

# Günter Theisen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11869103/publications.pdf>

Version: 2024-02-01

103  
papers

11,467  
citations

47006

47  
h-index

40979

93  
g-index

109  
all docs

109  
docs citations

109  
times ranked

8859  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Evolution of Floral Organ Identity. , 2021, , 697-713.		2
4	<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
5	A tale of two morphs: developmental patterns and mechanisms of seed coat differentiation in the dimorphic diaspore model <i>Aethionema arabicum</i> (Brassicaceae). <i>Plant Journal</i> , 2021, 107, 166-181.	5.7	8
6	Extending the Toolkit for Beauty: Differential Co-Expression of DROOPING LEAF-Like and Class B MADS-Box Genes during <i>Phalaenopsis</i> Flower Development. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7025.	4.1	9
7	DNA-binding properties of the MADS-domain transcription factor <i>SEPALLATA3</i> and mutant variants characterized by SELEX-seq. <i>Plant Molecular Biology</i> , 2021, 105, 543-557.	3.9	8
8	Independent origin of <i>MIRNA</i> genes controlling homologous target genes by partial inverted duplication of antisense-transcribed sequences. <i>Plant Journal</i> , 2020, 101, 401-419.	5.7	7
9	Structural Requirements of the Phytoplasma Effector Protein <i>SAP54</i> for Causing Homeotic Transformation of Floral Organs. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 1129-1141.	2.6	9
10	Morphologically and physiologically diverse fruits of two <i>Lepidium</i> species differ in allocation of glucosinolates into immature and mature seed and pericarp. <i>PLoS ONE</i> , 2020, 15, e0227528.	2.5	3
11	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
12	Reconstructing the ancestral flower of extant angiosperms: the "war of the whorls" is heating up. <i>Journal of Experimental Botany</i> , 2019, 70, 2615-2622.	4.8	14
13	Mechanismen der Evolution. , 2019, , 127-134.		0
14	A conserved leucine zipper-like motif accounts for strong tetramerization capabilities of <i>SEPALLATA</i> -like MADS-domain transcription factors. <i>Journal of Experimental Botany</i> , 2018, 69, 1943-1954.	4.8	24
15	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
16	Array of MADS-Box Genes: Facilitator for Rapid Adaptation?. <i>Trends in Plant Science</i> , 2018, 23, 563-576.	8.8	35
17	A Dead Gene Walking: Convergent Degeneration of a Clade of MADS-Box Genes in Crucifers. <i>Molecular Biology and Evolution</i> , 2018, 35, 2618-2638.	8.9	10
18	The Chara Genome: Secondary Complexity and Implications for Plant Terrestrialization. <i>Cell</i> , 2018, 174, 448-464.e24.	28.9	420

#	ARTICLE	IF	CITATIONS
19	The floral homeotic protein <i>SEPALLATA3</i> recognizes target DNA sequences by shape readout involving a conserved arginine residue in the MADS domain. <i>Plant Journal</i> , 2018, 95, 341-357.	5.7	17
20	Evolution of Floral Organ Identity. , 2018, , 1-17.		5
21	The ABCs of flower development: mutational analysis of <i>AP1</i> / <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
22	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
23	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
24	The significance of developmental robustness for species diversity. <i>Annals of Botany</i> , 2016, 117, 725-732.	2.9	25
25	Structure and Evolution of Plant MADS Domain Transcription Factors. , 2016, , 127-138.		30
26	Non-canonical structure, function and phylogeny of the B sister MADS box gene Os MADS 30 of rice ( ) Tj ETQq000 rgBTj/Overlock	3.7	16
27	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
28	Did Convergent Protein Evolution Enable Phytoplasmas to Generate "Zombie Plants"™?. <i>Trends in Plant Science</i> , 2015, 20, 798-806.	8.8	28
29	<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
30	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
31	Evolutionary game theory: molecules as players. <i>Molecular BioSystems</i> , 2014, 10, 3066-3074.	2.9	39
32	Evolutionary game theory: cells as players. <i>Molecular BioSystems</i> , 2014, 10, 3044-3065.	2.9	108
33	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
34	My favourite flowering image: a cob of pod corn. <i>Journal of Experimental Botany</i> , 2014, 65, 6751-6754.	4.8	0
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Molecular mechanisms involved in convergent crop domestication. <i>Trends in Plant Science</i> , 2013, 18, 704-714.	8.8	150
39	Evidence that an evolutionary transition from dehiscent to indehiscent fruits in <i>Lepidium</i> ( <i>Borragaceae</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
40	Functional Conservation of MIKC*-Type MADS Box Genes in <i>Arabidopsis</i> and Rice Pollen Maturation. <i>Plant Cell</i> , 2013, 25, 1288-1303.	6.6	106
41	Conservation of fruit dehiscence pathways between <i>Lepidium campestre</i> and <i>Arabidopsis thaliana</i> sheds light on the regulation of <i>INDEHISCENT</i> . <i>Plant Journal</i> , 2013, 76, 545-556.	5.7	42
42	Mapping a floral trait in Shepherds purse "Stamenoid petals" in natural populations of <i>Capsella bursa-pastoris</i> (L.) Medik. <i>Flora: Morphology, Distribution, Functional Ecology of Plants</i> , 2013, 208, 641-647.	1.2	13
43	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
44	The <i>seirena</i> B Class Floral Homeotic Mutant of California Poppy ( <i>Eschscholzia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 467 Td (ca MADS Domain Protein Complexes. <i>Plant Cell</i> , 2013, 25, 438-453.	6.6	52
45	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
46	Selaginella Genome Analysis " Entering the "Homoplasmy Heaven" of the MADS World. <i>Frontiers in Plant Science</i> , 2012, 3, 214.	3.6	31
47	Molecular genetic basis of pod corn ( <i>Tunicate</i> maize). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7115-7120.	7.1	48
48	Loss of deeply conserved C-class floral homeotic gene function and C- and E-class protein interaction in a double-flowered ranunculid mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2267-75.	7.1	96
49	Live and Let Die - The Sister MADS-Box Gene <i>OsMADS29</i> 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
50	MADS and More: Transcription Factors That Shape the Plant. <i>Methods in Molecular Biology</i> , 2011, 754, 3-18.	0.9	15
51	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	12.6	794
52	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
53	A double-flowered variety of lesser periwinkle ( <i>Vinca minor</i> fl. pl.) that has persisted in the wild for more than 160 years. <i>Annals of Botany</i> , 2011, 107, 1445-1452.	2.9	15
54	SplamiR" prediction of spliced miRNAs in plants. <i>Bioinformatics</i> , 2011, 27, 1215-1223.	4.1	15

#	ARTICLE	IF	CITATIONS
55	The Genetics of <i>Capsella</i> . , 2011, , 373-387.		2
56	Cooperation and cheating in microbial exoenzyme production – Theoretical analysis for biotechnological applications. <i>Biotechnology Journal</i> , 2010, 5, 751-758.	3.5	31
57	On the origin of MADS-domain transcription factors. <i>Trends in Genetics</i> , 2010, 26, 149-153.	6.7	123
58	Functional conservation and diversification of class E floral homeotic genes in rice ( <i>Oryza</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	5.7	223
59	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
60	GORDITA (AGL63) is a young paralog of the <i>Arabidopsis thaliana</i> B-sister MADS box gene ABS (TT16) that has undergone neofunctionalization. <i>Plant Journal</i> , 2010, 63, 914-924.	5.7	49
61	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
62	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
63	Developmental Robustness by Obligate Interaction of Class B Floral Homeotic Genes and Proteins. <i>PLoS Computational Biology</i> , 2009, 5, e1000264.	3.2	29
64	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
65	<i>Lepidium</i> as a model system for studying the evolution of fruit development in Brassicaceae. <i>Journal of Experimental Botany</i> , 2009, 60, 1503-1513.	4.8	64
66	Positive selection and ancient duplications in the evolution of class B floral homeotic genes of orchids and grasses. <i>BMC Evolutionary Biology</i> , 2009, 9, 81.	3.2	43
67	Floral visitation and reproductive traits of Stamenoid petals, a naturally occurring floral homeotic variant of <i>Capsella bursa-pastoris</i> (Brassicaceae). <i>Planta</i> , 2009, 230, 1239-1249.	3.2	15
68	Saltational evolution: hopeful monsters are here to stay. <i>Theory in Biosciences</i> , 2009, 128, 43-51.	1.4	99
69	Why are orchid flowers so diverse? Reduction of evolutionary constraints by paralogues of class B floral homeotic genes. <i>Annals of Botany</i> , 2009, 104, 583-594.	2.9	135
70	MADS about the evolution of orchid flowers. <i>Trends in Plant Science</i> , 2008, 13, 51-59.	8.8	139
71	Missing Links: DNA-binding and Target Gene Specificity of Floral Homeotic Proteins. <i>Advances in Botanical Research</i> , 2006, , 209-236.	1.1	14
72	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

#	ARTICLE	IF	CITATIONS
73	The proper place of hopeful monsters in evolutionary biology. <i>Theory in Biosciences</i> , 2006, 124, 349-369.	1.4	96
74	Plant Breeding: MADS ways of memorizing winter: vernalization in weed and wheat. , 2006, , 162-177.		1
75	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
76	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
77	Gymnosperm Orthologues of Class B Floral Homeotic Genes and Their Impact on Understanding Flower Origin. <i>Critical Reviews in Plant Sciences</i> , 2004, 23, 129-148.	5.7	58
78	Plant Breeding: The ABCs of Flower Development in Arabidopsis and Rice. <i>Progress in Botany Fortschritte Der Botanik</i> , 2004, , 193-215.	0.3	3
79	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
80	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
81	And then there were many: MADS goes genomic. <i>Trends in Plant Science</i> , 2003, 8, 475-483.	8.8	179
82	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
83	Evolution of Class B Floral Homeotic Proteins: Obligate Heterodimerization Originated from Homodimerization. <i>Molecular Biology and Evolution</i> , 2002, 19, 587-596.	8.9	167
84	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
85	Orthology: Secret life of genes. <i>Nature</i> , 2002, 415, 741-741.	27.8	66
86	Key Genes of Crop Domestication and Breeding: Molecular Analyses. <i>Progress in Botany Fortschritte Der Botanik</i> , 2002, , 189-203.	0.3	4
87	Characterization of three GLOBOSA -like MADS-box genes from maize: evidence for ancient paralogy in one class of floral homeotic B-function genes of grasses. <i>Gene</i> , 2001, 262, 1-13.	2.2	108
88	Why donâ€™t mosses flower?. <i>New Phytologist</i> , 2001, 150, 1-5.	7.3	41
89	Floral quartets. <i>Nature</i> , 2001, 409, 469-471.	27.8	826
90	Development of floral organ identity: stories from the MADS house. <i>Current Opinion in Plant Biology</i> , 2001, 4, 75-85.	7.1	799

#	ARTICLE	IF	CITATIONS
91	BiodiversitÄtsmessung bei Pflanzen anhand molekularer Daten: Ein Beitrag zur wissenschaftlichen Definition von BiodiversitÄt. Wissenschaftsethik Und Technikfolgenbeurteilung, 2001, , 181-234.	1.0	4
92	MADS-Box Gene Diversity in Seed Plants 300 Million Years Ago. Molecular Biology and Evolution, 2000, 17, 1425-1434.	8.9	145
93	Evolutionary developmental genetics of floral symmetry: The revealing power of Linnaeus' monstrous flower. BioEssays, 2000, 22, 209-213.	2.5	40
94	Shattering developments. Nature, 2000, 404, 711-713.	27.8	21
95	Plant Breeding: FLO-Like Meristem Identity Genes: from Basic Science to Crop Plant Design. Progress in Botany Fortschritte Der Botanik, 2000, , 167-183.	0.3	6
96	The golden decade of molecular floral development(1990â€“1999): A cheerful obituary. Genesis, 1999, 25, 181-193.	2.1	3
97	The golden decade of molecular floral development (1990-1999): A cheerful obituary. , 1999, 25, 181-193.		40
98	ADEF/GLO-like MADS-box gene from a gymnosperm:Pinus radiata contains an ortholog of angiosperm B class floral homeotic genes. Genesis, 1999, 25, 245-252.	2.1	87
99	MADS-box genes active in developing pollen cones of Norway spruce (Picea abies) are homologous to the B-class floral homeotic genes in angiosperms. Genesis, 1999, 25, 253-266.	2.1	103
100	Molecular Architects of Plant Body Plans. Progress in Botany Fortschritte Der Botanik, 1998, , 227-256.	0.3	14
101	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.	1.8	467
102	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.	1.8	47
103	Combinatorial Control of Floral Organ Identity by MADS-domain Transcription Factors. , 0, , 253-265.		3