

DanuÅ¡e TarkowskÃ¡

List of Publications by Year in descending order

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82
papers

10,204
citations

76326

40
h-index

85541

71
g-index

87
all docs

87
docs citations

87
times ranked

8940
citing authors

#	ARTICLE	IF	CITATIONS
1	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
2	The major clades of MADS-box genes and their role in the development and evolution of flowering plants. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 464-489.	2.7	827
3	Floral quartets. <i>Nature</i> , 2001, 409, 469-471.	27.8	826
4	Development of floral organ identity: stories from the MADS house. <i>Current Opinion in Plant Biology</i> , 2001, 4, 75-85.	7.1	799
5	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	12.6	794
6	MIKC-type MADS-domain proteins: structural modularity, protein interactions and network evolution in land plants. <i>Gene</i> , 2005, 347, 183-198.	2.2	484
7	Classification and phylogeny of the MADS-box multigene family suggest defined roles of MADS-box gene subfamilies in the morphological evolution of eukaryotes. <i>Journal of Molecular Evolution</i> , 1996, 43, 484-516.	1.8	467
8	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420
9	MADS-domain transcription factors and the floral quartet model of flower development: linking plant development and evolution. <i>Development (Cambridge)</i> , 2016, 143, 3259-3271.	2.5	346
10	Plant Hormonomics: Multiple Phytohormone Profiling by Targeted Metabolomics. <i>Plant Physiology</i> , 2018, 177, 476-489.	4.8	293
11	Functional conservation and diversification of class E floral homeotic genes in rice (<i>Oryza</i>). <i>Journal of Molecular Evolution</i> , 2011, 72, 223-233.	5.7	223
12	Two Ancient Classes of MIKC-type MADS-box Genes are Present in the Moss <i>Physcomitrella patens</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 801-814.	8.9	216
13	UHPLC-MS/MS based target profiling of stress-induced phytohormones. <i>Phytochemistry</i> , 2014, 105, 147-157.	2.9	184
14	FLOWERING LOCUS C in monocots and the tandem origin of angiosperm-specific MADS-box genes. <i>Nature Communications</i> , 2013, 4, 2280.	12.8	142
15	The class E floral homeotic protein SEPALLATA3 is sufficient to loop DNA in floral quartet-like complexes in vitro. <i>Nucleic Acids Research</i> , 2009, 37, 144-157.	14.5	141
16	MADS about the evolution of orchid flowers. <i>Trends in Plant Science</i> , 2008, 13, 51-59.	8.8	139
17	Reconstitution of floral quartets in vitro involving class B and class E floral homeotic proteins. <i>Nucleic Acids Research</i> , 2009, 37, 2723-2736.	14.5	133
18	Conserved differential expression of paralogous <i>DEFICIENS</i> and <i>GLOBOSA</i> -like MADS-box genes in the flowers of Orchidaceae: refining the orchid code. <i>Plant Journal</i> , 2011, 66, 1008-1019.	5.7	125

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19	On the origin of MADS-domain transcription factors. <i>Trends in Genetics</i> , 2010, 26, 149-153.	6.7	123
20	Horizontal gene transfer and functional diversification of plant cell wall degrading polygalacturonases: Key events in the evolution of herbivory in beetles. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 52, 33-50.	2.7	116
21	Genomewide Structural Annotation and Evolutionary Analysis of the Type I MADS-Box Genes in Plants. <i>Journal of Molecular Evolution</i> , 2003, 56, 573-586.	1.8	109
22	MADS goes genomic in conifers: towards determining the ancestral set of MADS-box genes in seed plants. <i>Annals of Botany</i> , 2014, 114, 1407-1429.	2.9	101
23	Saltational evolution: hopeful monsters are here to stay. <i>Theory in Biosciences</i> , 2009, 128, 43-51.	1.4	99
24	Structural Basis for the Oligomerization of the MADS Domain Transcription Factor SEPALLATA3 in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 3603-3615.	6.6	97
25	The proper place of hopeful monsters in evolutionary biology. <i>Theory in Biosciences</i> , 2006, 124, 349-369.	1.4	96
26	The naked and the dead: The ABCs of gymnosperm reproduction and the origin of the angiosperm flower. <i>Seminars in Cell and Developmental Biology</i> , 2010, 21, 118-128.	5.0	93
27	On the origin of class B floral homeotic genes: functional substitution and dominant inhibition in <i>Arabidopsis</i> by expression of an orthologue from the gymnosperm <i>Gnetum</i> . <i>Plant Journal</i> , 2002, 31, 457-475.	5.7	81
28	The ABCs of flower development: mutational analysis of <i>AP1</i> and <i>FUL</i> -like genes in rice provides evidence for a homeotic (A) function in grasses. <i>Plant Journal</i> , 2017, 89, 310-324.	5.7	76
29	Live and Let Die - The Sister MADS-Box Gene OsMADS29 Controls the Degeneration of Cells in Maternal Tissues during Seed Development of Rice (<i>Oryza sativa</i>). <i>PLoS ONE</i> , 2012, 7, e51435.	2.5	73
30	Quo vadis plant hormone analysis?. <i>Planta</i> , 2014, 240, 55-76.	3.2	72
31	Evidence that an evolutionary transition from dehiscent to indehiscent fruits in <i>Lepidium</i> (<i>Brassicaceae</i>) was caused by a change in the control of valve margin identity genes. <i>Plant Journal</i> , 2013, 73, 824-835.	5.7	71
32	Phylogenomics of MADS-Box Genes in Plants – Two Opposing Life Styles in One Gene Family. <i>Biology</i> , 2013, 2, 1150-1164.	2.8	70
33	Phylogenomics reveals surprising sets of essential and dispensable clades of MIKC group MADS-box genes in flowering plants. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2015, 324, 353-362.	1.3	69
34	Molecular interactions of orthologues of floral homeotic proteins from the gymnosperm <i>Gnetum gnemon</i> provide a clue to the evolutionary origin of floral quartets. <i>Plant Journal</i> , 2010, 64, 177-190.	5.7	68
35	<i>Arabidopsis</i> SEPALLATA proteins differ in cooperative DNA-binding during the formation of floral quartet-like complexes. <i>Nucleic Acids Research</i> , 2014, 42, 10927-10942.	14.5	68
36	Orthology: Secret life of genes. <i>Nature</i> , 2002, 415, 741-741.	27.8	66

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37	Developmental Control and Plasticity of Fruit and Seed Dimorphism in <i>Aethionema arabicum</i> . <i>Plant Physiology</i> , 2016, 172, 1691-1707.	4.8	59
38	Petaloidy and petal identity MADS-box genes in the balsaminoid genera <i>Impatiens</i> and <i>Marcgravia</i> . <i>Plant Journal</i> , 2006, 47, 501-518.	5.7	54
39	GORDITA (AGL63) is a young paralog of the <i>Arabidopsis thaliana</i> B1 MADS box gene ABS (TT16) that has undergone neofunctionalization. <i>Plant Journal</i> , 2010, 63, 914-924.	5.7	49
40	DEF- and GLO-like proteins may have lost most of their interaction partners during angiosperm evolution. <i>Annals of Botany</i> , 2014, 114, 1431-1443.	2.9	49
41	Conservation of fruit dehiscence pathways between <i>Lepidium campestre</i> and <i>Arabidopsis thaliana</i> sheds light on the regulation of INDEHISCENT. <i>Plant Journal</i> , 2013, 76, 545-556.	5.7	42
42	The pleiotropic SEPALLATA-like gene Os MADS 34 reveals that the "empty glumes" of rice (<i>Oryza sativa</i>) spikelets are in fact rudimentary lemmas. <i>New Phytologist</i> , 2014, 202, 689-702.	7.3	42
43	Array of MADS-Box Genes: Facilitator for Rapid Adaptation?. <i>Trends in Plant Science</i> , 2018, 23, 563-576.	8.8	35
44	Cooperation and cheating in microbial exoenzyme production – Theoretical analysis for biotechnological applications. <i>Biotechnology Journal</i> , 2010, 5, 751-758.	3.5	31
45	<i>Aethionema arabicum</i> : a novel model plant to study the light control of seed germination. <i>Journal of Experimental Botany</i> , 2019, 70, 3313-3328.	4.8	31
46	Structure and Evolution of Plant MADS Domain Transcription Factors. , 2016, , 127-138.		30
47	Developmental Robustness by Obligate Interaction of Class B Floral Homeotic Genes and Proteins. <i>PLoS Computational Biology</i> , 2009, 5, e1000264.	3.2	29
48	Did Convergent Protein Evolution Enable Phytoplasmas to Generate "Zombie Plants"? <i>Trends in Plant Science</i> , 2015, 20, 798-806.	8.8	28
49	The significance of developmental robustness for species diversity. <i>Annals of Botany</i> , 2016, 117, 725-732.	2.9	25
50	A conserved leucine zipper-like motif accounts for strong tetramerization capabilities of SEPALLATA-like MADS-domain transcription factors. <i>Journal of Experimental Botany</i> , 2018, 69, 1943-1954.	4.8	24
51	When the BRANCHED network bears fruit: how carpel dominance causes fruit dimorphism in <i>Aethionema</i> . <i>Plant Journal</i> , 2018, 94, 352-371.	5.7	20
52	<i>Aethionema arabicum</i> genome annotation using PacBio full-length transcripts provides a valuable resource for seed dormancy and Brassicaceae evolution research. <i>Plant Journal</i> , 2021, 106, 275-293.	5.7	20
53	Birth, life and death of developmental control genes: New challenges for the homology concept. <i>Theory in Biosciences</i> , 2005, 124, 199-212.	1.4	18
54	OsMADS14 and NF-YB1 cooperate in the direct activation of <i>OsAGPL2</i> and <i>Waxy</i> during starch synthesis in rice endosperm. <i>New Phytologist</i> , 2022, 234, 77-92.	7.3	18

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55	The floral homeotic protein <sc>SEPALLATA</sc>3 recognizes target <sc>DNA</sc> sequences by shape readout involving a conserved arginine residue in the <sc>MADS</sc> domain. Plant Journal, 2018, 95, 341-357.	5.7	17
56	Non-canonical structure, function and phylogeny of the B sister MADS box gene OsMADS30 of rice (<i>Oryza sativa</i>). Tj ETQq0,0 0 rgBTJ/Overlock	3.7	16
57	Floral visitation and reproductive traits of Stamenoid petals, a naturally occurring floral homeotic variant of <i>Capsella bursa-pastoris</i> (Brassicaceae). Planta, 2009, 230, 1239-1249.	3.2	15
58	A double-flowered variety of lesser periwinkle (<i>Vinca minor</i> fl. pl.) that has persisted in the wild for more than 160 years. Annals of Botany, 2011, 107, 1445-1452.	2.9	15
59	Missing Links: DNA-binding and Target Gene Specificity of Floral Homeotic Proteins. Advances in Botanical Research, 2006, , 209-236.	1.1	14
60	Plant miRNA Conservation and Evolution. Methods in Molecular Biology, 2019, 1932, 41-50.	0.9	14
61	Reconstructing the ancestral flower of extant angiosperms: the "war of the whorls"™ is heating up. Journal of Experimental Botany, 2019, 70, 2615-2622.	4.8	14
62	Genetics of identity. Nature, 2001, 414, 491-491.	27.8	13
63	A Dead Gene Walking: Convergent Degeneration of a Clade of MADS-Box Genes in Crucifers. Molecular Biology and Evolution, 2018, 35, 2618-2638.	8.9	10
64	Structural Requirements of the Phytoplasma Effector Protein SAP54 for Causing Homeotic Transformation of Floral Organs. Molecular Plant-Microbe Interactions, 2020, 33, 1129-1141.	2.6	9
65	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.	4.1	9
66	A tale of two morphs: developmental patterns and mechanisms of seed coat differentiation in the dimorphic diaspore model <i>Aethionema arabicum</i> (Brassicaceae). Plant Journal, 2021, 107, 166-181.	5.7	8
67	DNA-binding properties of the MADS-domain transcription factor SEPALLATA3 and mutant variants characterized by SELEX-seq. Plant Molecular Biology, 2021, 105, 543-557.	3.9	8
68	Independent origin of <i>MIRNA</i> genes controlling homologous target genes by partial inverted duplication of antisense-transcribed sequences. Plant Journal, 2020, 101, 401-419.	5.7	7
69	Evolution of Floral Organ Identity. , 2018, , 1-17.		5
70	Morphologically and physiologically diverse fruits of two <i>Lepidium</i> species differ in allocation of glucosinolates into immature and mature seed and pericarp. PLoS ONE, 2020, 15, e0227528.	2.5	3
71	New phytoplasma effector: 50 shades of green. Cell Host and Microbe, 2021, 29, 1601-1603.	11.0	3
72	Studying the Function of Phytoplasma Effector Proteins Using a Chemical-Inducible Expression System in Transgenic Plants. International Journal of Molecular Sciences, 2021, 22, 13582.	4.1	3

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73	Comparative transcriptomics identifies candidate genes involved in the evolutionary transition from dehiscent to indehiscent fruits in <i>Lepidium</i> (Brassicaceae). <i>BMC Plant Biology</i> , 2022, 22, .	3.6	3
74	Evolution of Floral Organ Identity. , 2021, , 697-713.		2
75	Stranger than Fiction; Loss of MADS-Box Genes During Evolutionary Miniaturization of the Duckweed Body Plan. <i>Compendium of Plant Genomes</i> , 2020, , 91-101.	0.5	1
76	My favourite flowering image: a cob of pod corn. <i>Journal of Experimental Botany</i> , 2014, 65, 6751-6754.	4.8	0
77	Title is missing!. , 2020, 15, e0227528.		0
78	Title is missing!. , 2020, 15, e0227528.		0
79	Title is missing!. , 2020, 15, e0227528.		0
80	Title is missing!. , 2020, 15, e0227528.		0
81	Title is missing!. , 2020, 15, e0227528.		0
82	Title is missing!. , 2020, 15, e0227528.		0