Koen Geuten

List of Publications by Year
in descending order

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35 papers	1,809 citations	346980 22 h-index	406436 35 g-index
38 all docs	38 docs citations	38 times ranked	3151 citing authors

#	Article	IF	Citations
1	Insights Into Natural Genetic Resistance to Rice Yellow Mottle Virus and Implications on Breeding for Durable Resistance. Frontiers in Plant Science, 2021, 12, 671355.	1.7	10
2	Single and Combined Methods to Specifically or Bulk-Purify RNAâ€"Protein Complexes. Biomolecules, 2020, 10, 1160.	1.8	13
3	The Role of FLOWERING LOCUS C Relatives in Cereals. Frontiers in Plant Science, 2020, 11, 617340.	1.7	17
4	The molecular mechanism of vernalization in Arabidopsis and cereals: role of Flowering Locus C and its homologs. Physiologia Plantarum, 2020, 170, 373-383.	2.6	34
5	Cold Induced Antisense Transcription of FLOWERING LOCUS C in Distant Grasses. Frontiers in Plant Science, 2019, 10, 72.	1.7	20
6	The Effect of Ambient Temperature on Brachypodium distachyon Development. Frontiers in Plant Science, 2019, 10, 1011.	1.7	5
7	Resurrected Protein Interaction Networks Reveal the Innovation Potential of Ancient Whole-Genome Duplication. Plant Cell, 2018, 30, 2741-2760.	3.1	13
8	TM8 represses developmental timing in Nicotiana benthamiana and has functionally diversified in angiosperms. BMC Plant Biology, 2018, 18, 129.	1.6	3
9	The Origin of Floral Organ Identity Quartets. Plant Cell, 2017, 29, 229-242.	3.1	44
10	A Flowering Locus C Homolog Is a Vernalization-Regulated Repressor in <i>Brachypodium</i> and Is Cold Regulated in Wheat. Plant Physiology, 2017, 173, 1301-1315.	2.3	78
11	Exploiting DELLA Signaling in Cereals. Trends in Plant Science, 2017, 22, 880-893.	4.3	115
12	mRNA Interactome Capture from Plant Protoplasts. Journal of Visualized Experiments, 2017, , .	0.2	1
13	Extensive gene content variation in the Brachypodium distachyon pan-genome correlates with population structure. Nature Communications, 2017, 8, 2184.	5.8	269
14	UV crosslinked mRNA-binding proteins captured from leaf mesophyll protoplasts. Plant Methods, 2016, 12, 42.	1.9	53
15	Evolution of DNA-Binding Sites of a Floral Master Regulatory Transcription Factor. Molecular Biology and Evolution, 2016, 33, 185-200.	3.5	32
16	FLOWERING LOCUS C in monocots and the tandem origin of angiosperm-specific MADS-box genes. Nature Communications, 2013, 4, 2280.	5.8	142
17	When paleontology and molecular genetics meet: a genetic context for the evolution of conifer ovuliferous scales. New Phytologist, 2013, 200, 10-12.	3.5	6
18	The hybrid Fourâ€<scp>CBS</scp>â€Domain <scp>KIN</scp>Î²Î³ subunit functions as the canonical Î³ subunit of the plant energy sensor Sn<scp>RK</scp>1. Plant Journal, 2013, 75, 11-25.	2.8	77

#	ARTICLE	IF	CITATIONS
19	Analysis of Developmental Control Genes Using Virus-Induced Gene Silencing. Methods in Molecular Biology, 2013, 975, 61-69.	0.4	4
20	Heterochronic genes in plant evolution and development. Frontiers in Plant Science, 2013, 4, 381.	1.7	30
21	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. Molecular Biology and Evolution, 2012, 29, 3793-3806.	3.5	127
22	Transference of function shapes organ identity in the dove tree inflorescence. New Phytologist, 2012, 193, 216-228.	3.5	23
23	Robustness and evolvability in the B-system of flower development. Annals of Botany, 2011, 107, 1545-1556.	1.4	19
24	Unraveling the Phylogeny of Heptacodium and Zabelia (Caprifoliaceae): An Interdisciplinary Approach. Systematic Botany, 2011, 36, 231-252.	0.2	27
25	Expression divergence of the AGL6 MADS domain transcription factor lineage after a core eudicot duplication suggests functional diversification. BMC Plant Biology, 2010, 10, 148.	1.6	28
26	Hidden Variability of Floral Homeotic B Genes in Solanaceae Provides a Molecular Basis for the Evolution of Novel Functions Â. Plant Cell, 2010, 22, 2562-2578.	3.1	64
27	Pistillataâ€"Duplications as a Mode for Floral Diversification in (Basal) Asterids. Molecular Biology and Evolution, 2009, 26, 2627-2645.	3.5	38
28	Experimental Design Criteria in Phylogenetics: Where to Add Taxa. Systematic Biology, 2007, 56, 609-622.	2.7	65
29	Phylogenetic utility of the AP3/DEF K-domain and its molecular evolution in Impatiens (Balsaminaceae). Molecular Phylogenetics and Evolution, 2007, 43, 225-239.	1.2	49
30	The rice genome encodes two vacuolar invertases with fructan exohydrolase activity but lacks the related fructan biosynthesis genes of the Pooideae. New Phytologist, 2007, 173, 50-62.	3.5	58
31	Phylogenetics of <I>Impatiens</I> and <I>Hydrocera</I> (Balsaminaceae) Using Chloroplast <I>atpB-rbcL</I> Spacer Sequences. Systematic Botany, 2006, 31, 171-180.	0.2	112
32	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
33	Palynological Variation in Balsaminoid Ericales. II. Balsaminaceae, Tetrameristaceae, Pellicieraceae and General Conclusions. Annals of Botany, 2005, 96, 1061-1073.	1.4	26
34	<i>Gomphocalyx</i> and <i>Phylohydrax</i> (Rubiaceae): sister taxa excluded from Spermacoceae s.s., featuring a remarkable case of convergent evolution. Taxon, 2005, 54, 91-107.	0.4	19
35	Phylogeny and biogeography of Balsaminaceae inferred from ITS sequences. Taxon, 2004, 53, 391-404.	0.4	133