

Michael Freeling

List of Publications by Year in descending order

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73
papers

10,976
citations

66343

42
h-index

88630

70
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77
all docs

77
docs citations

77
times ranked

9849
citing authors

#	ARTICLE	IF	CITATIONS
1	A cluster of transcripts identifies a transition stage initiating leafy head growth in heading morphotypes of <i>Brassica</i> . <i>Plant Journal</i> , 2022, 110, 688-706.	5.7	7
2	Ovule siRNAs methylate protein-coding genes in trans. <i>Plant Cell</i> , 2022, 34, 3647-3664.	6.6	17
3	Evolution of Conserved Noncoding Sequences in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 2692-2703.	8.9	14
4	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	5.5	21
5	Impacts of allopolyploidization and structural variation on intraspecific diversification in <i>Brassica rapa</i> . <i>Genome Biology</i> , 2021, 22, 166.	8.8	80
6	qTeller: a tool for comparative multi-genomic gene expression analysis. <i>Bioinformatics</i> , 2021, 38, 236-242.	4.1	15
7	Abundant expression of maternal siRNAs is a conserved feature of seed development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15305-15315.	7.1	49
8	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019, 51, 541-547.	21.4	469
9	Maternal components of <i>RNA-directed DNA</i> methylation are required for seed development in <i>Brassica rapa</i> . <i>Plant Journal</i> , 2018, 94, 575-582.	5.7	72
10	Gene retention, fractionation and subgenome differences in polyploid plants. <i>Nature Plants</i> , 2018, 4, 258-268.	9.3	257
11	FAIR: A Call to Make Published Data More Findable, Accessible, Interoperable, and Reusable. <i>Molecular Plant</i> , 2018, 11, 1105-1108.	8.3	31
12	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. <i>Plant Cell</i> , 2017, 29, 202-206.	6.6	33
13	Epigenetic regulation of subgenome dominance following whole genome triplication in <i>Brassica rapa</i> . <i>New Phytologist</i> , 2016, 211, 288-299.	7.3	100
14	A Solution to the C-Value Paradox and the Function of Junk DNA: The Genome Balance Hypothesis. <i>Molecular Plant</i> , 2015, 8, 899-910.	8.3	36
15	Fractionation and subfunctionalization following genome duplications: mechanisms that drive gene content and their consequences. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 110-118.	3.3	94
16	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . <i>Nature</i> , 2015, 527, 508-511.	27.8	291
17	Advances in understanding cis regulation of the plant gene with an emphasis on comparative genomics. <i>Current Opinion in Plant Biology</i> , 2015, 27, 141-147.	7.1	20
18	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472

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19	A Short Course on the Impact of Gene Duplications on the Evolution of Novelty. <i>Advances in Botanical Research</i> , 2014, 69, 335-361.	1.1	1
20	Two Evolutionarily Distinct Classes of Paleopolyploidy. <i>Molecular Biology and Evolution</i> , 2014, 31, 448-454.	8.9	159
21	The Most Deeply Conserved Noncoding Sequences in Plants Serve Similar Functions to Those in Vertebrates Despite Large Differences in Evolutionary Rates. <i>Plant Cell</i> , 2014, 26, 946-961.	6.6	38
22	Origin, inheritance, and gene regulatory consequences of genome dominance in polyploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5283-5288.	7.1	172
23	Co-option of the polarity gene network shapes filament morphology in angiosperms. <i>Scientific Reports</i> , 2014, 4, 6194.	3.3	37
24	Automated conserved non-coding sequence (CNS) discovery reveals differences in gene content and promoter evolution among grasses. <i>Frontiers in Plant Science</i> , 2013, 4, 170.	3.6	32
25	The Fate of <i>Arabidopsis thaliana</i> Homeologous CNSs and Their Motifs in the Paleohexaploid <i>Brassica rapa</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 646-660.	2.5	8
26	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 94.	3.6	73
27	High-resolution mapping of open chromatin in the rice genome. <i>Genome Research</i> , 2012, 22, 151-162.	5.5	205
28	Maize (<i>Zea Mays</i>) as a Model for Studying the Impact of Gene and Regulatory Sequence Loss Following Whole-Genome Duplication. , 2012, , 137-145.		5
29	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. <i>Genetics</i> , 2012, 190, 1563-1574.	2.9	163
30	Evidence of function for conserved noncoding sequences in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2012, 193, 241-252.	7.3	13
31	Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. <i>Current Opinion in Plant Biology</i> , 2012, 15, 131-139.	7.1	194
32	Dose-Sensitivity, Conserved Non-Coding Sequences, and Duplicate Gene Retention Through Multiple Tetraploidies in the Grasses. <i>Frontiers in Plant Science</i> , 2011, 2, 2.	3.6	35
33	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
34	Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011, 12, 102.	2.6	142
35	Inna Golubovskaya: The Life of a Geneticist Studying Meiosis. <i>Genetics</i> , 2011, 188, 491-498.	2.9	13
36	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4069-4074.	7.1	644

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37	Genes Identified by Visible Mutant Phenotypes Show Increased Bias toward One of Two Subgenomes of Maize. <i>PLoS ONE</i> , 2011, 6, e17855.	2.5	145
38	Epigenetic reprogramming during vegetative phase change in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 22184-22189.	7.1	69
39	Transposed Genes in Arabidopsis Are Often Associated with Flanking Repeats. <i>PLoS Genetics</i> , 2010, 6, e1000949.	3.5	52
40	Following Tetraploidy in Maize, a Short Deletion Mechanism Removed Genes Preferentially from One of the Two Homeologs. <i>PLoS Biology</i> , 2010, 8, e1000409.	5.6	260
41	Conserved noncoding sequences (CNSs) in higher plants. <i>Current Opinion in Plant Biology</i> , 2009, 12, 126-132.	7.1	75
42	Bias in Plant Gene Content Following Different Sorts of Duplication: Tandem, Whole-Genome, Segmental, or by Transposition. <i>Annual Review of Plant Biology</i> , 2009, 60, 433-453.	18.7	838
43	The Value of Nonmodel Genomes and an Example Using SynMap Within CoGe to Dissect the Hexaploidy that Predates the Rosids. <i>Tropical Plant Biology</i> , 2008, 1, 181-190.	1.9	193
44	How to usefully compare homologous plant genes and chromosomes as DNA sequences. <i>Plant Journal</i> , 2008, 53, 661-673.	5.7	469
45	Many or most genes in <i>Arabidopsis</i> transposed after the origin of the order Brassicales. <i>Genome Research</i> , 2008, 18, 1924-1937.	5.5	157
46	Finding and Comparing Syntenic Regions among Arabidopsis and the Outgroups Papaya, Poplar, and Grape: CoGe with Rosids. <i>Plant Physiology</i> , 2008, 148, 1772-1781.	4.8	376
47	G-Boxes, Bigfoot Genes, and Environmental Response: Characterization of Intragenomic Conserved Noncoding Sequences in Arabidopsis. <i>Plant Cell</i> , 2007, 19, 1441-1457.	6.6	42
48	Arabidopsis intragenomic conserved noncoding sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3348-3353.	7.1	55
49	Following tetraploidy in an Arabidopsis ancestor, genes were removed preferentially from one homeolog leaving clusters enriched in dose-sensitive genes. <i>Genome Research</i> , 2006, 16, 934-946.	5.5	393
50	Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity. <i>Genome Research</i> , 2006, 16, 805-814.	5.5	421
51	Genomic Duplication, Fractionation and the Origin of Regulatory Novelty. <i>Genetics</i> , 2004, 166, 935-945.	2.9	205
52	Genomic Duplication, Fractionation and the Origin of Regulatory Novelty. <i>Genetics</i> , 2004, 166, 935-945.	2.9	45
53	Utility and distribution of conserved noncoding sequences in the grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6147-6151.	7.1	93
54	Expression of a mutant maize gene in the ventral leaf epidermis is sufficient to signal a switch of the leaf's dorsoventral axis. <i>Development (Cambridge)</i> , 2002, 129, 4581-4589.	2.5	76

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55	Genetic Evidence and the Origin of Maize. <i>Latin American Antiquity</i> , 2001, 12, 84-86.	0.6	39
56	Grasses as a Single Genetic System. Reassessment 2001. <i>Plant Physiology</i> , 2001, 125, 1191-1197.	4.8	78
57	Mutator Transposase Is Widespread in the Grasses. <i>Plant Physiology</i> , 2001, 125, 1293-1303.	4.8	59
58	Biomechanical analysis of the Rolled (RLD) leaf phenotype of maize. <i>American Journal of Botany</i> , 2000, 87, 625-633.	1.7	23
59	Mutator-Suppressible Alleles of rough sheath1 and liguleless3 in Maize Reveal Multiple Mechanisms for Suppression. <i>Genetics</i> , 2000, 154, 437-446.	2.9	27
60	Ectopic Expression of the Maize Homeobox Gene <i>Liguleless3</i> Alters Cell Fates in the Leaf1. <i>Plant Physiology</i> , 1999, 119, 651-662.	4.8	80
61	Regulatory changes as a consequence of transposon insertion. <i>Genesis</i> , 1999, 25, 291-296.	2.1	53
62	The Maize rough sheath2 Gene and Leaf Development Programs in Monocot and Dicot Plants. <i>Science</i> , 1999, 284, 154-156.	12.6	307
63	Regulatory changes as a consequence of transposon insertion. , 1999, 25, 291.		1
64	Functional Analysis of Deletion Derivatives of the Maize Transposon MuDR Delineates Roles for the MURA and MURB Proteins. <i>Genetics</i> , 1999, 151, 331-341.	2.9	61
65	Lax Midrib1-O, A systemic, heterochronic mutant of maize. <i>American Journal of Botany</i> , 1998, 85, 481-491.	1.7	17
66	The maize gene empty pericarp-2 is required for progression beyond early stages of embryogenesis. <i>Plant Journal</i> , 1997, 12, 901-909.	5.7	16
67	ACQUISITION OF IDENTITY IN THE DEVELOPING LEAF. <i>Annual Review of Cell and Developmental Biology</i> , 1996, 12, 257-304.	9.4	98
68	Genetic analysis of mutations that alter cell fates in maize leaves: Dominant <i>Liguleless</i> mutations. , 1996, 18, 198-222.		57
69	Maize mutants and variants altering developmental time and their heterochronic interactions. <i>BioEssays</i> , 1992, 14, 227-236.	2.5	52
70	Expression and distribution of cytosolic 6-phosphogluconate dehydrogenase isozymes in maize. <i>Biochemical Genetics</i> , 1992, 30, 233-246.	1.7	0
71	HAIRY SHEATH FRAYED #1: A SYSTEMIC, HETEROCHRONIC MUTANT OF MAIZE THAT SPECIFIES SLOW DEVELOPMENTAL STAGE TRANSITIONS. <i>American Journal of Botany</i> , 1991, 78, 747-765.	1.7	23
72	Cell lineage and its consequences in higher plants. <i>Plant Journal</i> , 1991, 1, 3-8.	5.7	81

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73	Hairy-Sheath Frayed # 1-0: A Systemic, Heterochronic Mutant of Maize that Specifies Slow Developmental Stage Transitions. American Journal of Botany, 1991, 78, 747.	1.7	17