

# A Mark Settles

## List of Publications by Year in descending order

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48  
papers

2,114  
citations

304743

22  
h-index

243625

44  
g-index

55  
all docs

55  
docs citations

55  
times ranked

2583  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	12.8	37
2	Accelerating Biological Insight for Understudied Genes. <i>Integrative and Comparative Biology</i> , 2021, , .	2.0	2
3	Characterization of pea seed nutritional value within a diverse population of <i>Pisum sativum</i> . <i>PLoS ONE</i> , 2021, 16, e0259565.	2.5	10
4	Classification approaches for sorting maize ( <i>Zea mays</i> subsp. <i>mays</i> ) haploids using single-kernel near-infrared spectroscopy. <i>Plant Breeding</i> , 2020, 139, 1103-1112.	1.9	4
5	Engineering 6-phosphogluconate dehydrogenase improves grain yield in heat-stressed maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33177-33185.	7.1	22
6	Competitive Growth Assay of Mutagenized <i>Chlamydomonas reinhardtii</i> Compatible With the International Space Station Veggie Plant Growth Chamber. <i>Frontiers in Plant Science</i> , 2020, 11, 631.	3.6	12
7	Protein, weight, and oil prediction by single-seed near-infrared spectroscopy for selection of seed quality and yield traits in pea ( <i>Pisum sativum</i> ). <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 3488-3497.	3.5	19
8	EMS Mutagenesis of Maize Pollen. <i>Methods in Molecular Biology</i> , 2020, 2122, 25-33.	0.9	6
9	Genetic Screens to Target Embryo and Endosperm Pathways in Arabidopsis and Maize. <i>Methods in Molecular Biology</i> , 2020, 2122, 3-14.	0.9	1
10	Maize defective kernel5 is a bacterial TamB homologue required for chloroplast envelope biogenesis. <i>Journal of Cell Biology</i> , 2019, 218, 2638-2658.	5.2	19
11	Effects of long-term exposure to elevated temperature on <i>Zea mays</i> endosperm development during grain fill. <i>Plant Journal</i> , 2019, 99, 23-40.	5.7	37
12	RNA Binding Motif Protein 48 Is Required for U12 Splicing and Maize Endosperm Differentiation. <i>Plant Cell</i> , 2019, 31, 715-733.	6.6	27
13	Functions of maize genes encoding pyruvate phosphate dikinase in developing endosperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E24-E33.	7.1	35
14	Restorer-of-Fertility Mutations Recovered in Transposon-Active Lines of S Male-Sterile Maize. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 291-302.	1.8	5
15	Quantitative trait loci associated with soybean seed weight and composition under different phosphorus levels. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 232-241.	8.5	32
16	Modulation of early maize seedling performance via priming under sub-optimal temperatures. <i>PLoS ONE</i> , 2018, 13, e0206861.	2.5	9
17	Ovary abortion is prevalent in diverse maize inbred lines and is under genetic control. <i>Scientific Reports</i> , 2018, 8, 13032.	3.3	12
18	The maize W22 genome provides a foundation for functional genomics and transposon biology. <i>Nature Genetics</i> , 2018, 50, 1282-1288.	21.4	183

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19	Aberrant splicing in maize <i>rough endosperm3</i> reveals a conserved role for U12 splicing in eukaryotic multicellular development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2195-E2204.	7.1	38
20	Quantification of seed ionome variation in 90 diverse soybean ( <i>Glycine max</i> ) lines. <i>Journal of Plant Nutrition</i> , 2017, 40, 2808-2817.	1.9	16
21	Parent-of-Origin-Effect <i>rough endosperm</i> Mutants in Maize. <i>Genetics</i> , 2016, 204, 221-231.	2.9	16
22	Enhanced Single Seed Trait Predictions in Soybean ( <i>Glycine max</i> ) and Robust Calibration Model Transfer with Near-Infrared Reflectance Spectroscopy. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 1079-1086.	5.2	23
23	Seed Phenomics. , 2015, , 67-82.		8
24	Efficient Molecular Marker Design Using the MaizeGDB Mo17 SNPs and Indels Track. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1143-1145.	1.8	12
25	Analysis of Maize ( <i>Zea mays</i> ) Kernel Density and Volume Using Microcomputed Tomography and Single-Kernel Near-Infrared Spectroscopy. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 10872-10880.	5.2	38
26	NATURAL VARIATION IN SEED COMPOSITION OF 91 COMMON BEAN GENOTYPES AND THEIR POSSIBLE ASSOCIATION WITH SEED COAT COLOR. <i>Journal of Plant Nutrition</i> , 2013, 36, 772-780.	1.9	21
27	Chloroplast-localized 6-phosphogluconate dehydrogenase is critical for maize endosperm starch accumulation. <i>Journal of Experimental Botany</i> , 2013, 64, 2231-2242.	4.8	38
28	Ionic Characterization of Maize Kernels in the Intermated B73 × Mo17 Population. <i>Crop Science</i> , 2013, 53, 208-220.	1.8	65
29	Maize <i>Rough Endosperm3</i> Encodes an RNA Splicing Factor Required for Endosperm Cell Differentiation and Has a Nonautonomous Effect on Embryo Development. <i>Plant Cell</i> , 2011, 23, 4280-4297.	6.6	71
30	Distributed simple sequence repeat markers for efficient mapping from maize public mutagenesis populations. <i>Theoretical and Applied Genetics</i> , 2010, 121, 697-704.	3.6	9
31	RepFrag. , 2010, , .		0
32	Near-Infrared Reflectance Spectroscopy Predicts Protein, Starch, and Seed Weight in Intact Seeds of Common Bean ( <i>Phaseolus vulgaris</i> L.). <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 702-706.	5.2	70
33	High-Throughput Near-Infrared Reflectance Spectroscopy for Predicting Quantitative and Qualitative Composition Phenotypes of Individual Maize Kernels. <i>Cereal Chemistry</i> , 2009, 86, 556-564.	2.2	78
34	Transposon Tagging and Reverse Genetics. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 143-159.	0.2	10
35	The Maize <i>Viviparous8</i> Locus, Encoding a Putative ALTERED MERISTEM PROGRAM1-Like Peptidase, Regulates Abscisic Acid Accumulation and Coordinates Embryo and Endosperm Development. <i>Plant Physiology</i> , 2008, 146, 1193-1206.	4.8	61
36	A novel genome-scale repeat finder geared towards transposons. <i>Bioinformatics</i> , 2008, 24, 468-476.	4.1	14

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37	Sequence-indexed mutations in maize using the UniformMu transposon-tagging population. <i>BMC Genomics</i> , 2007, 8, 116.	2.8	124
38	The maizeviviparous15locus encodes the molybdopterin synthase small subunit. <i>Plant Journal</i> , 2006, 45, 264-274.	5.7	50
39	The maizeViviparous10/Viviparous13locus encodes theCnx1gene required for molybdenum cofactor biosynthesis. <i>Plant Journal</i> , 2006, 45, 250-263.	5.7	41
40	Development of a calibration to predict maize seed composition using single kernel near infrared spectroscopy. <i>Journal of Cereal Science</i> , 2006, 43, 236-243.	3.7	103
41	Steady-state transposon mutagenesis in inbred maize. <i>Plant Journal</i> , 2005, 44, 52-61.	5.7	234
42	Molecular analysis of high-copy insertion sites in maize. <i>Nucleic Acids Research</i> , 2004, 32, e54-e54.	14.5	82
43	Duplication and Suppression of Chloroplast Protein Translocation Genes in Maize. <i>Genetics</i> , 2001, 157, 349-360.	2.9	25
44	The Thylakoid $\text{H}^+$ pH-dependent Pathway Machinery Facilitates RR-independent N-Tail Protein Integration. <i>Journal of Biological Chemistry</i> , 2000, 275, 23483-23490.	3.4	38
45	Old and new pathways of protein export in chloroplasts and bacteria. <i>Trends in Cell Biology</i> , 1998, 8, 494-501.	7.9	71
46	Opportunities and Challenges Grow from <i>Arabidopsis</i> Genome Sequencing. <i>Genome Research</i> , 1998, 8, 83-85.	5.5	5
47	Sec-Independent Protein Translocation by the Maize Hcf106 Protein. <i>Science</i> , 1997, 278, 1467-1470.	12.6	268
48	Ion transport in rat tongue epithelium in vitro: A developmental study. <i>Pharmacology Biochemistry and Behavior</i> , 1993, 46, 83-88.	2.9	5