Joachim Messing

List of Publications by Year in Descending Order

219 papers	56,946 citations	69 h-index	238 g-index
253 ext. papers	59,237 ext. citations	8.6 avg, IF	7.76 L-index

#	Paper	IF	Citations
219	Flowering and Seed Production across the Lemnaceae. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	5
218	Natural variants of Egliadin peptides within wheat proteins with reduced toxicity in coeliac disease. *British Journal of Nutrition*, **2020**, 123, 1382-1389	3.6	1
217	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. *Nature Communications*, **2020**, 11, 884	17.4	51
216	Towards coeliac-safe bread. *Plant Biotechnology Journal*, **2020**, 18, 1056-1065	11.6	0
215	Long-read sequencing reveals genomic structural variations that underlie creation of quality protein maize. *Nature Communications*, **2020**, 11, 17	17.4	19
214	Plant evolution and environmental adaptation unveiled by long-read whole-genome sequencing of. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 18893-18899	11.5	35
213	NAC-type transcription factors regulate accumulation of starch and protein in maize seeds. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 11223-11228	11.5	47
212	Post-transcriptional adaptation of the aquatic plant Spirodela polyrhiza under stress and hormonal stimuli. *Plant Journal*, **2019**, 98, 1120-1133	6.9	5
211	Transcriptome and metabolome reveal distinct carbon allocation patterns during internode sugar accumulation in different sorghum genotypes. *Plant Biotechnology Journal*, **2019**, 17, 472-487	11.6	25
210	Common metabolic networks contribute to carbon sink strength of sorghum internodes: implications for bioenergy improvement. *Biotechnology for Biofuels*, **2019**, 12, 274	7.8	3
209	Candidate gene identification of existing or induced mutations with pipelines applicable to large genomes. *Plant Journal*, **2019**, 97, 673-682	6.9	9
208	Genetic diversity and evolution of reduced sulfur storage during domestication of maize. *Plant Journal*, **2018**, 94, 943-955	6.9	4
207	Overexpression of serine acetyltransferase in maize leaves increases seed-specific methionine-rich zeins. *Plant Biotechnology Journal*, **2018**, 16, 1057-1067	11.6	18
206	A new high-throughput assay for determining soluble sugar in sorghum internode-extracted juice. *Planta*, **2018**, 248, 785-793	4.7	7
205	PacBio for Haplotyping in Gene Families. *Methods in Molecular Biology*, **2017**, 1551, 61-71	1.4	
204	Maize mutant generated by insertion of a element in a gene encoding a highly conserved TTI2 cochaperone. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 5165-5170	11.5	18
203	Engineering sulfur storage in maize seed proteins without apparent yield loss. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 11386-11391	11.5	37

202	Quality Protein Maize Based on Reducing Sulfur in Leaf Cells. *Genetics*, **2017**, 207, 1687-1697	4	7
201	TTT and PIKK Complex Genes Reverted to Single Copy Following Polyploidization and Retain Function Despite Massive Retrotransposition in Maize. *Frontiers in Plant Science*, **2017**, 8, 1723	6.2	3
200	Maize seed storage proteins. **2017**, 175-189		7
199	Maize endosperm-specific transcription factors O2 and PBF network the regulation of protein and starch synthesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 10842-7	11.5	83
198	Genome-wide analysis of pentatricopeptide-repeat proteins of an aquatic plant. *Planta*, **2016**, 244, 893-9	4.7	8
197	Teff, an Orphan Cereal in the Chloridoideae, Provides Insights into the Evolution of Storage Proteins in Grasses. *Genome Biology and Evolution*, **2016**, 8, 1712-21	3.9	11
196	Analysis of tandem gene copies in maize chromosomal regions reconstructed from long sequence reads. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 7949-56	11.5	33
195	Phage M13 for the treatment of Alzheimer and Parkinson disease. *Gene*, **2016**, 583, 85-89	3.8	17
194	Locus- and Site-Specific DNA Methylation of 19 kDa Zein Genes in Maize. *PLoS ONE*, **2016**, 11, e0146416	3.7	2
193	The map-based genome sequence of Spirodela polyrhiza aligned with its chromosomes, a reference for karyotype evolution. *New Phytologist*, **2016**, 209, 354-63	9.8	33
192	Dynamics of chloroplast genomes in green plants. *Genomics*, **2015**, 106, 221-31	4.3	58
191	Chromatin organisation in duckweed interphase nuclei in relation to the nuclear DNA content. *Plant Biology*, **2015**, 17 Suppl 1, 120-4	3.7	15
190	Status of duckweed genomics and transcriptomics. *Plant Biology*, **2015**, 17 Suppl 1, 10-5	3.7	18
189	Molecular Genetics of Corn. *Agronomy*, **2015**, 389-429	0.8	1
188	RNA Editing in Chloroplasts of Spirodela polyrhiza, an Aquatic Monocotelydonous Species. *PLoS ONE*, **2015**, 10, e0140285	3.7	23
187	Genome-wide histone acetylation correlates with active transcription in maize. *Genomics*, **2015**, 106, 214-20	4.3	15
186	The Wukong Terminal-Repeat Retrotransposon in Miniature (TRIM) Elements in Diverse Maize Germplasm. *G3: Genes, Genomes, Genetics*, **2015**, 5, 1585-92	3.2	6
185	Evolution of gene expression after gene amplification. *Genome Biology and Evolution*, **2015**, 7, 1303-12	3.9	5

184	RNA-Seq transcriptome analysis of Spirodela dormancy without reproduction. *BMC Genomics*, **2014**, 15, 60	4.5	27
183	Defining the Role of prolamin-box binding factor1 Gene During Maize Domestication. *Journal of Heredity*, **2014**, 105, 576-582	2.4	13
182	PacBio sequencing of gene families - a case study with wheat gluten genes. *Gene*, **2014**, 533, 541-6	3.8	24
181	Genome diversity in Brachypodium distachyon: deep sequencing of highly diverse inbred lines. *Plant Journal*, **2014**, 79, 361-74	6.9	58
180	Proteome balancing of the maize seed for higher nutritional value. *Frontiers in Plant Science*, **2014**, 5, 240	6.2	64
179	The Spirodela polyrhiza genome reveals insights into its neotenous reduction fast growth and aquatic lifestyle. *Nature Communications*, **2014**, 5, 3311	17.4	180
178	Microbiology Spurred Massively Parallel Genomic Sequencing and Biotechnology. *Microbe Magazine* , **2014**, 9, 271-277		3
177	Divergent properties of prolamins in wheat and maize. *Planta*, **2013**, 237, 1465-73	4.7	9
176	Evolution, Structure, and Function of Prolamin Storage Proteins **2013**, 138-158		4
175	Mutation in the seed storage protein kafirin creates a high-value food trait in sorghum. *Nature Communications*, **2013**, 4, 2217	17.4	44
174	Paramutagenicity of a p1 epiallele in maize. *Theoretical and Applied Genetics*, **2013**, 126, 159-77	6	14
173	Epiallele biogenesis in maize. *Gene*, **2013**, 516, 8-23	3.8	11
172	Genomic resources for gene discovery, functional genome annotation, and evolutionary studies of maize and its close relatives. *Genetics*, **2013**, 195, 723-37	4	13
171	Discovery of MicroRNA169 gene copies in genomes of flowering plants through positional information. *Genome Biology and Evolution*, **2013**, 5, 402-17	3.9	17
170	Balancing of sulfur storage in maize seed. *BMC Plant Biology*, **2012**, 12, 77	5.3	40
169	Sweet sorghum as a model system for bioenergy crops. *Current Opinion in Biotechnology*, **2012**, 23, 323-9	11.4	107
168	RNA interference can rebalance the nitrogen sink of maize seeds without losing hard endosperm. *PLoS ONE*, **2012**, 7, e32850	3.7	34
167	Analysis of ADP-glucose pyrophosphorylase expression during turion formation induced by abscisic acid in Spirodela polyrhiza (greater duckweed). *BMC Plant Biology*, **2012**, 12, 5	5.3	34

166	Rapid divergence of prolamin gene promoters of maize after gene amplification and dispersal. *Genetics*, **2012**, 192, 507-19	4	25
165	Dynamic gene copy number variation in collinear regions of grass genomes. *Molecular Biology and Evolution*, **2012**, 29, 861-71	8.3	21
164	The mitochondrial genome of an aquatic plant, Spirodela polyrhiza. *PLoS ONE*, **2012**, 7, e46747	3.7	28
163	Miniature Inverted-Repeat Transposable Element Identification and Genetic Marker Development in Agrostis. *Crop Science*, **2011**, 51, 854-861	2.4	8
162	Characterization of the small RNA component of the transcriptome from grain and sweet sorghum stems. *BMC Genomics*, **2011**, 12, 356	4.5	46
161	The maize high-lysine mutant opaque7 is defective in an acyl-CoA synthetase-like protein. *Genetics*, **2011**, 189, 1271-80	4	31
160	Novel genetic selection system for quantitative trait loci of quality protein maize. *Genetics*, **2011**, 188, 1019-22	4	25
159	Differential gene expression and epiregulation of alpha zein gene copies in maize haplotypes. *PLoS Genetics*, **2011**, 7, e1002131	6	30
158	High-throughput sequencing of three Lemnoideae (duckweeds) chloroplast genomes from total DNA. *PLoS ONE*, **2011**, 6, e24670	3.7	96
157	Genome sequencing and analysis of the model grass Brachypodium distachyon. *Nature*, **2010**, 463, 763-85	0.4	1399
156	Rescue of a dominant mutant with RNA interference. *Genetics*, **2010**, 186, 1493-6	4	6
155	Gamma-zeins are essential for endosperm modification in quality protein maize. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 12810-5	11.5	92
154	Palaeogenomics of plants: synteny-based modelling of extinct ancestors. *Trends in Plant Science*, **2010**, 15, 479-87	13.1	103
153	RNA interference-mediated change in protein body morphology and seed opacity through loss of different zein proteins. *Plant Physiology*, **2010**, 153, 337-47	6.6	76
152	Ancestral grass karyotype reconstruction unravels new mechanisms of genome shuffling as a source of plant evolution. *Genome Research*, **2010**, 20, 1545-57	9.7	136
151	Divergence of gene regulation through chromosomal rearrangements. *BMC Genomics*, **2010**, 11, 678	4.5	15
150	DNA barcoding of the Lemnaceae, a family of aquatic monocots. *BMC Plant Biology*, **2010**, 10, 205	5.3	94
149	Synergy of two reference genomes for the grass family. *Plant Physiology*, **2009**, 149, 117-24	6.6	6

148	Change of gene structure and function by non-homologous end-joining, homologous recombination, and transposition of DNA. *PLoS Genetics*, **2009**, 5, e1000516	6	23
147	The Inner circle of the cereal genomes. *Current Opinion in Plant Biology*, **2009**, 12, 119-25	9.9	128
146	Molecular Markers for Sweet Sorghum Based on Microarray Expression Data. *Rice*, **2009**, 2, 129-142	5.8	16
145	Non-Mendelian regulation and allelic variation of methionine-rich delta-zein genes in maize. *Theoretical and Applied Genetics*, **2009**, 119, 721-31	6	22
144	Amplification of prolamin storage protein genes in different subfamilies of the Poaceae. *Theoretical and Applied Genetics*, **2009**, 119, 1397-412	6	99
143	The Sorghum bicolor genome and the diversification of grasses. *Nature*, **2009**, 457, 551-6	50.4	2200
142	Reconstruction of monocotelydoneous proto-chromosomes reveals faster evolution in plants than in animals. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 14908-13	11.5	125
141	The Structure of the Maize Genome. *Biotechnology in Agriculture and Forestry*, **2009**, 213-230		
140	The Polyploid Origin of Maize **2009**, 221-238		4
139	Methylation-sensitive linking libraries enhance gene-enriched sequencing of complex genomes and map DNA methylation domains. *BMC Genomics*, **2008**, 9, 621	4.5	8
138	Grass genome structure and evolution. *Genome Dynamics*, **2008**, 4, 41-56		16
137	Organization of the prolamin gene family provides insight into the evolution of the maize genome and gene duplications in grass species. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 14330-5	11.5	88
136	Diverged copies of the seed regulatory Opaque-2 gene by a segmental duplication in the progenitor genome of rice, sorghum, and maize. *Molecular Plant*, **2008**, 1, 760-9	14.4	24
135	Genetic analysis of opaque2 modifier loci in quality protein maize. *Theoretical and Applied Genetics*, **2008**, 117, 157-70	6	69
134	Screen of Genes Linked to High-Sugar Content in Stems by Comparative Genomics. *Rice*, **2008**, 1, 166-176	5.8	33
133	The Rice Annotation Project Database (RAP-DB): 2008 update. *Nucleic Acids Research*, **2008**, 36, D1028-33	30.1	262
132	Sequence-indexed mutations in maize using the UniformMu transposon-tagging population. *BMC Genomics*, **2007**, 8, 116	4.5	91
131	Analysis of EST sequences suggests recent origin of allotetraploid colonial and creeping bentgrasses. *Molecular Genetics and Genomics*, **2007**, 278, 197-209	3.1	18

130	Physical and genetic structure of the maize genome reflects its complex evolutionary history. *PLoS Genetics*, **2007**, 3, e123	6	234
129	Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana. *Genome Research*, **2007**, 17, 175-83	9.7	200
128	Efficacy of clone fingerprinting methodologies. *Genomics*, **2007**, 89, 160-5	4.3	20
127	Organization and variability of the maize genome. *Current Opinion in Plant Biology*, **2006**, 9, 157-63	9.9	72
126	Retrotranspositions in orthologous regions of closely related grass species. *BMC Evolutionary Biology*, **2006**, 6, 62	3	35
125	Uneven chromosome contraction and expansion in the maize genome. *Genome Research*, **2006**, 16, 1241-54	9.7	95
124	Maize haplotype with a helitron-amplified cytidine deaminase gene copy. *BMC Genetics*, **2006**, 7, 52	2.6	41
123	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, 9068-73	11.5	222
122	Steady-state transposon mutagenesis in inbred maize. *Plant Journal*, **2005**, 44, 52-61	6.9	184
121	The map-based sequence of the rice genome. *Nature*, **2005**, 436, 793-800	50.4	2923
120	Structure and evolution of the r/b chromosomal regions in rice, maize and sorghum. *Genetics*, **2005**, 169, 891-906	4	44
119	Structure and architecture of the maize genome. *Plant Physiology*, **2005**, 139, 1612-24	6.6	130
118	DNA rearrangement in orthologous orp regions of the maize, rice and sorghum genomes. *Genetics*, **2005**, 170, 1209-20	4	55
117	Whole-genome validation of high-information-content fingerprinting. *Plant Physiology*, **2005**, 139, 27-38	6.6	81
116	Expression of the sorghum 10-member kafirin gene cluster in maize endosperm. *Nucleic Acids Research*, **2004**, 32, e189	20.1	36
115	Pattern of diversity in the genomic region near the maize domestication gene tb1. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 700-7	11.5	240
114	Asymmetric localization of seed storage protein RNAs to distinct subdomains of the endoplasmic reticulum in developing maize endosperm cells. *Plant and Cell Physiology*, **2004**, 45, 1830-7	4.9	29
113	Gene loss and movement in the maize genome. *Genome Research*, **2004**, 14, 1924-31	9.7	144

112	Close split of sorghum and maize genome progenitors. *Genome Research*, **2004**, 14, 1916-23	9.7	347
111	Characterization of the maize endosperm transcriptome and its comparison to the rice genome. *Genome Research*, **2004**, 14, 1932-7	9.7	68
110	Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. *Functional and Integrative Genomics*, **2004**, 4, 102-17	3.8	40
109	On the tetraploid origin of the maize genome. *Comparative and Functional Genomics*, **2004**, 5, 281-4		54
108	Sequence composition and genome organization of maize. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 14349-54	11.5	247
107	In-depth view of structure, activity, and evolution of rice chromosome 10. *Science*, **2003**, 300, 1566-9	33.3	234
106	Dual regulated RNA transport pathways to the cortical region in developing rice endosperm. *Plant Cell*, **2003**, 15, 2265-72	11.6	62
105	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, 9055-60	11.5	219
104	A new opaque variant of maize by a single dominant RNA-interference-inducing transgene. *Genetics* , **2003**, 165, 387-97	4	162
103	CARPEL FACTORY, a Dicer homolog, and HEN1, a novel protein, act in microRNA metabolism in Arabidopsis thaliana. *Current Biology*, **2002**, 12, 1484-95	6.3	999
102	Frequent genic rearrangements in two regions of grass genomes identified by comparative sequence analysis. *Comparative and Functional Genomics*, **2002**, 3, 165-6		5
101	Increasing maize seed methionine by mRNA stability. *Plant Journal*, **2002**, 30, 395-402	6.9	79
100	Mosaic organization of orthologous sequences in grass genomes. *Genome Research*, **2002**, 12, 1549-55	9.7	114
99	Comparative sequence analysis of the sorghum Rph region and the maize Rp1 resistance gene complex. *Plant Physiology*, **2002**, 130, 1728-38	6.6	41
98	Contiguous genomic DNA sequence comprising the 19-kD zein gene family from maize. *Plant Physiology*, **2002**, 130, 1626-35	6.6	52
97	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. *Plant Physiology*, **2002**, 130, 1686-96	6.6	60
96	The universal primers and the shotgun DNA sequencing method. *Methods in Molecular Biology*, **2001**, 167, 13-31	1.4	3
95	Do plants have more genes than humans?. *Trends in Plant Science*, **2001**, 6, 195-6	13.1	9

94	Sequence, regulation, and evolution of the maize 22-kD alpha zein gene family. *Genome Research*, **2001**, 11, 1817-25	9.7	100
93	Genomic imprinting in plants. *Results and Problems in Cell Differentiation*, **1999**, 25, 23-40	1.4	29
92	Amplicons of maize zein genes are conserved within genic but expanded and constricted in intergenic regions. *Plant Journal*, **1998**, 15, 211-20	6.9	53
91	Characterization of the maize prolamin box-binding factor-1 (PBF-1) and its role in the developmental regulation of the zein multigene family. *Gene*, **1998**, 223, 321-32	3.8	28
90	Modulation of gene expression by DNA-protein and protein-protein interactions in the promoter region of the zein multigene family. *Gene*, **1998**, 223, 333-45	3.8	9
89	A Plant Genome Initiative. *Plant Cell*, **1998**, 10, 488-493	11.6	13
88	A Plant Genome Initiative. *Plant Cell*, **1998**, 10, 488	11.6	
87	Plant science in lac: A continuation of using tools from Escherichia coli in studying gene function in heterologous systems. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 93-4	11.5	6
86	Importance of anchor genomes for any plant genome project. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 2017-20	11.5	36
85	Interchromosomal recombination in Zea mays. *Genetics*, **1998**, 150, 1229-37	4	13
84	Dynamic genome organization and gene evolution by positive selection in geminivirus (Geminiviridae). *Molecular Biology and Evolution*, **1997**, 14, 1114-24	8.3	11
83	Region-specific cis- and trans-acting factors contribute to genetic variability in meiotic recombination in maize. *Genetics*, **1997**, 146, 1101-13	4	20
82	Cloning single-stranded DNA. *Molecular Biotechnology*, **1996**, 5, 39-47	3	5
81	Characterization of a meiotic crossover in maize identified by a restriction fragment length polymorphism-based method. *Genetics*, **1996**, 143, 1771-83	4	21
80	Tissue-specific DNase I-sensitive sites of the maize P gene and their changes upon epimutation. *Plant Journal*, **1995**, 7, 797-807	6.9	46
79	The formation of mRNA 3Sends in plants. *Plant Journal*, **1995**, 8, 323-9	6.9	73
78	Determinants of the high-methionine trait in wild and exotic germplasm may have escaped selection during early cultivation of maize. *Plant Journal*, **1995**, 8, 359-68	6.9	48
77	RFLP mapping of the maize dzr1 locus, which regulates methionine-rich 10 kDa zein accumulation. *Molecular Genetics and Genomics*, **1995**, 246, 707-15		13

76	Endosperm-specific demethylation and activation of specific alleles of alpha-tubulin genes of Zea mays L. *Molecular Genetics and Genomics*, **1995**, 246, 716-22		70
75	Zeon-1, a member of a new maize retrotransposon family. *Molecular Genetics and Genomics*, **1995**, 248, 471-80		49
74	Tissue-specific DNase I-sensitive sites of the maize P gene and their changes upon epimutation. *Plant Journal*, **1995**, 7, 797-807	6.9	14
73	Geminiviruses and Their Uses as Extrachromosomal Replicons. *Annual Review of Plant Biology*, **1994**, 45, 79-112		72
72	Sequence and spatial requirements for the tissue- and species-independent 3Send processing mechanism of plant mRNA. *Molecular and Cellular Biology*, **1994**, 14, 6829-38	4.8	14
71	Allele-specific parental imprinting of dzr1, a posttranscriptional regulator of zein accumulation. *Proceedings of the National Academy of Sciences of the United States of America*, **1994**, 91, 4867-71	11.5	92
70	Identification of a transcriptional activator-binding element in the 27-kilodalton zein promoter, the -300 element. *Molecular and Cellular Biology*, **1994**, 14, 4350-9	4.8	42
69	Variegated phenotype and developmental methylation changes of a maize allele originating from epimutation. *Genetics*, **1994**, 136, 1121-41	4	85
68	Identification of a transcriptional activator-binding element in the 27-kilodalton zein promoter, the -300 element. *Molecular and Cellular Biology*, **1994**, 14, 4350-4359	4.8	19
67	Sequence and spatial requirements for the tissue- and species-independent 3Send processing mechanism of plant mRNA. *Molecular and Cellular Biology*, **1994**, 14, 6829-6838	4.8	6
66	M13 cloning vehicles. Their contribution to DNA sequencing. *Methods in Molecular Biology*, **1993**, 23, 9-22	1.4	18
65	3Send processing of the maize 27 kDa zein mRNA. *Plant Journal*, **1993**, 4, 535-44	6.9	42
64	Repression of the high-methionine zein gene in the maize inbred line Mo17. *Plant Journal*, **1993**, 3, 221-229	6.9	27
63	Manipulation of amino acid balance in maize seeds. *Genetic Engineering*, **1993**, 15, 109-30		11
62	Mutations of the 22- and 27-kD zein promoters affect transactivation by the Opaque-2 protein. *Plant Cell*, **1992**, 4, 701-9	11.6	87
61	Trans replication and high copy numbers of wheat dwarf virus vectors in maize cells. *Nucleic Acids Research*, **1992**, 20, 4047-54	20.1	38
60	Mutations of the 22- and 27-kD Zein Promoters Affect Transactivation by the Opaque-2 Protein. *Plant Cell*, **1992**, 4, 701	11.6	9
59	Cytological aberrations in maize populations exhibiting unusual recombinational behaviour. *Cytobios*, **1992**, 70, 203-8		1

58	A homologous expression system for cloned zein genes. *Theoretical and Applied Genetics*, **1991**, 82, 93-100	6	40
57	Post-transcriptional regulation of methionine content in maize kernels. *Molecular Genetics and Genomics*, **1991**, 225, 331-9		31
56	A new allele of the duplicated 27kD zein locus of maize generated by homologous recombination. *Nucleic Acids Research*, **1991**, 19, 3325-30	20.1	33
55	Replication of a geminivirus derived shuttle vector in maize endosperm cells. *Nucleic Acids Research* , **1991**, 19, 371-7	20.1	50
54	Sequence variation between alleles reveals two types of copy correction at the 27-kDa zein locus of maize. *Genomics*, **1991**, 11, 849-56	4.3	21
53	Highly clustered zein gene sequences reveal evolutionary history of the multigene family. *Genomics* , **1991**, 10, 719-32	4.3	31
52	Maternal effect on high methionine levels in hybrid corn. *Journal of Biotechnology*, **1991**, 21, 229-237	3.7	13
51	New pUC-derived cloning vectors with different selectable markers and DNA replication origins. *Gene*, **1991**, 100, 189-94	3.8	459
50	Cloning in M13 phage or how to use biology at its best. *Gene*, **1991**, 100, 3-12	3.8	37
49	A somatic gene rearrangement contributing to genetic diversity in maize. *Proceedings of the National Academy of Sciences of the United States of America*, **1990**, 87, 7809-13	11.5	59
48	The pFF plasmids: cassettes utilising CaMV sequences for expression of foreign genes in plants. *Journal of Biotechnology*, **1990**, 14, 333-44	3.7	135
47	Genetic analysis of methionine-rich storage protein accumulation in maize. *Theoretical and Applied Genetics*, **1989**, 78, 761-7	6	42
46	Differential expression of a gene for a methionine-rich storage protein in maize. *Molecular Genetics and Genomics*, **1988**, 211, 477-84		67
45	Cloned genes of storage proteins. *Plant Molecular Biology Reporter*, **1988**, 6, 22-22	1.7	4
44	Isolation and sequence of a gene encoding a methionine-rich 10-kDa zein protein from maize. *Gene*, **1988**, 71, 359-70	3.8	101
43	Maize glutamine synthetase cDNAs: isolation by direct genetic selection in Escherichia coli. *Genetics* , **1988**, 120, 1111-23	4	48
42	A method for cloning full-length cDNA in plasmid vectors. *Methods in Enzymology*, **1987**, 154, 28-41	1.7	7
41	Production of single-stranded plasmid DNA. *Methods in Enzymology*, **1987**, 153, 3-11	1.7	2282

40	Structural Analysis of Plant Genes. *Annual Review of Plant Physiology*, **1986**, 37, 439-466		209
39	High frequency callus formation from maize protoplasts. *Theoretical and Applied Genetics*, **1985**, 71, 344-50		47
38	The nucleotide sequence of a mitochondrial replicon from maize. *Gene*, **1985**, 38, 131-8	3.8	31
37	Manipulation and expression of the maize zein storage proteins in Escherichia coli. *Journal of Biotechnology*, **1985**, 2, 157-175	3.7	16
36	Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors. *Gene*, **1985**, 33, 103-19	3.8	14870
35	Cloning and sequencing of the ribosomal RNA genes in maize: the 17S region. *DNA and Cell Biology*, **1984**, 3, 31-40		108
34	Data storage and handling of plant nucleotide sequences. *Plant Molecular Biology Reporter*, **1984**, 2, 32-35	1.57	4
33	Nucleotide sequence analysis of a zein genomic clone with a short open reading frame. *Gene*, **1984**, 28, 113-8	3.8	62
32	The nucleotide sequence of the maize controlling element Activator. *Cell*, **1984**, 37, 635-43	56.2	287
31	Efficiency in cloning and sequencing using the single-stranded bacteriophage M13. *Journal of Biotechnology*, **1984**, 1, 253-264	3.7	34
30	Primary structure of the Escherichia coli ribonucleoside diphosphate reductase operon. *Proceedings of the National Academy of Sciences of the United States of America*, **1984**, 81, 4294-7	11.5	113
29	Construction of improved M13 vectors using oligodeoxynucleotide-directed mutagenesis. *Gene*, **1983**, 26, 101-6	3.8	2419
28	New M13 vectors for cloning. *Methods in Enzymology*, **1983**, 101, 20-78	1.7	4726
27	Apple II computer software for DNA and protein sequence data. *DNA and Cell Biology*, **1983**, 2, 31-5		74
26	Sequence analysis of zein cDNAs obtained by an efficient mRNA cloning method. *Nucleic Acids Research*, **1983**, 11, 4891-906	20.1	127
25	The manipulation of zein genes to improve the nutritional value of corn. *Trends in Biotechnology*, **1983**, 1, 54-59	15.1	10
24	In vitro DNA synthesis as a tool to analyze and alter genes. *Basic Life Sciences*, **1983**, 25, 9-15		1
23	Plant Gene Structure **1983**, 211-227		92

22	Apple II software for M13 shotgun DNA sequencing. *Nucleic Acids Research*, **1982**, 10, 39-49	20.1	114
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