DanuÅ¡e TarkowskÃ¡

List of Publications by Year
in descending order

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82
papers

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76196
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docs citations

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times ranked

8940
citing authors

#	ARTICLE	IF	CITATIONS
1	OsMADS14 and NFâ€YB1 cooperate in the direct activation of <i>OsAGPL2</i> and <i>Waxy</i> during starch synthesis in rice endosperm. New Phytologist, 2022, 234, 77-92.	3.5	18
2	Comparative transcriptomics identifies candidate genes involved in the evolutionary transition from dehiscent to indehiscent fruits in Lepidium (Brassicaceae). BMC Plant Biology, 2022, 22, .	1.6	3
3	Evolution of Floral Organ Identity. , 2021, , 697-713.		2
4	<i>Aethionema arabicum</i> genome annotation using PacBio fullâ€length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. Plant Journal, 2021, 106, 275-293.	2.8	20
5	A tale of two morphs: developmental patterns and mechanisms of seed coat differentiation in the dimorphic diaspore model Aethionema arabicum (Brassicaceae). Plant Journal, 2021, 107, 166-181.	2.8	8
6	Extending the Toolkit for Beauty: Differential Co-Expression of DROOPING LEAF-Like and Class B MADS-Box Genes during Phalaenopsis Flower Development. International Journal of Molecular Sciences, 2021, 22, 7025.	1.8	9
7	DNA-binding properties of the MADS-domain transcription factor SEPALLATA3 and mutant variants characterized by SELEX-seq. Plant Molecular Biology, 2021, 105, 543-557.	2.0	8
8	New phytoplasma effector: 50 shades of green. Cell Host and Microbe, 2021, 29, 1601-1603.	5.1	3
9	Studying the Function of Phytoplasma Effector Proteins Using a Chemical-Inducible Expression System in Transgenic Plants. International Journal of Molecular Sciences, 2021, 22, 13582.	1.8	3
10	Independent origin of <i>MIRNA</i> genes controlling homologous target genes by partial inverted duplication of antisenseâ€transcribed sequences. Plant Journal, 2020, 101, 401-419.	2.8	7
11	Structural Requirements of the Phytoplasma Effector Protein SAP54 for Causing Homeotic Transformation of Floral Organs. Molecular Plant-Microbe Interactions, 2020, 33, 1129-1141.	1.4	9
12	Morphologically and physiologically diverse fruits of two Lepidium species differ in allocation of glucosinolates into immature and mature seed and pericarp. PLoS ONE, 2020, 15, e0227528.	1.1	3
13	Stranger than Fiction: Loss of MADS-Box Genes During Evolutionary Miniaturization of the Duckweed Body Plan. Compendium of Plant Genomes, 2020, , 91-101.	0.3	1
14	Title is missing!. , 2020, 15, e0227528.		0
15	Title is missing!. , 2020, 15, e0227528.		0
16	Title is missing!. , 2020, 15, e0227528.		0
17	Title is missing!. , 2020, 15, e0227528.		0
18	Title is missing!. , 2020, 15, e0227528.		0

#	Article	IF	Citations
19	Title is missing!. , 2020, 15, e0227528.		0
20	Plant miRNA Conservation and Evolution. Methods in Molecular Biology, 2019, 1932, 41-50.	0.4	14
21	Reconstructing the ancestral flower of extant angiosperms: the â€˜war of the whorlsâ€™ is heating up. Journal of Experimental Botany, 2019, 70, 2615-2622.	2.4	14
22	Aethionema arabicum: a novel model plant to study the light control of seed germination. Journal of Experimental Botany, 2019, 70, 3313-3328.	2.4	31
23	A conserved leucine zipper-like motif accounts for strong tetramerization capabilities of SEPALLATA-like MADS-domain transcription factors. Journal of Experimental Botany, 2018, 69, 1943-1954.	2.4	24
24	When the BRANCHED network bears fruit: how carpic dominance causes fruit dimorphism in <i>Aethionema</i>. Plant Journal, 2018, 94, 352-371.	2.8	20
25	Plant Hormonomics: Multiple Phytohormone Profiling by Targeted Metabolomics. Plant Physiology, 2018, 177, 476-489.	2.3	293
26	Array of MADS-Box Genes: Facilitator for Rapid Adaptation?. Trends in Plant Science, 2018, 23, 563-576.	4.3	35
27	A Dead Gene Walking: Convergent Degeneration of a Clade of MADS-Box Genes in Crucifers. Molecular Biology and Evolution, 2018, 35, 2618-2638.	3.5	10
28	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. Cell, 2018, 174, 448-464.e24.	13.5	420
29	The floral homeotic protein <scp>SEPALLATA</scp>3 recognizes target <scp>DNA</scp> sequences by shape readout involving a conserved arginine residue in the <scp>MADS</scp>â€domain. Plant Journal, 2018, 95, 341-357.	2.8	17
30	Evolution of Floral Organ Identity. , 2018, , 1-17.		5
31	The <scp>ABC</scp>s of flower development: mutational analysis of <i><scp>AP</scp>1</i>/<i><scp>FUL</scp></i>â€like genes in rice provides evidence for a homeotic (A)â€function in grasses. Plant Journal, 2017, 89, 310-324.	2.8	76
32	Developmental Control and Plasticity of Fruit and Seed Dimorphism in <i>Aethionema arabicum</i>. Plant Physiology, 2016, 172, 1691-1707.	2.3	59
33	MADS-domain transcription factors and the floral quartet model of flower development: linking plant development and evolution. Development (Cambridge), 2016, 143, 3259-3271.	1.2	346
34	The significance of developmental robustness for species diversity. Annals of Botany, 2016, 117, 725-732.	1.4	25
35	Structure and Evolution of Plant MADS Domain Transcription Factors. , 2016, , 127-138.		30
36	Nonâ€canonical structure, function and phylogeny of the B sister MADS â€box gene O s MADS 30 of rice () Tj ETQq0 0 0 rgBT /Overlock	2.8	16

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37	Phylogenomics reveals surprising sets of essential and dispensable clades of MIKC^câ€group MADSâ€box genes in flowering plants. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2015, 324, 353-362.	0.6	69
38	Did Convergent Protein Evolution Enable Phytoplasmas to Generate â€˜Zombie Plantsâ€™?. Trends in Plant Science, 2015, 20, 798-806.	4.3	28
39	Arabidopsis SEPALLATA proteins differ in cooperative DNA-binding during the formation of floral quartet-like complexes. Nucleic Acids Research, 2014, 42, 10927-10942.	6.5	68
40	The pleiotropic SEPALLATA â€like gene Os MADS 34 reveals that the â€˜empty glumesâ€™ of rice (Oryza sativa) spikelets are in fact rudimentary lemmas. New Phytologist, 2014, 202, 689-702.	3.5	42
41	Horizontal gene transfer and functional diversification of plant cell wall degrading polygalacturonases: Key events in the evolution of herbivory in beetles. Insect Biochemistry and Molecular Biology, 2014, 52, 33-50.	1.2	116
42	UHPLCâ€“MS/MS based target profiling of stress-induced phytohormones. Phytochemistry, 2014, 105, 147-157.	1.4	184
43	Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in <i>Arabidopsis</i> Â. Plant Cell, 2014, 26, 3603-3615.	3.1	97
44	Quo vadis plant hormone analysis?. Planta, 2014, 240, 55-76.	1.6	72
45	My favourite flowering image: a cob of pod corn. Journal of Experimental Botany, 2014, 65, 6751-6754.	2.4	0
46	DEF- and GLO-like proteins may have lost most of their interaction partners during angiosperm evolution. Annals of Botany, 2014, 114, 1431-1443.	1.4	49
47	MADS goes genomic in conifers: towards determining the ancestral set of MADS-box genes in seed plants. Annals of Botany, 2014, 114, 1407-1429.	1.4	101
48	FLOWERING LOCUS C in monocots and the tandem origin of angiosperm-specific MADS-box genes. Nature Communications, 2013, 4, 2280.	5.8	142
49	Evidence that an evolutionary transition from dehiscent to indehiscent fruits in <i><scp>L</scp>epidium</i> (<scp>B</scp>rassicaceae) was caused by a change in the control of valve margin identity genes. Plant Journal, 2013, 73, 824-835.	2.8	71
50	Conservation of fruit dehiscence pathways between <i><scp>L</scp>epidium campestre</i> and <i><scp>A</scp>rabidopsis thaliana</i> sheds light on the regulation of <i><scp>INDEHISCENT</scp></i>. Plant Journal, 2013, 76, 545-556.	2.8	42
51	The Norway spruce genome sequence and conifer genome evolution. Nature, 2013, 497, 579-584.	13.7	1,303
52	Phylogenomics of MADS-Box Genes in Plants â€” Two Opposing Life Styles in One Gene Family. Biology, 2013, 2, 1150-1164.	1.3	70
53	Live and Let Die - The Bsister MADS-Box Gene OsMADS29 Controls the Degeneration of Cells in Maternal Tissues during Seed Development of Rice (Oryza sativa). PLoS ONE, 2012, 7, e51435.	1.1	73
54	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	6.0	794

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55	Conserved differential expression of paralogous <i>DEFICIENS</i>â€•and <i>GLOBOSA</i>â€•like MADSâ€•box genes in the flowers of Orchidaceae: refining the â€˜orchid codeâ€™. Plant Journal, 2011, 66, 1008-1019.	2.8	125
56	A double-flowered variety of lesser periwinkle (Vinca minor fl. pl.) that has persisted in the wild for more than 160 years. Annals of Botany, 2011, 107, 1445-1452.	1.4	15
57	Cooperation and cheating in microbial exoenzyme production â€“ Theoretical analysis for biotechnological applications. Biotechnology Journal, 2010, 5, 751-758.	1.8	31
58	On the origin of MADS-domain transcription factors. Trends in Genetics, 2010, 26, 149-153.	2.9	123
59	Functional conservation and diversification of class E floral homeotic genes in rice (<i>Oryza) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.8	223
60	Molecular interactions of orthologues of floral homeotic proteins from the gymnosperm Gnetum gnemon provide a clue to the evolutionary origin of â€˜floral quartetsâ€™. Plant Journal, 2010, 64, 177-190.	2.8	68
61	GORDITA (AGL63) is a young paralog of the Arabidopsis thaliana Bsister MADS box gene ABS (TT16) that has undergone neofunctionalization. Plant Journal, 2010, 63, 914-924.	2.8	49
62	The naked and the dead: The ABCs of gymnosperm reproduction and the origin of the angiosperm flower. Seminars in Cell and Developmental Biology, 2010, 21, 118-128.	2.3	93
63	Reconstitution of â€˜floral quartetsâ€™ in vitro involving class B and class E floral homeotic proteins. Nucleic Acids Research, 2009, 37, 2723-2736.	6.5	133
64	Developmental Robustness by Obligate Interaction of Class B Floral Homeotic Genes and Proteins. PLoS Computational Biology, 2009, 5, e1000264.	1.5	29
65	The class E floral homeotic protein SEPALLATA3 is sufficient to loop DNA in â€˜floral quartetâ€™-like complexes in vitro. Nucleic Acids Research, 2009, 37, 144-157.	6.5	141
66	Floral visitation and reproductive traits of Stamenoid petals, a naturally occurring floral homeotic variant of Capsella bursa-pastoris (Brassicaceae). Planta, 2009, 230, 1239-1249.	1.6	15
67	Saltational evolution: hopeful monsters are here to stay. Theory in Biosciences, 2009, 128, 43-51.	0.6	99
68	MADS about the evolution of orchid flowers. Trends in Plant Science, 2008, 13, 51-59.	4.3	139
69	Missing Links: DNAâ€•Binding and Target Gene Specificity of Floral Homeotic Proteins. Advances in Botanical Research, 2006, , 209-236.	0.5	14
70	Petaloidy and petal identity MADSâ€•box genes in the balsaminoid genera <i>Impatiens</i> and <i>Marcgravia</i>. Plant Journal, 2006, 47, 501-518.	2.8	54
71	The proper place of hopeful monsters in evolutionary biology. Theory in Biosciences, 2006, 124, 349-369.	0.6	96
72	Birth, life and death of developmental control genes: New challenges for the homology concept. Theory in Biosciences, 2005, 124, 199-212.	0.6	18

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73	MIKC-type MADS-domain proteins: structural modularity, protein interactions and network evolution in land plants. Gene, 2005, 347, 183-198.	1.0	484
74	Genomewide Structural Annotation and Evolutionary Analysis of the Type I MADS-Box Genes in Plants. Journal of Molecular Evolution, 2003, 56, 573-586.	0.8	109
75	The major clades of MADS-box genes and their role in the development and evolution of flowering plants. Molecular Phylogenetics and Evolution, 2003, 29, 464-489.	1.2	827
76	Two Ancient Classes of MIKC-type MADS-box Genes are Present in the Moss Physcomitrella patens. Molecular Biology and Evolution, 2002, 19, 801-814.	3.5	216
77	On the origin of class B floral homeotic genes: functional substitution and dominant inhibition inArabidopsisby expression of an orthologue from the gymnospermGnetum. Plant Journal, 2002, 31, 457-475.	2.8	81
78	Orthology: Secret life of genes. Nature, 2002, 415, 741-741.	13.7	66
79	Floral quartets. Nature, 2001, 409, 469-471.	13.7	826
80	Genetics of identity. Nature, 2001, 414, 491-491.	13.7	13
81	Development of floral organ identity: stories from the MADS house. Current Opinion in Plant Biology, 2001, 4, 75-85.	3.5	799
82	Classification and phylogeny of the MADS-box multigene family suggest defined roles of MADS-box gene subfamilies in the morphological evolution of eukaryotes. Journal of Molecular Evolution, 1996, 43, 484-516.	0.8	467