Michael Freeling

List of Publications by Year in Descending Order

70 papers	8,078 citations	41 h-index	77 g-index
77 ext. papers	9,876 ext. citations	9.9 avg, IF	6.13 L-index

#	Paper	IF	Citations
70	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. *Genome Research*, **2021**, 31, 799-810	9.7	4
69	Impacts of allopolyploidization and structural variation on intraspecific diversification in Brassica rapa. *Genome Biology*, **2021**, 22, 166	18.3	12
68	Evolution of Conserved Noncoding Sequences in Arabidopsis thaliana. *Molecular Biology and Evolution*, **2021**, 38, 2692-2703	8.3	3
67	qTeller: A tool for comparative multi-genomic gene expression analysis. *Bioinformatics*, **2021**,	7.2	2
66	Abundant expression of maternal siRNAs is a conserved feature of seed development. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 15305-15315	11.5	17
65	Origin and evolution of the octoploid strawberry genome. *Nature Genetics*, **2019**, 51, 541-547	36.3	242
64	Maternal components of RNA-directed DNA methylation are required for seed development in Brassica rapa. *Plant Journal*, **2018**, 94, 575-582	6.9	38
63	Gene retention, fractionation and subgenome differences in polyploid plants. *Nature Plants*, **2018**, 4, 258-268	11.5	123
62	Picking up the Ball at the K/Pg Boundary: The Distribution of Ancient Polyploidies in the Plant Phylogenetic Tree as a Spandrel of Asexuality with Occasional Sex. *Plant Cell*, **2017**, 29, 202-206	11.6	22
61	Epigenetic regulation of subgenome dominance following whole genome triplication in Brassica rapa. *New Phytologist*, **2016**, 211, 288-99	9.8	55
60	Advances in understanding cis regulation of the plant gene with an emphasis on comparative genomics. *Current Opinion in Plant Biology*, **2015**, 27, 141-7	9.9	17
59	The pineapple genome and the evolution of CAM photosynthesis. *Nature Genetics*, **2015**, 47, 1435-42	36.3	309
58	A Solution to the C-Value Paradox and the Function of Junk DNA: The Genome Balance Hypothesis. *Molecular Plant*, **2015**, 8, 899-910	14.4	31
57	Fractionation and subfunctionalization following genome duplications: mechanisms that drive gene content and their consequences. *Current Opinion in Genetics and Development*, **2015**, 35, 110-8	4.9	51
56	Single-molecule sequencing of the desiccation-tolerant grass Oropetium thomaeum. *Nature*, **2015**, 527, 508-11	50.4	208
55	Co-option of the polarity gene network shapes filament morphology in angiosperms. *Scientific Reports*, **2014**, 4, 6194	4.9	21
54	Two evolutionarily distinct classes of paleopolyploidy. *Molecular Biology and Evolution*, **2014**, 31, 448-54	8.3	119

53	The most deeply conserved noncoding sequences in plants serve similar functions to those in vertebrates despite large differences in evolutionary rates. *Plant Cell*, **2014**, 26, 946-61	11.6	30
52	Origin, inheritance, and gene regulatory consequences of genome dominance in polyploids. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 5283-8	11.5	132
51	A Short Course on the Impact of Gene Duplications on the Evolution of Novelty. *Advances in Botanical Research*, **2014**, 69, 335-361	2.2	1
50	Automated conserved non-coding sequence (CNS) discovery reveals differences in gene content and promoter evolution among grasses. *Frontiers in Plant Science*, **2013**, 4, 170	6.2	23
49	The fate of Arabidopsis thaliana homeologous CNSs and their motifs in the Paleohexaploid Brassica rapa. *Genome Biology and Evolution*, **2013**, 5, 646-60	3.9	8
48	Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. *Current Opinion in Plant Biology*, **2012**, 15, 131-9	9.9	145
47	Maize (Zea Mays) as a Model for Studying the Impact of Gene and Regulatory Sequence Loss Following Whole-Genome Duplication **2012**, 137-145		4
46	Altered patterns of fractionation and exon deletions in Brassica rapa support a two-step model of paleohexaploidy. *Genetics*, **2012**, 190, 1563-74	4	129
45	Evidence of function for conserved noncoding sequences in Arabidopsis thaliana. *New Phytologist*, **2012**, 193, 241-252	9.8	13
44	Escape from preferential retention following repeated whole genome duplications in plants. *Frontiers in Plant Science*, **2012**, 3, 94	6.2	52
43	High-resolution mapping of open chromatin in the rice genome. *Genome Research*, **2012**, 22, 151-62	9.7	168
42	Dose-sensitivity, conserved non-coding sequences, and duplicate gene retention through multiple tetraploidies in the grasses. *Frontiers in Plant Science*, **2011**, 2, 2	6.2	27
41	The genome of the mesopolyploid crop species Brassica rapa. *Nature Genetics*, **2011**, 43, 1035-9	36.3	1490
40	Screening synteny blocks in pairwise genome comparisons through integer programming. *BMC Bioinformatics*, **2011**, 12, 102	3.6	99
39	Inna Golubovskaya: the life of a geneticist studying meiosis. *Genetics*, **2011**, 188, 491-8	4	8
38	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 4069-74	11.5	462
37	Genes identified by visible mutant phenotypes show increased bias toward one of two subgenomes of maize. *PLoS ONE*, **2011**, 6, e17855	3.7	117
36	Epigenetic reprogramming during vegetative phase change in maize. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 22184-9	11.5	60

35	Transposed genes in Arabidopsis are often associated with flanking repeats. *PLoS Genetics*, **2010**, 6, e1000949	6	43
34	Following tetraploidy in maize, a short deletion mechanism removed genes preferentially from one of the two homologs. *PLoS Biology*, **2010**, 8, e1000409	9.7	202
33	Conserved noncoding sequences (CNSs) in higher plants. *Current Opinion in Plant Biology*, **2009**, 12, 126-32	9.9	65
32	Bias in plant gene content following different sorts of duplication: tandem, whole-genome, segmental, or by transposition. *Annual Review of Plant Biology*, **2009**, 60, 433-53	30.7	563
31	How to usefully compare homologous plant genes and chromosomes as DNA sequences. *Plant Journal*, **2008**, 53, 661-73	6.9	344
30	Many or most genes in Arabidopsis transposed after the origin of the order Brassicales. *Genome Research*, **2008**, 18, 1924-37	9.7	131
29	Finding and comparing syntenic regions among Arabidopsis and the outgroups papaya, poplar, and grape: CoGe with rosids. *Plant Physiology*, **2008**, 148, 1772-81	6.6	285
28	The Value of Nonmodel Genomes and an Example Using SynMap Within CoGe to Dissect the Hexaploidy that Predates the Rosids. *Tropical Plant Biology*, **2008**, 1, 181-190	1.6	166
27	G-boxes, bigfoot genes, and environmental response: characterization of intragenomic conserved noncoding sequences in Arabidopsis. *Plant Cell*, **2007**, 19, 1441-57	11.6	38
26	Arabidopsis intragenomic conserved noncoding sequence. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 3348-53	11.5	52
25	Following tetraploidy in an Arabidopsis ancestor, genes were removed preferentially from one homeolog leaving clusters enriched in dose-sensitive genes. *Genome Research*, **2006**, 16, 934-46	9.7	321
24	Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity. *Genome Research*, **2006**, 16, 805-14	9.7	355
23	Genomic duplication, fractionation and the origin of regulatory novelty. *Genetics*, **2004**, 166, 935-45	4	150
22	Genomic Duplication, Fractionation and the Origin of Regulatory Novelty. *Genetics*, **2004**, 166, 935-945	4	17
21	Utility and distribution of conserved noncoding sequences in the grasses. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 6147-51	11.5	84
20	Expression of a mutant maize gene in the ventral leaf epidermis is sufficient to signal a switch of the leaf's dorsoventral axis. *Development (Cambridge)*, **2002**, 129, 4581-4589	6.6	64
19	Grasses as a single genetic system: reassessment 2001. *Plant Physiology*, **2001**, 125, 1191-7	6.6	63
18	Mutator transposase is widespread in the grasses. *Plant Physiology*, **2001**, 125, 1293-303	6.6	56

17	Genetic Evidence and the Origin of Maize. *Latin American Antiquity*, **2001**, 12, 84-86	0.5	34
16	Biomechanical analysis of the Rolled (RLD) leaf phenotype of maize. *American Journal of Botany*, **2000**, 87, 625-633	2.7	16
15	Mutator-suppressible alleles of rough sheath1 and liguleless3 in maize reveal multiple mechanisms for suppression. *Genetics*, **2000**, 154, 437-46	4	22
14	Ectopic expression of the maize homeobox gene liguleless3 alters cell fates in the leaf. *Plant Physiology*, **1999**, 119, 651-62	6.6	72
13	Regulatory changes as a consequence of transposon insertion. *Genesis*, **1999**, 25, 291-6		48
12	The maize rough sheath2 gene and leaf development programs in monocot and dicot plants. *Science*, **1999**, 284, 154-6	33.3	265
11	Functional analysis of deletion derivatives of the maize transposon MuDR delineates roles for the MURA and MURB proteins. *Genetics*, **1999**, 151, 331-41	4	50
10	Regulatory changes as a consequence of transposon insertion **1999**, 25, 291		1
9	Lax Midrib1-O, A systemic, heterochronic mutant of maize. *American Journal of Botany*, **1998**, 85, 481-491	1.7	14
8	The maize gene empty pericarp-2 is required for progression beyond early stages of embryogenesis. *Plant Journal*, **1997**, 12, 901-909	6.9	14
7	Acquisition of identity in the developing leaf. *Annual Review of Cell and Developmental Biology*, **1996**, 12, 257-304	12.6	86
6	Genetic analysis of mutations that alter cell fates in maize leaves: dominant Liguleless mutations. *Genesis*, **1996**, 18, 198-222		44
5	Maize mutants and variants altering developmental time and their heterochronic interactions. *BioEssays*, **1992**, 14, 227-36	4.1	47
4	Expression and distribution of cytosolic 6-phosphogluconate dehydrogenase isozymes in maize. *Biochemical Genetics*, **1992**, 30, 233-246	2.4	
3	Cell lineage and its consequences in higher plants. *Plant Journal*, **1991**, 1, 3-8	6.9	69
2	HAIRY-SHEATH FRAYED #1-O: A SYSTEMIC, HETEROCHRONIC MUTANT OF MAIZE THAT SPECIFIES SLOW DEVELOPMENTAL STAGE TRANSITIONS. *American Journal of Botany*, **1991**, 78, 747-765	2.7	13
1	HAIRY-SHEATH FRAYED #1-O: A SYSTEMIC, HETEROCHRONIC MUTANT OF MAIZE THAT SPECIFIES SLOW DEVELOPMENTAL STAGE TRANSITIONS **1991**, 78, 747		14