

Martin M Kater

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

9,219
citations

50276

46
h-index

71685

76
g-index

82
all docs

82
docs citations

82
times ranked

8327
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome analysis reveals rice MADS13 as an important repressor of the carpel development pathway in ovules. <i>Journal of Experimental Botany</i> , 2021, 72, 398-414.	4.8	7
2	Alternative Splicing Generates a MONOPTEROS Isoform Required for Ovule Development. <i>Current Biology</i> , 2021, 31, 892-899.e3.	3.9	22
3	Cauliflower fractal forms arise from perturbations of floral gene networks. <i>Science</i> , 2021, 373, 192-197.	12.6	37
4	BPC transcription factors and a Polycomb Group protein confine the expression of the ovule identity gene <i><i>SEEDSTICK</i></i> in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2020, 102, 582-599.	5.7	34
5	MADS-Box and bHLH Transcription Factors Coordinate Transmitting Tract Development in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 526.	3.6	25
6	Genes of the <i><i>RAV</i></i> Family Control Heading Date and Carpel Development in Rice. <i>Plant Physiology</i> , 2020, 183, 1663-1680.	4.8	25
7	Functionally Divergent Splicing Variants of the Rice AGAMOUS Ortholog OsMADS3 Are Evolutionary Conserved in Grasses. <i>Frontiers in Plant Science</i> , 2020, 11, 637.	3.6	2
8	CRISPR-mediated accelerated domestication of African rice landraces. <i>PLoS ONE</i> , 2020, 15, e0229782.	2.5	53
9	Gynoecium size and ovule number are interconnected traits that impact seed yield. <i>Journal of Experimental Botany</i> , 2020, 71, 2479-2489.	4.8	51
10	Crop reproductive meristems in the genomic era: a brief overview. <i>Biochemical Society Transactions</i> , 2020, 48, 853-865.	3.4	3
11	REM34 and REM35 Control Female and Male Gametophyte Development in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1351.	3.6	19
12	Early cold stress responses in post-meiotic anthers from tolerant and sensitive rice cultivars. <i>Rice</i> , 2019, 12, 94.	4.0	11
13	A Genomic View of Alternative Splicing of Long Non-coding RNAs during Rice Seed Development Reveals Extensive Splicing and lncRNA Gene Families. <i>Frontiers in Plant Science</i> , 2018, 9, 115.	3.6	31
14	Gene expression profiling of reproductive meristem types in early rice inflorescences by laser microdissection. <i>Plant Journal</i> , 2016, 86, 75-88.	5.7	56
15	Genome-Wide Transcriptome Analysis During Anthesis Reveals New Insights into the Molecular Basis of Heat Stress Responses in Tolerant and Sensitive Rice Varieties. <i>Plant and Cell Physiology</i> , 2016, 57, 57-68.	3.1	118
16	PGR5-PGRL1-Dependent Cyclic Electron Transport Modulates Linear Electron Transport Rate in <i>Arabidopsis thaliana</i> . <i>Molecular Plant</i> , 2016, 9, 271-288.	8.3	119
17	Peptide aptamers: The versatile role of specific protein function inhibitors in plant biotechnology. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 892-901.	8.5	33
18	SHORT VEGETATIVE PHASE reduces gibberellin biosynthesis at the <i><i>Arabidopsis</i></i> shoot apex to regulate the floral transition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2760-9.	7.1	132

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19	SEEDSTICK is a Master Regulator of Development and Metabolism in the Arabidopsis Seed Coat. PLoS Genetics, 2014, 10, e1004856.	3.5	86
20	<i>MADS</i> reloaded: evolution of the <i>AGAMOUS</i> subfamily genes. New Phytologist, 2014, 201, 717-732.	7.3	116
21	Class I BASIC PENTACYSTEINE factors regulate HOMEBOX genes involved in meristem size maintenance. Journal of Experimental Botany, 2014, 65, 1455-1465.	4.8	57
22	Analysis of the arabidopsis REM gene family predicts functions during flower development. Annals of Botany, 2014, 114, 1507-1515.	2.9	55
23	OsJAR1 is required for JA-regulated floret opening and anther dehiscence in rice. Plant Molecular Biology, 2014, 86, 19-33.	3.9	85
24	Gene coexpression patterns during early development of the native Arabidopsis reproductive meristem: novel candidate developmental regulators and patterns of functional redundancy. Plant Journal, 2014, 79, 861-877.	5.7	29
25	Flower Development: Open Questions and Future Directions. Methods in Molecular Biology, 2014, 1110, 103-124.	0.9	26
26	Identification of pathways directly regulated by SHORT VEGETATIVE PHASE during vegetative and reproductive development in Arabidopsis. Genome Biology, 2013, 14, R56.	8.8	134
27	OsMADS16 Genetically Interacts with OsMADS3 and OsMADS58 in Specifying Floral Patterning in Rice. Molecular Plant, 2013, 6, 743-756.	8.3	46
28	MADS Domain Transcription Factors Mediate Short-Range DNA Looping That Is Essential for Target Gene Expression in Arabidopsis. Plant Cell, 2013, 25, 2560-2572.	6.6	65
29	The Ins and Outs of the Rice AGAMOUS Subfamily. Molecular Plant, 2013, 6, 650-664.	8.3	29
30	TAF13 interacts with PRC2 members and is essential for Arabidopsis seed development. Developmental Biology, 2013, 379, 28-37.	2.0	22
31	Arabidopsis plants lacking PsbQ and PsbR subunits of the oxygen-evolving complex show altered ^{PSII} supercomplex organization and short-term adaptive mechanisms. Plant Journal, 2013, 75, 671-684.	5.7	99
32	Panicle Development. , 2013, , 279-295.		18
33	BASIC PENTACYSTEINE Proteins Mediate MADS Domain Complex Binding to the DNA for Tissue-Specific Expression of Target Genes in <i>Arabidopsis</i>. Plant Cell, 2012, 24, 4163-4172.	6.6	75
34	Versatile roles of Arabidopsis plastid ribosomal proteins in plant growth and development. Plant Journal, 2012, 72, 922-934.	5.7	89
35	Uncovering genetic and molecular interactions among floral meristem identity genes in <i>Arabidopsis thaliana</i>. Plant Journal, 2012, 69, 881-893.	5.7	42
36	The MADS box genes <i>SEEDSTICK</i> and <i>ARABIDOPSIS B</i> _{<i>sister</i>} play a maternal role in fertilization and seed development. Plant Journal, 2012, 70, 409-420.	5.7	109

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37	Reversible male sterility in eggplant (<i>Solanum melongena</i> L.) by artificial microRNA-mediated silencing of general transcription factor genes. <i>Plant Biotechnology Journal</i> , 2011, 9, 684-692.	8.3	48
38	The Arabidopsis <i>SOC1</i> -like genes <i>AGL42</i> , <i>AGL71</i> and <i>AGL72</i> promote flowering in the shoot apical and axillary meristems. <i>Plant Journal</i> , 2011, 67, 1006-1017.	5.7	117
39	Functional Analysis of All AGAMOUS Subfamily Members in Rice Reveals Their Roles in Reproductive Organ Identity Determination and Meristem Determinacy. <i>Plant Cell</i> , 2011, 23, 2850-2863.	6.6	140
40	The Emerging Importance of Type I MADS Box Transcription Factors for Plant Reproduction. <i>Plant Cell</i> , 2011, 23, 865-872.	6.6	177
41	Rice <i>MADS6</i> Interacts with the Floral Homeotic Genes <i>SUPERWOMAN1</i> , <i>MADS3</i> , <i>MADS58</i> , <i>MADS13</i> , and <i>DROOPING LEAF</i> in Specifying Floral Organ Identities and Meristem Fate. <i>Plant Cell</i> , 2011, 23, 2536-2552.	6.6	131
42	The Arabidopsis BET Bromodomain Factor GTE4 Is Involved in Maintenance of the Mitotic Cell Cycle during Plant Development. <i>Plant Physiology</i> , 2010, 152, 1320-1334.	4.8	34
43	The genome of the domesticated apple (<i>Malus domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
44	<i>VERDANDI</i> Is a Direct Target of the MADS Domain Ovule Identity Complex and Affects Embryo Sac Differentiation in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010, 22, 1702-1715.	6.6	92
45	The Arabidopsis BET bromodomain factor GTE4 regulates the mitotic cell cycle. <i>Plant Signaling and Behavior</i> , 2010, 5, 677-680.	2.4	10
46	A new role for the SHATTERPROOF genes during Arabidopsis gynoecium development. <i>Developmental Biology</i> , 2010, 337, 294-302.	2.0	76
47	The Arabidopsis floral meristem identity genes AP1, AGL24 and SVP directly repress class B and C floral homeotic genes. <i>Plant Journal</i> , 2009, 60, 626-637.	5.7	182
48	<i>AGL23</i> , a type I MADS-box gene that controls female gametophyte and embryo development in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 54, 1037-1048.	5.7	130
49	<i>AGAMOUS-LIKE24</i> and <i>SHORT VEGETATIVE PHASE</i> determine floral meristem identity in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2008, 56, 891-902.	5.7	116
50	Arabidopsis ovule development and its evolutionary conservation. <i>Trends in Plant Science</i> , 2008, 13, 444-450.	8.8	95
51	The rice StMADS11-like genes OsMADS22 and OsMADS47 cause floral reversions in Arabidopsis without complementing the <i>svp</i> and <i>agl24</i> mutants. <i>Journal of Experimental Botany</i> , 2008, 59, 2181-2190.	4.8	58
52	Genetic and Molecular Interactions between BELL1 and MADS Box Factors Support Ovule Development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2007, 19, 2544-2556.	6.6	178
53	The lineage MADS-box gene <i>OsMADS13</i> controls ovule identity in rice. <i>Plant Journal</i> , 2007, 52, 690-699.	5.7	190
54	Functional analysis of MADS-box genes controlling ovule development in Arabidopsis using the ethanol-inducible alc gene-expression system. <i>Mechanisms of Development</i> , 2006, 123, 267-276.	1.7	24

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55	Functional conservation of MADS-box factors controlling floral organ identity in rice and Arabidopsis. <i>Journal of Experimental Botany</i> , 2006, 57, 3433-3444.	4.8	165
56	AGL24, SHORT VEGETATIVE PHASE, and APETALA1 Redundantly Control AGAMOUS during Early Stages of Flower Development in Arabidopsis. <i>Plant Cell</i> , 2006, 18, 1373-1382.	6.6	207
57	Comprehensive Interaction Map of the Arabidopsis MADS Box Transcription Factors. <i>Plant Cell</i> , 2005, 17, 1424-1433.	6.6	528
58	BASIC PENTACYSSTEINE1, a GA Binding Protein That Induces Conformational Changes in the Regulatory Region of the Homeotic Arabidopsis Gene SEEDSTICK. <i>Plant Cell</i> , 2005, 17, 722-729.	6.6	126
59	The Arabidopsis TFIIID factor AtTAF6 controls pollen tube growth. <i>Developmental Biology</i> , 2005, 285, 91-100.	2.0	42
60	Functional Characterization of OsMADS18, a Member of the AP1/SQUA Subfamily of MADS Box Genes. <i>Plant Physiology</i> , 2004, 135, 2207-2219.	4.8	164
61	TBP-associated factors in Arabidopsis. <i>Gene</i> , 2004, 342, 231-241.	2.2	51
62	The use of floral homeotic mutants as a novel way to obtain durable resistance to insect pests. <i>Plant Biotechnology Journal</i> , 2003, 1, 123-127.	8.3	5
63	Molecular and Phylogenetic Analyses of the Complete MADS-Box Transcription Factor Family in Arabidopsis. <i>Plant Cell</i> , 2003, 15, 1538-1551.	6.6	758
64	MADS-Box Protein Complexes Control Carpel and Ovule Development in Arabidopsis. <i>Plant Cell</i> , 2003, 15, 2603-2611.	6.6	499
65	Ternary Complex Formation between MADS-box Transcription Factors and the Histone Fold Protein NF-YB. <i>Journal of Biological Chemistry</i> , 2002, 277, 26429-26435.	3.4	104
66	Comparative analysis of rice MADS-box genes expressed during flower development. <i>Sexual Plant Reproduction</i> , 2002, 15, 113-122.	2.2	91
67	Sex Determination in the Monoecious Species Cucumber Is Confined to Specific Floral Whorls. <i>Plant Cell</i> , 2001, 13, 481-493.	6.6	117
68	Suppression of cell expansion by ectopic expression of the Arabidopsis SUPERMAN gene in transgenic petunia and tobacco. <i>Plant Journal</i> , 2000, 23, 407-413.	5.7	26
69	NEC1, a novel gene, highly expressed in nectary tissue of <i>Petunia hybrida</i> . <i>Plant Journal</i> , 2000, 24, 725-734.	5.7	82
70	OsMADS13, a novel rice MADS-box gene expressed during ovule development. , 1999, 25, 237-244.		137
71	The NADH-specific enoyl-acyl carrier protein reductase: Characterization of a housekeeping gene involved in storage lipid synthesis in seeds of arabidopsis and other plant species. <i>Plant Physiology and Biochemistry</i> , 1998, 36, 473-486.	5.8	10
72	Multiple AGAMOUS Homologs from Cucumber and Petunia Differ in Their Ability to Induce Reproductive Organ Fate. <i>Plant Cell</i> , 1998, 10, 171-182.	6.6	154

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73	The use of a hybrid genetic system to study the functional relationship between prokaryotic and plant multi-enzyme fatty acid synthetase complexes. <i>Plant Molecular Biology</i> , 1994, 25, 771-790.	3.9	44
74	cDNA cloning and expression of <i>Brassica napus</i> enoyl-acyl carrier protein reductase in <i>Escherichia coli</i> . <i>Plant Molecular Biology</i> , 1991, 17, 895-909.	3.9	65
75	Lipid production in wheypermeate by an unsaturated fatty acid mutant of the oleaginous yeast <i>Apiotrichum curvatum</i> . <i>Biotechnology Letters</i> , 1989, 11, 477-482.	2.2	17
76	Optimization of lipid production in the oleaginous yeast <i>Apiotrichum curvatum</i> in wheypermeate. <i>Applied Microbiology and Biotechnology</i> , 1988, 29, 211-218.	3.6	99
77	Optimization of lipid production in the oleaginous yeast <i>Apiotrichum curvatum</i> in wheypermeate. <i>Applied Microbiology and Biotechnology</i> , 1988, 29, 211-218.	3.6	72
78	Optimization of lipid production in the oleaginous yeast <i>Apiotrichum curvatum</i> in wheypermeate. <i>Applied Microbiology and Biotechnology</i> , 1988, 29, 211-218.	3.6	6