-9073.	7.1	244
28	Steady-state transposon mutagenesis in inbred maize. Plant Journal, 2005, 44, 52-61.	5.7	234
29	Structural Analysis of Plant Genes. Annual Review of Plant Physiology, 1986, 37, 439-466.	10.9	233
30	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . Genome Research, 2007, 17, 175-183.	5.5	218
31	A New Opaque Variant of Maize by a Single Dominant RNA-Interference-Inducing Transgene. Genetics, 2003, 165, 387-397.	2.9	188
32	Gene Loss and Movement in the Maize Genome. Genome Research, 2004, 14, 1924-1931.	5.5	186
33	Ancestral grass karyotype reconstruction unravels new mechanisms of genome shuffling as a source of plant evolution. Genome Research, 2010, 20, 1545-1557.	5.5	180
34	Nucleotide sequence of naturally occurring deletion mutants of cauliflower mosaic virus. Virology, 1981, 112, 678-685.	2.4	165
35	The primary structure of a plant storage protein: zein. Nucleic Acids Research, 1981, 9, 5163-5174.	14.5	163
36	Structure and Architecture of the Maize Genome. Plant Physiology, 2005, 139, 1612-1624.	4.8	159

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37	The pFF plasmids: cassettes utilising CaMV sequences for expression of foreign genes in plants. <i>Journal of Biotechnology</i> , 1990, 14, 333-344.	3.8	151
38	Reconstruction of monocotyledonous proto-chromosomes reveals faster evolution in plants than in animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14908-14913.	7.1	144
39	The "inner circle"™ of the cereal genomes. <i>Current Opinion in Plant Biology</i> , 2009, 12, 119-125.	7.1	143
40	Sweet sorghum as a model system for bioenergy crops. <i>Current Opinion in Biotechnology</i> , 2012, 23, 323-329.	6.6	141
41	High-Throughput Sequencing of Three Lemnoideae (Duckweeds) Chloroplast Genomes from Total DNA. <i>PLoS ONE</i> , 2011, 6, e24670.	2.5	139
42	DNA barcoding of the Lemnaceae, a family of aquatic monocots. <i>BMC Plant Biology</i> , 2010, 10, 205.	3.6	137
43	Sequence analysis of zein cDNAs obtained by an efficient mRNA cloning method. <i>Nucleic Acids Research</i> , 1983, 11, 4891-4906.	14.5	136
44	Maize endosperm-specific transcription factors O2 and PBF network the regulation of protein and starch synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10842-10847.	7.1	136
45	Primary structure of the <i>Escherichia coli</i> ribonucleoside diphosphate reductase operon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1984, 81, 4294-4297.	7.1	132
46	Mosaic Organization of Orthologous Sequences in Grass Genomes. <i>Genome Research</i> , 2002, 12, 1549-1555.	5.5	130
47	Amplification of prolamin storage protein genes in different subfamilies of the Poaceae. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1397-1412.	3.6	126
48	Apple II software for M13 shotgun DNA sequencing. <i>Nucleic Acids Research</i> , 1982, 10, 39-49.	14.5	124
49	Sequence-indexed mutations in maize using the UniformMu transposon-tagging population. <i>BMC Genomics</i> , 2007, 8, 116.	2.8	124
50	Cloning and Sequencing of the Ribosomal RNA Genes in Maize: The 17S Region. <i>DNA and Cell Biology</i> , 1984, 3, 31-40.	5.2	121
51	Î³-Zeins are essential for endosperm modification in quality protein maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12810-12815.	7.1	120
52	Sequence, Regulation, and Evolution of the Maize 22-kD Î± Zein Gene Family. <i>Genome Research</i> , 2001, 11, 1817-1825.	5.5	118
53	NAC-type transcription factors regulate accumulation of starch and protein in maize seeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11223-11228.	7.1	114
54	Isolation and sequence of a gene encoding a methionine-rich 10-kDa zein protein from maize. <i>Gene</i> , 1988, 71, 359-370.	2.2	112

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55	Palaeogenomics of plants: synteny-based modelling of extinct ancestors. <i>Trends in Plant Science</i> , 2010, 15, 479-487.	8.8	111
56	Plant Gene Structure. , 1983, , 211-227.		111
57	Proteome balancing of the maize seed for higher nutritional value. <i>Frontiers in Plant Science</i> , 2014, 5, 240.	3.6	109
58	Variegated phenotype and developmental methylation changes of a maize allele originating from epimutation.. <i>Genetics</i> , 1994, 136, 1121-1141.	2.9	109
59	Allele-specific parental imprinting of <i>dzr1</i> , a posttranscriptional regulator of zein accumulation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 4867-4871.	7.1	108
60	Uneven chromosome contraction and expansion in the maize genome. <i>Genome Research</i> , 2006, 16, 1241-1251.	5.5	105
61	Mutations of the 22- and 27-kD zein promoters affect transactivation by the Opaque-2 protein.. <i>Plant Cell</i> , 1992, 4, 701-709.	6.6	102
62	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020, 11, 884.	12.8	101
63	Organization of the prolamin gene family provides insight into the evolution of the maize genome and gene duplications in grass species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14330-14335.	7.1	99
64	RNA Interference-Mediated Change in Protein Body Morphology and Seed Opacity through Loss of Different Zein Proteins. <i>Plant Physiology</i> , 2010, 153, 337-347.	4.8	97
65	Geminiviruses and Their Uses as Extrachromosomal Replicons. <i>Annual Review of Plant Biology</i> , 1994, 45, 79-112.	14.3	96
66	Increasing maize seed methionine by mRNA stability. <i>Plant Journal</i> , 2002, 30, 395-402.	5.7	94
67	The formation of mRNA 3'-ends in plants. <i>Plant Journal</i> , 1995, 8, 323-329.	5.7	87
68	Whole-Genome Validation of High-Information-Content Fingerprinting. <i>Plant Physiology</i> , 2005, 139, 27-38.	4.8	86
69	Differential expression of a gene for a methionine-rich storage protein in maize. <i>Molecular Genetics and Genomics</i> , 1988, 211, 477-484.	2.4	82
70	Organization and variability of the maize genome. <i>Current Opinion in Plant Biology</i> , 2006, 9, 157-163.	7.1	82
71	Genetic analysis of opaque2 modifier loci in quality protein maize. <i>Theoretical and Applied Genetics</i> , 2008, 117, 157-170.	3.6	81
72	Endosperm-specific demethylation and activation of specific alleles of β -tubulin genes of <i>Zea mays</i> L.. <i>Molecular Genetics and Genomics</i> , 1995, 246, 716-722.	2.4	80

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73	Characterization of the Maize Endosperm Transcriptome and Its Comparison to the Rice Genome. <i>Genome Research</i> , 2004, 14, 1932-1937.	5.5	80
74	Genome diversity in <i>Brachypodium distachyon</i> : deep sequencing of highly diverse inbred lines. <i>Plant Journal</i> , 2014, 79, 361-374.	5.7	80
75	Dynamics of chloroplast genomes in green plants. <i>Genomics</i> , 2015, 106, 221-231.	2.9	80
76	Apple II Computer Software for DNA and Protein Sequence Data. <i>DNA and Cell Biology</i> , 1983, 2, 31-35.	5.2	77
77	A somatic gene rearrangement contributing to genetic diversity in maize.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 7809-7813.	7.1	77
78	Plant evolution and environmental adaptation unveiled by long-read whole-genome sequencing of <i>Spirodela</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18893-18899.	7.1	76
79	Dual Regulated RNA Transport Pathways to the Cortical Region in Developing Rice Endosperm. <i>Plant Cell</i> , 2003, 15, 2265-2272.	6.6	69
80	Nucleotide sequence analysis of a zein genomic clone with a short open reading frame. <i>Gene</i> , 1984, 28, 113-118.	2.2	66
81	Characterization of Three Maize Bacterial Artificial Chromosome Libraries toward Anchoring of the Physical Map to the Genetic Map Using High-Density Bacterial Artificial Chromosome Filter Hybridization. <i>Plant Physiology</i> , 2002, 130, 1686-1696.	4.8	65
82	Primary structure of a genomic zein sequence of maize.. <i>EMBO Journal</i> , 1982, 1, 1337-1342.	7.8	64
83	DNA Rearrangement in Orthologous Orp Regions of the Maize, Rice and Sorghum Genomes. <i>Genetics</i> , 2005, 170, 1209-1220.	2.9	62
84	Contiguous Genomic DNA Sequence Comprising the 19-kD Zein Gene Family from Maize. <i>Plant Physiology</i> , 2002, 130, 1626-1635.	4.8	61
85	On the Tetraploid Origin of the Maize Genome. <i>Comparative and Functional Genomics</i> , 2004, 5, 281-284.	2.0	61
86	Zeon-1, a member of a new maize retrotransposon family. <i>Molecular Genetics and Genomics</i> , 1995, 248, 471-480.	2.4	59
87	Mutation in the seed storage protein kafirin creates a high-value food trait in sorghum. <i>Nature Communications</i> , 2013, 4, 2217.	12.8	59
88	Sequence analysis and comparison of cDNAs of the zein multigene family .. <i>EMBO Journal</i> , 1982, 1, 1329-1335.	7.8	58
89	Transcriptome and metabolome reveal distinct carbon allocation patterns during internode sugar accumulation in different sorghum genotypes. <i>Plant Biotechnology Journal</i> , 2019, 17, 472-487.	8.3	57
90	Cloning and Sequencing of Restriction Fragments Generated by <i>Eco</i> RI*. <i>DNA and Cell Biology</i> , 1982, 1, 109-115.	5.2	56

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91	Amplicons of maize zein genes are conserved within genic but expanded and constricted in intergenic regions. <i>Plant Journal</i> , 1998, 15, 211-220.	5.7	56
92	Cloning in M13 phage or how to use biology at its best. <i>Gene</i> , 1991, 100, 3-12.	2.2	55
93	Replication of a geminivirus derived shuttle vector in maize endosperm cells. <i>Nucleic Acids Research</i> , 1991, 19, 371-377.	14.5	54
94	Determinants of the high-methionine trait in wild and exotic germplasm may have escaped selection during early cultivation of maize. <i>Plant Journal</i> , 1995, 8, 359-368.	5.7	54
95	Balancing of sulfur storage in maize seed. <i>BMC Plant Biology</i> , 2012, 12, 77.	3.6	54
96	Engineering sulfur storage in maize seed proteins without apparent yield loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11386-11391.	7.1	53
97	3'-end processing of the maize 27 kDa zein mRNA. <i>Plant Journal</i> , 1993, 4, 535-544.	5.7	52
98	Characterization of the small RNA component of the transcriptome from grain and sweet sorghum stems. <i>BMC Genomics</i> , 2011, 12, 356.	2.8	52
99	Maize glutamine synthetase cDNAs: isolation by direct genetic selection in <i>Escherichia coli</i> . <i>Genetics</i> , 1988, 120, 1111-1123.	2.9	52
100	Structure and Evolution of the r/b Chromosomal Regions in Rice, Maize and Sorghum Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY542311, AF466202, AF466203, and AY542310. <i>Genetics</i> , 2005, 169, 891-906.	2.9	51
101	Tissue-specific DNase I-sensitive sites of the maize P gene and their changes upon epimutation. <i>Plant Journal</i> , 1995, 7, 797-807.	5.7	50
102	Analysis of tandem gene copies in maize chromosomal regions reconstructed from long sequence reads. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7949-7956.	7.1	50
103	High frequency callus formation from maize protoplasts. <i>Theoretical and Applied Genetics</i> , 1985, 71, 344-350.	3.6	48
104	Genetic analysis of methionine-rich storage protein accumulation in maize. <i>Theoretical and Applied Genetics</i> , 1989, 78, 761-767.	3.6	48
105	Trans replication and high copy numbers of wheat dwarf virus vectors in maize cells. <i>Nucleic Acids Research</i> , 1992, 20, 4047-4054.	14.5	47
106	Identification of a transcriptional activator-binding element in the 27-kilodalton zein promoter, the -300 element. <i>Molecular and Cellular Biology</i> , 1994, 14, 4350-4359.	2.3	47
107	Maize haplotype with a helitron-amplified cytidine deaminase gene copy. <i>BMC Genetics</i> , 2006, 7, 52.	2.7	46
108	Analysis of ADP-glucose pyrophosphorylase expression during turion formation induced by abscisic acid in <i>Spirodela polyrhiza</i> (greater duckweed). <i>BMC Plant Biology</i> , 2012, 12, 5.	3.6	46

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109	A homologous expression system for cloned zein genes. Theoretical and Applied Genetics, 1991, 82, 93-100.	3.6	45
110	Long-read sequencing reveals genomic structural variations that underlie creation of quality protein maize. Nature Communications, 2020, 11, 17.	12.8	45
111	Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. Functional and Integrative Genomics, 2004, 4, 102-117.	3.5	44
112	Comparative Sequence Analysis of the Sorghum RphRegion and the Maize Rp1 Resistance Gene Complex. Plant Physiology, 2002, 130, 1728-1738.	4.8	42
113	Inhibition of Minicircular DNA Replication in Escherichia coli 15 by Rifampicin. Nature: New Biology, 1972, 238, 202-203.	4.5	41
114	RNA Interference Can Rebalance the Nitrogen Sink of Maize Seeds without Losing Hard Endosperm. PLoS ONE, 2012, 7, e32850.	2.5	41
115	Importance of anchor genomes for any plant genome project. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 2017-2020.	7.1	40
116	The map-based genome sequence of <i>Sorghum polyrhiza</i> aligned with its chromosomes, a reference for karyotype evolution. New Phytologist, 2016, 209, 354-363.	7.3	40
117	A new allele of the duplicated 27kD zein locus of maize generated by homologous recombination. Nucleic Acids Research, 1991, 19, 3325-3330.	14.5	39
118	Expression of the sorghum 10-member kafirin gene cluster in maize endosperm. Nucleic Acids Research, 2004, 32, e189-e189.	14.5	39
119	Genomic Imprinting in Plants. Results and Problems in Cell Differentiation, 1999, 25, 23-40.	0.7	39
120	Retrotranspositions in orthologous regions of closely related grass species. BMC Evolutionary Biology, 2006, 6, 62.	3.2	38
121	Screen of Genes Linked to High-Sugar Content in Stems by Comparative Genomics. Rice, 2008, 1, 166-176.	4.0	38
122	Overexpression of serine acetyltransferase in maize leaves increases seed-specific methionine-rich zeins. Plant Biotechnology Journal, 2018, 16, 1057-1067.	8.3	37
123	Efficiency in cloning and sequencing using the single-stranded bacteriophage M13. Journal of Biotechnology, 1984, 1, 253-264.	3.8	36
124	Post-transcriptional regulation of methionine content in maize kernels. Molecular Genetics and Genomics, 1991, 225, 331-339.	2.4	36
125	Highly clustered zein gene sequences reveal evolutionary history of the multigene family. Genomics, 1991, 10, 719-732.	2.9	35
126	The nucleotide sequence of a mitochondrial replicon from maize. Gene, 1985, 38, 131-138.	2.2	34

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127	The Maize High-Lysine Mutant opaque7 Is Defective in an Acyl-CoA Synthetase-Like Protein. <i>Genetics</i> , 2011, 189, 1271-1280.	2.9	34
128	Differential Gene Expression and Epiregulation of Alpha Zein Gene Copies in Maize Haplotypes. <i>PLoS Genetics</i> , 2011, 7, e1002131.	3.5	34
129	RNA-Seq transcriptome analysis of <i>Spirodela</i> dormancy without reproduction. <i>BMC Genomics</i> , 2014, 15, 60.	2.8	34
130	Asymmetric Localization of Seed Storage Protein RNAs to Distinct Subdomains of the Endoplasmic Reticulum in Developing Maize Endosperm Cells. <i>Plant and Cell Physiology</i> , 2004, 45, 1830-1837.	3.1	33
131	Diverged Copies of the Seed Regulatory Opaque-2 Gene by a Segmental Duplication in the Progenitor Genome of Rice, Sorghum, and Maize. <i>Molecular Plant</i> , 2008, 1, 760-769.	8.3	33
132	Characterization of the maize prolamin box-binding factor-1 (PBF-1) and its role in the developmental regulation of the zein multigene family1Published in conjunction with A Wisconsin Gathering Honoring Waclaw Szybalski on occasion of his 75th year and 20 years of Editorship-in-Chief of <i>Gene</i> , 10â€“11 August 1997, University of Wisconsin, Madison, WI, USA.1. <i>Gene</i> , 1998, 223, 321-332.	2.2	32
133	Rapid Divergence of Prolamin Gene Promoters of Maize After Gene Amplification and Dispersal. <i>Genetics</i> , 2012, 192, 507-519.	2.9	32
134	The Mitochondrial Genome of an Aquatic Plant, <i>Spirodela polyrhiza</i> . <i>PLoS ONE</i> , 2012, 7, e46747.	2.5	31
135	Repression of the high-methionine zein gene in the maize inbred line Mo17. <i>Plant Journal</i> , 1993, 3, 221-229.	5.7	30
136	Non-Mendelian regulation and allelic variation of methionine-rich delta-zein genes in maize. <i>Theoretical and Applied Genetics</i> , 2009, 119, 721-731.	3.6	30
137	Sequence variation between alleles reveals two types of copy correction at the 27-kDa zein locus of maize. <i>Genomics</i> , 1991, 11, 849-856.	2.9	28
138	Change of Gene Structure and Function by Non-Homologous End-Joining, Homologous Recombination, and Transposition of DNA. <i>PLoS Genetics</i> , 2009, 5, e1000516.	3.5	28
139	M13 Cloning Vehicles: Their Contribution to DNA Sequencing. , 1993, 23, 9-22.		27
140	Novel Genetic Selection System for Quantitative Trait Loci of Quality Protein Maize. <i>Genetics</i> , 2011, 188, 1019-1022.	2.9	27
141	PacBio sequencing of gene families â€” A case study with wheat gluten genes. <i>Gene</i> , 2014, 533, 541-546.	2.2	27
142	RNA Editing in Chloroplasts of <i>Spirodela polyrhiza</i> , an Aquatic Monocotyledonous Species. <i>PLoS ONE</i> , 2015, 10, e0140285.	2.5	27
143	Maize <i>defective kernel</i> mutant generated by insertion of a <i>Ds</i> element in a gene encoding a highly conserved TTI2 cochaperone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5165-5170.	7.1	25
144	Primary structure of a genomic zein sequence of maize. <i>EMBO Journal</i> , 1982, 1, 1337-42.	7.8	25

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145	Dynamic Gene Copy Number Variation in Collinear Regions of Grass Genomes. <i>Molecular Biology and Evolution</i> , 2012, 29, 861-871.	8.9	24
146	Characterization of a Meiotic Crossover in Maize Identified by a Restriction Fragment Length Polymorphism-Based Method. <i>Genetics</i> , 1996, 143, 1771-1783.	2.9	24
147	Region-Specific <i>Cis</i> - and <i>Trans</i> -Acting Factors Contribute to Genetic Variability in Meiotic Recombination in Maize. <i>Genetics</i> , 1997, 146, 1101-1113.	2.9	24
148	Sequence analysis and comparison of cDNAs of the zein multigene family. <i>EMBO Journal</i> , 1982, 1, 1329-35.	7.8	24
149	Analysis of EST sequences suggests recent origin of allotetraploid colonial and creeping bentgrasses. <i>Molecular Genetics and Genomics</i> , 2007, 278, 197-209.	2.1	22
150	RFLP mapping of the maize <i>dzr1</i> locus, which regulates methionine-rich 10 kDa zein accumulation. <i>Molecular Genetics and Genomics</i> , 1995, 246, 707-715.	2.4	21
151	Efficacy of clone fingerprinting methodologies. <i>Genomics</i> , 2007, 89, 160-165.	2.9	21
152	Genome-wide histone acetylation correlates with active transcription in maize. <i>Genomics</i> , 2015, 106, 214-220.	2.9	21
153	Status of duckweed genomics and transcriptomics. <i>Plant Biology</i> , 2015, 17, 10-15.	3.8	21
154	Discovery of MicroRNA169 Gene Copies in Genomes of Flowering Plants through Positional Information. <i>Genome Biology and Evolution</i> , 2013, 5, 402-417.	2.5	20
155	Phage M13 for the treatment of Alzheimer and Parkinson disease. <i>Gene</i> , 2016, 583, 85-89.	2.2	20
156	Identification of a Transcriptional Activator-Binding Element in the 27-Kilodalton Zein Promoter, the α "300 Element. <i>Molecular and Cellular Biology</i> , 1994, 14, 4350-4359.	2.3	20
157	Mutations of the 22- and 27-kD Zein Promoters Affect Transactivation by the Opaque-2 Protein. <i>Plant Cell</i> , 1992, 4, 701.	6.6	19
158	Molecular Markers for Sweet Sorghum Based on Microarray Expression Data. <i>Rice</i> , 2009, 2, 129-142.	4.0	19
159	Grass Genome Structure and Evolution. , 2008, 4, 41-56.		18
160	Chromatin organisation in duckweed interphase nuclei in relation to the nuclear <i>scp</i> DNA content. <i>Plant Biology</i> , 2015, 17, 120-124.	3.8	18
161	Interchromosomal Recombination in <i>Zea mays</i> . <i>Genetics</i> , 1998, 150, 1229-1237.	2.9	18
162	Manipulation and expression of the maize zein storage proteins in <i>Escherichia coli</i> . <i>Journal of Biotechnology</i> , 1985, 2, 157-175.	3.8	17

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163	Maternal effect on high methionine levels in hybrid corn. <i>Journal of Biotechnology</i> , 1991, 21, 229-237.	3.8	17
164	Divergence of gene regulation through chromosomal rearrangements. <i>BMC Genomics</i> , 2010, 11, 678.	2.8	17
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