

Michael Freeling

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5851868/michael-freeling-publications-by-citations.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011 , 43, 1035-9	36.3	1490
69	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, 433-53	30.7	563
68	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, 4069-74	11.5	462
67	Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity. <i>Genome Research</i> , 2006 , 16, 805-14	9.7	355
66	How to usefully compare homologous plant genes and chromosomes as DNA sequences. <i>Plant Journal</i> , 2008 , 53, 661-73	6.9	344
65	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, 934-46	9.7	321
64	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015 , 47, 1435-42	36.3	309
63	Finding and comparing syntenic regions among Arabidopsis and the outgroups papaya, poplar, and grape: CoGe with rosids. <i>Plant Physiology</i> , 2008 , 148, 1772-81	6.6	285
62	The maize rough sheath2 gene and leaf development programs in monocot and dicot plants. <i>Science</i> , 1999 , 284, 154-6	33.3	265
61	Origin and evolution of the octoploid strawberry genome. <i>Nature Genetics</i> , 2019 , 51, 541-547	36.3	242
60	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . <i>Nature</i> , 2015 , 527, 508-11	50.4	208
59	Following tetraploidy in maize, a short deletion mechanism removed genes preferentially from one of the two homologs. <i>PLoS Biology</i> , 2010 , 8, e1000409	9.7	202
58	High-resolution mapping of open chromatin in the rice genome. <i>Genome Research</i> , 2012 , 22, 151-62	9.7	168
57	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	1.6	166
56	Genomic duplication, fractionation and the origin of regulatory novelty. <i>Genetics</i> , 2004 , 166, 935-45	4	150
55	Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. <i>Current Opinion in Plant Biology</i> , 2012 , 15, 131-9	9.9	145
54	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, 5283-8	11.5	132

53	Many or most genes in Arabidopsis transposed after the origin of the order Brassicales. <i>Genome Research</i> , 2008 , 18, 1924-37	9.7	131
52	Altered patterns of fractionation and exon deletions in Brassica rapa support a two-step model of paleohexaploidy. <i>Genetics</i> , 2012 , 190, 1563-74	4	129
51	Gene retention, fractionation and subgenome differences in polyploid plants. <i>Nature Plants</i> , 2018 , 4, 258-268	11.5	123
50	Two evolutionarily distinct classes of paleopolyploidy. <i>Molecular Biology and Evolution</i> , 2014 , 31, 448-54	8.3	119
49	Genes identified by visible mutant phenotypes show increased bias toward one of two subgenomes of maize. <i>PLoS ONE</i> , 2011 , 6, e17855	3.7	117
48	Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011 , 12, 102	3.6	99
47	Acquisition of identity in the developing leaf. <i>Annual Review of Cell and Developmental Biology</i> , 1996 , 12, 257-304	12.6	86
46	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, 6147-51	11.5	84
45	Ectopic expression of the maize homeobox gene liguleless3 alters cell fates in the leaf. <i>Plant Physiology</i> , 1999 , 119, 651-62	6.6	72
44	Cell lineage and its consequences in higher plants. <i>Plant Journal</i> , 1991 , 1, 3-8	6.9	69
43	Conserved noncoding sequences (CNSs) in higher plants. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 126-32	3.9	65
42	Expression of a mutant maize gene in the ventral leaf epidermis is sufficient to signal a switch of the leaf dorsoventral axis. <i>Development (Cambridge)</i> , 2002 , 129, 4581-4589	6.6	64
41	Grasses as a single genetic system: reassessment 2001. <i>Plant Physiology</i> , 2001 , 125, 1191-7	6.6	63
40	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, 22184-9	11.5	60
39	Mutator transposase is widespread in the grasses. <i>Plant Physiology</i> , 2001 , 125, 1293-303	6.6	56
38	Epigenetic regulation of subgenome dominance following whole genome triplication in Brassica rapa. <i>New Phytologist</i> , 2016 , 211, 288-99	9.8	55
37	Escape from preferential retention following repeated whole genome duplications in plants. <i>Frontiers in Plant Science</i> , 2012 , 3, 94	6.2	52
36	Arabidopsis intragenomic conserved noncoding sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3348-53	11.5	52

35	Fractionation and subfunctionalization following genome duplications: mechanisms that drive gene content and their consequences. <i>Current Opinion in Genetics and Development</i> , 2015 , 35, 110-8	4.9	51
34	Functional analysis of deletion derivatives of the maize transposon MuDR delineates roles for the MURA and MURB proteins. <i>Genetics</i> , 1999 , 151, 331-41	4	50
33	Regulatory changes as a consequence of transposon insertion. <i>Genesis</i> , 1999 , 25, 291-6		48
32	Maize mutants and variants altering developmental time and their heterochronic interactions. <i>BioEssays</i> , 1992 , 14, 227-36	4.1	47
31	Genetic analysis of mutations that alter cell fates in maize leaves: dominant Liguleless mutations. <i>Genesis</i> , 1996 , 18, 198-222		44
30	Transposed genes in Arabidopsis are often associated with flanking repeats. <i>PLoS Genetics</i> , 2010 , 6, e1000949		43
29	Maternal components of RNA-directed DNA methylation are required for seed development in Brassica rapa. <i>Plant Journal</i> , 2018 , 94, 575-582	6.9	38
28	G-boxes, bigfoot genes, and environmental response: characterization of intragenomic conserved noncoding sequences in Arabidopsis. <i>Plant Cell</i> , 2007 , 19, 1441-57	11.6	38
27	Genetic Evidence and the Origin of Maize. <i>Latin American Antiquity</i> , 2001 , 12, 84-86	0.5	34
26	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	14.4	31
25	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, 946-61	11.6	30
24	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	6.2	27
23	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	6.2	23
22	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	11.6	22
21	Mutator-suppressible alleles of rough sheath1 and liguleless3 in maize reveal multiple mechanisms for suppression. <i>Genetics</i> , 2000 , 154, 437-46	4	22
20	Co-option of the polarity gene network shapes filament morphology in angiosperms. <i>Scientific Reports</i> , 2014 , 4, 6194	4.9	21
19	Advances in understanding cis regulation of the plant gene with an emphasis on comparative genomics. <i>Current Opinion in Plant Biology</i> , 2015 , 27, 141-7	9.9	17
18	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	11.5	17

17	Genomic Duplication, Fractionation and the Origin of Regulatory Novelty. <i>Genetics</i> , 2004 , 166, 935-945	4	17
16	Biomechanical analysis of the Rolled (RLD) leaf phenotype of maize. <i>American Journal of Botany</i> , 2000 , 87, 625-633	2.7	16
15	The maize gene empty pericarp-2 is required for progression beyond early stages of embryogenesis. <i>Plant Journal</i> , 1997 , 12, 901-909	6.9	14
14	Lax Midrib1-O, A systemic, heterochronic mutant of maize. <i>American Journal of Botany</i> , 1998 , 85, 481-491	1.7	14
13	HAIRY-SHEATH FRAYED #1-O: A SYSTEMIC, HETEROCHRONIC MUTANT OF MAIZE THAT SPECIFIES SLOW DEVELOPMENTAL STAGE TRANSITIONS 1991 , 78, 747		14
12	Evidence of function for conserved noncoding sequences in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2012 , 193, 241-252	9.8	13
11	HAIRY-SHEATH FRAYED #1-O: A SYSTEMIC, HETEROCHRONIC MUTANT OF MAIZE THAT SPECIFIES SLOW DEVELOPMENTAL STAGE TRANSITIONS. <i>American Journal of Botany</i> , 1991 , 78, 747-765	2.7	13
10	Impacts of allopolyploidization and structural variation on intraspecific diversification in <i>Brassica rapa</i> . <i>Genome Biology</i> , 2021 , 22, 166	18.3	12
9	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, 646-60	3.9	8
8	Inna Golubovskaya: the life of a geneticist studying meiosis. <i>Genetics</i> , 2011 , 188, 491-8	4	8
7	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		4
6	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021 , 31, 799-810	9.7	4
5	Evolution of Conserved Noncoding Sequences in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021 , 38, 2692-2703	8.3	3
4	qTeller: A tool for comparative multi-genomic gene expression analysis. <i>Bioinformatics</i> , 2021 ,	7.2	2
3	A Short Course on the Impact of Gene Duplications on the Evolution of Novelty. <i>Advances in Botanical Research</i> , 2014 , 69, 335-361	2.2	1
2	Regulatory changes as a consequence of transposon insertion 1999 , 25, 291		1
1	Expression and distribution of cytosolic 6-phosphogluconate dehydrogenase isozymes in maize. <i>Biochemical Genetics</i> , 1992 , 30, 233-246	2.4	