Matthias Fladung

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2060733/publications.pdf

Version: 2024-02-01

104 papers	2,768 citations	201674 27 h-index	206112 48 g-index
111 all docs	111 docs citations	111 times ranked	2840 citing authors

#	Article	IF	Citations
1	Transgenic potato plants resistant to the phytopathogenic bacterium Erwinia carotovora. Plant Journal, 1993, 3, 587-598.	5.7	179
2	Hormonal content and sensitivity of transgenic tobacco and potato plants expressing single rol genes of Agrobacterium rhizogenes T-DNA. Plant Journal, 1993, 3, 371-382.	5.7	151
3	Over-expression of an FT-homologous gene of apple induces early flowering in annual and perennial plants. Planta, 2010, 232, 1309-1324.	3.2	144
4	A single gene underlies the dynamic evolution of poplar sex determination. Nature Plants, 2020, 6, 630-637.	9.3	138
5	Gene stability in transgenic aspen (Populus). II. Molecular characterization of variable expression of transgene in wild and hybrid aspen. Planta, 2001, 213, 731-740.	3.2	100
6	Genetic linkage mapping in aspen (Populus tremula L. and Populus tremuloides Michx.). Tree Genetics and Genomes, 2009, 5, 505-515.	1.6	97
7	Title is missing!. Transgenic Research, 1997, 6, 111-121.	2.4	88
8	Effects of altered phosphoenolpyruvate carboxylase activities on transgenic C3 plant Solanum tuberosum. Plant Molecular Biology, 1996, 32, 831-848.	3.9	83
9	Transgene integration in aspen: structures of integration sites and mechanism of T-DNA integration. Plant Journal, 2002, 31, 543-551.	5.7	82
10	Function of defensive volatiles in pedunculate oak (Quercus robur) is tricked by the moth Tortrix viridana. Plant, Cell and Environment, 2012, 35, 2192-2207.	5.7	80
11	Characterization and spatial distribution of ectomycorrhizas colonizing aspen clones released in an experimental field. Mycorrhiza, 2004, 14, 295-306.	2.8	64
12	Mycorrhizal colonization of transgenic aspen in a field trial. Planta, 2002, 214, 653-660.	3.2	61
13	Controlling transgene integration in plants. Trends in Plant Science, 2001, 6, 155-159.	8.8	57
14	Heterologous overexpression of the birch FRUITFULL-like MADS-box gene BpMADS4 prevents normal senescence and winter dormancy in Populus tremula L.. Planta, 2008, 227, 1001-1011.	3.2	56
15	The 20-year environmental safety record of GM trees. Nature Biotechnology, 2010, 28, 656-658.	17.5	55
16	Biosafety in Populus spp. and other forest trees: from non-native species to taxa derived from traditional breeding and genetic engineering. Trees - Structure and Function, 2006, 20, 131-144.	1.9	54
17	A Reference Genome Sequence for the European Silver Fir (Abies alba Mill.): A Community-Generated Genomic Resource. G3: Genes, Genomes, Genetics, 2019, 9, 2039-2049.	1.8	53
18	Genome Sequences of Populus tremula Chloroplast and Mitochondrion: Implications for Holistic Poplar Breeding. PLoS ONE, 2016, 11, e0147209.	2.5	48

#	Article	IF	Citations
19	Alterations in hormonal and developmental characteristics in transgenic Populus conditioned by the rolC gene from Agrobacterium rhizogenes. Journal of Plant Physiology, 1997, 150, 420-427.	3.5	44
20	Evaluating the Efficiency of gRNAs in CRISPR/Cas9 Mediated Genome Editing in Poplars. International Journal of Molecular Sciences, 2019, 20, 3623.	4.1	43
21	Genetic mapping of linkage group XIX and identification of sex-linked SSR markers in a Populus tremulaÂÃ— Populus tremuloides cross. Canadian Journal of Forest Research, 2011, 41, 245-253.	1.7	42
22	Elimination of marker genes and targeted integration via FLP/FRT recombination system from yeast in hybrid aspen (Populus tremula L. Ã— P. tremuloides Michx.). Tree Genetics and Genomes, 2010, 6, 205-217.	1.6	40
23	Molecular identification of individual oak and fir trees from maternal tissues of their fruits or seeds. Trees - Structure and Function, 2003, 17, 345-350.	1.9	37
24	Integrated transcriptomics and metabolomics decipher differences in the resistance of pedunculate oak to the herbivore Tortrix viridanaL.. BMC Genomics, 2013, 14, 737.	2.8	35
25	Stable haploid poplar callus lines from immature pollen culture. Physiologia Plantarum, 2004, 120, 613-622.	5.2	34
26	The ectomycorrhizal morphotype Pinirhiza sclerotia is formed by Acephala macrosclerotiorum sp. nov., a close relative of Phialocephala fortinii. Mycorrhiza, 2009, 19, 481-492.	2.8	34
27	Ac/Ds-transposon activation tagging in poplar: a powerful tool for gene discovery. BMC Genomics, 2012, 13, 61.	2.8	33
28	Whole-genome draft assembly of Populus tremula x P. alba clone INRA 717-1B4. Silvae Genetica, 2016, 65, 74-79.	0.8	29
29	The Diversity and Dynamics of Sex Determination in Dioecious Plants. Frontiers in Plant Science, 2020, 11, 580488.	3.6	29
30	Genetic Variants of Panicum maximum (Jacq.) in C4 Photosynthetic Traits. Journal of Plant Physiology, 1994, 143, 165-172.	3.5	27
31	Resistance reactions of leaves and tubers of rolC transgenic tetraploid potato to bacterial and fungal pathogens. Correlation with sugar, starch and chlorophyll content. Physiological and Molecular Plant Pathology, 1993, 42, 123-132.	2.5	26
32	High Level of Conservation of Mitochondrial RNA Editing Sites Among Four Populus Species. G3: Genes, Genomes, Genetics, 2019, 9, 709-717.	1.8	26
33	Influence of over-expression of the FLOWERING PROMOTING FACTOR 1 gene (FPF1) from Arabidopsis on wood formation in hybrid poplar (Populus tremula L. Ã— P. tremuloides Michx.). Planta, 2012, 235, 359-373.	3.2	25
34	Excision of the maize transposable element Ac in periclinal chimeric leaves of 35S-Ac-rolC transgenic aspen-Populus. , 1997, 33, 1097-1103.		23
35	Genomics of sex determination in dioecious trees and woody plants. Trees - Structure and Function, 2017, 31, 1113-1125.	1.9	23
36	European discussion forum on transgenic tree biosafety. Nature Biotechnology, 2012, 30, 37-38.	17.5	21

#	Article	IF	Citations
37	Constitutive or light-regulated expression of the rolC gene in transgenic potato plants has different effects on yield attributes and tuber carbohydrate composition. Plant Molecular Biology, 1993, 23, 749-757.	3.9	20
38	Insertional mutagenesis in Populus: relevance and feasibility. Tree Genetics and Genomes, 2005, 1, 135-142.	1.6	20
39	Successful crossings with early flowering transgenic poplar: interspecific crossings, but not transgenesis, promoted aberrant phenotypes in offspring. Plant Biotechnology Journal, 2014, 12, 1066-1074.	8.3	20
40	Determination of Transgene Repeat Formation and Promoter Methylation in Transgenic Plants. BioTechniques, 2000, 28, 1128-1137.	1.8	19
41	Somatic mobility of the maize element Ac and its utility for gene tagging in aspen. Plant Molecular Biology, 2003, 51, 643-650.	3.9	19
42	Low temperatures are required to induce the development of fertile flowers in transgenic male and female early flowering poplar (Populus tremulaL.). Tree Physiology, 2016, 36, 667-677.	3.1	19
43	Morphology, wood structure and cell wall composition of rolC transgenic and non-transformed aspen trees. Trees - Structure and Function, 2001, 15, 503-517.	1.9	17
44	Genome Instability in Woody Plants Derived from Genetic Engineering. , 2006, , 301-321.		16
45	Influence of overexpression of a gibberellin 20-oxidase gene on the kinetics of xylem cell development in hybrid poplar (Populus tremula L. and P. tremuloides Michx.). Holzforschung, 2006, 60, 608-617.	1.9	16
46	Identification of single nucleotide polymorphisms in different Populus species. Trees - Structure and Function, 2009, 23, 1199-1212.	1.9	16
47	Spatial genetic structure in fourPinusspecies in the Sierra Madre Occidental, Durango, Mexico. Canadian Journal of Forest Research, 2017, 47, 73-80.	1.7	16
48	Faster Evaluation of Induced Floral Sterilit. Silvae Genetica, 2006, 55, 285-291.	0.8	16
49	ARR17 controls dioecy in Populus by repressing B-class MADS-box gene expression. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20210217.	4.0	16
50	Vegetative and generative dispersal capacity of field released transgenic aspen trees. Trees - Structure and Function, 2003, 17, 412-416.	1.9	15
51	Old methods rediscovered: application and improvement of two direct transformation methods to hybrid poplar (Populus tremulaâ€‰Ã—â€‰P. alba). Plant Cell, Tissue and Organ Culture, 2017, 130, 183-196.	2.3	15
52	Callus induction and plant regeneration in Panicum bisulcatum and Panicum milioides. Plant Cell Reports, 1986, 5, 169-173.	5.6	14
53	Development of DNA-based methods to identify CITES-protected timber species: a case study in the Meliaceae family. Holzforschung, 2012, 66, .	1.9	14
54	Genomic stability and long-term transgene expression in poplar. Transgenic Research, 2013, 22, 1167-1178.	2.4	14

#	Article	IF	Citations
55	European oak chemical diversity â€“ from ecotypes to herbivore resistance. New Phytologist, 2021, 232, 818-834.	7.3	14
56	Towards construction of an ultra high density linkage map for Pinus pinaster. Annals of Forest Science, 2002, 59, 637-643.	2.0	14
57	Knockdown of PCBER1, a gene of neolignan biosynthesis, resulted in increased poplar growth. Planta, 2019, 249, 515-525.	3.2	13
58	Effect of varying environments on photosynthetic parameters of C3, C3-C4 and C4 species of Panicum. Oecologia, 1989, 79, 168-173.	2.0	11
59	Analysis of re-integrated Ac element positions in the genome of Populus provides a basis for Ac/Ds-transposon activation tagging in trees. Trees - Structure and Function, 2011, 25, 551-557.	1.9	10
60	Transgene copy number estimation and analysis of gene expression levels in Populus spp. transgenic lines. BMC Proceedings, 2011, 5, P152.	1.6	10
61	Potentials and limitations of the cross-species transfer of nuclear microsatellite marker in six species belonging to three sections of the genus Populus L.. Tree Genetics and Genomes, 2013, 9, 1413-1421.	1.6	10
62	Cibus' herbicide-resistant canola in European limbo. Nature Biotechnology, 2016, 34, 473-474.	17.5	10
63	Methyl salicylate as a signaling compound that contributes to forest ecosystem stability. Trees - Structure and Function, 2021, 35, 1755-1769.	1.9	10
64	Genetic Engineering Contribution to Forest Tree Breeding Efforts. Forestry Sciences, 2016, , 11-29.	0.4	10
65	Developmental Studies on Photosynthetic Parameters in C3, C3 - C4 and C4 Plants of Panicum. Journal of Plant Physiology, 1987, 130, 461-470.	3.5	9
66	Chloroplast SNP-marker as powerful tool for differentiation of Populus species in reliable poplar breeding and barcoding approaches. BMC Proceedings, 2011, 5, .	1.6	9
67	Development of Multiplexed Marker Sets to Identify the Most Relevant Poplar Species for Breeding. Forests, 2017, 8, 492.	2.1	9
68	Targeted CRISPR/Cas9-Based Knock-Out of the Rice Orthologs TILLER ANGLE CONTROL 1 (TAC1) in Poplar Induces Erect Leaf Habit and Shoot Growth. Forests, 2021, 12, 1615.	2.1	9
69	Individual tree genotypes do not explain ectomycorrhizal biodiversity in soil cores of a pure stand of beech (Fagus sylvatica L.). Trees - Structure and Function, 2013, 27, 1327-1338.	1.9	8
70	Genetic structure of remnant black poplar (Populus nigra L.) populations along biggest rivers in Serbia assessed by SSR markers. Silvae Genetica, 2016, 65, 12-19.	0.8	7
71	Poplar Transformation. Methods in Molecular Biology, 2019, 1864, 165-177.	0.9	7
72	Oaks as Beacons of Hope for Threatened Mixed Forests in Central Europe. Frontiers in Forests and Global Change, 2021, 4, .	2.3	7

#	Article	IF	Citations
73	The genetic basis of sex determination in Populus provides molecular markers across the genus and indicates convergent evolution. Silvae Genetica, 2021, 70, 145-155.	0.8	7
74	TallPinus luzmariaetrees with genes fromP. herrerae. PeerJ, 2020, 8, e8648.	2.0	7
75	Identification of transgenes from wood of genetically transformed poplar trees. Wood Science and Technology, 2004, 38, 207-215.	3.2	6
76	Development of mitochondrial SNP markers in different Populus species. Trees - Structure and Function, 2015, 29, 575-582.	1.9	6
77	EU Regulations Impede Market Introduction of GM Forest Trees. Trends in Plant Science, 2016, 21, 283-285.	8.8	6
78	Identification and analysis of key genes involved in methyl salicylate biosynthesis in different birch species. PLoS ONE, 2020, 15, e0240246.	2.5	6
79	Species determination and phylogenetic relationships of the genus Betula inferred from multiple chloroplast and nuclear regions reveal the high methyl salicylate-producing ability of the ancestor. Trees - Structure and Function, 2020, 34, 1131-1146.	1.9	6
80	Efficient evaluation of a gene containment system for poplar through early flowering induction. Plant Cell Reports, 2020, 39, 577-587.	5.6	6
81	Functional Genomics of Flowering Time in Trees. , 2012, , 39-69.		5
82	Level of tissue differentiation influences the activation of a heat-inducible flower-specific system for genetic containment in poplar (Populus tremula L.). Plant Cell Reports, 2016, 35, 369-384.	5.6	5
83	Long-term study of a subdioecious Populusâ€‰Ã—canescens family reveals sex lability of females and reproduction behaviour of cosexual plants. Plant Reproduction, 2020, 33, 1-17.	2.2	5
84	Gene Targeting in Plants. , 2002, , 481-499.		5
85	Flexible DNA isolation procedure for different tree species as a convenient lab routine. Silvae Genetica, 2022, 71, 20-30.	0.8	5
86	Growth of Mixoploid GIBBERELLIC ACIDÂ20 OXIDASE (GA20-OXIDASE) Overexpressing Transgenic Populus. Gesunde Pflanzen, 2018, 70, 91-98.	3.0	4
87	Overexpression of both flowering time genes AtSOC1 and SaFUL revealed huge influence onto plant habitus in poplar. Tree Genetics and Genomes, 2019, 15, 1.	1.6	4
88	Targeted integration and removal of transgenes in hybrid aspen (Populus tremula L.â€ƒÃ—â€ƒP.Âtremuloides) Tj ETQq0 0 0 rgBT /Overlo	3.8	3
89	RNA-seq of eight different poplar clones reveals conserved up-regulation of gene expression in response to insect herbivory. BMC Genomics, 2019, 20, 673.	2.8	3
90	Selfing of a single monoecious Populus tremula tree produces viable males, females and â€œsupermalesâ€• Trees - Structure and Function, 2019, 33, 803-816.	1.9	3

#	Article	IF	Citations
91	Sequencing of two transgenic early-flowering poplar lines confirmed vector-free single-locus T-DNA integration. Transgenic Research, 2020, 29, 321-337.	2.4	3
92	Genome-wide bioinformatics analysis revealed putative substrate specificities of SABATH and MES family members in silver birch (Betula pendula). Silvae Genetica, 2021, 70, 57-74.	0.8	3
93	Modification of Cellulose in Wood. , 2006, , 123-136.		2
94	Spatial Genetic Structure within and among Seed Stands of Pinus engelmannii Carr. and Pinus leiophylla Schiede ex Schltdl. & Cham, in Durango, Mexico. Forests, 2017, 8, 22.	2.1	2
95	Investigation of Horizontal Gene Transfer from Transgenic Aspen to Ectomycorrhizal Fungi. , 2006, , 323-333.		2
96	Public Knowledge and Perceptions of Safety Issues Towards the Use of Genetically Modified Forest Trees: A Cross-Country Pilot Survey. Forestry Sciences, 2016, , 223-244.	0.4	2
97	Xylem-specific Overexpression of the GIBBERELLIN ACIDÂ20 OXIDASE Gene (GA20-OXIDASE) from Pine in Hybrid Poplar (Populus tremula L.â€Ã—â€‰P.ÂalbaÂL.) Revealed Reliable Increase in Growth and Biomass Production Just in aÂSingle-copy-line. Gesunde Pflanzen, 2022, 74, 239-248.	3.0	2
98	Activation tagging in poplar by using an inducible Ac/Ds transposon system. BMC Proceedings, 2011, 5, .	1.6	1
99	Transposon Activation Tagging in Plants for Gene Function Discovery. Progress in Botany Fortschritte Der Botanik, 2016, , 265-289.	0.3	1
100	Transcriptome analysis of North American sweet birch (Betula lenta) revealed a higher expression of genes involved in the biosynthesis of secondary metabolites than European silver birch (B. pendula). Journal of Plant Research, 2021, 134, 1253-1264.	2.4	1
101	Debate is failing Europe's geneticists. Nature, 2017, 544, 35-35.	27.8	0
102	Editorial: Advances and Challenges of RNAi Based Technologies for Plants. Frontiers in Plant Science, 2021, 12, 680242.	3.6	0
103	Soil Effects of Genetically Modified Trees (GMTs). Forestry Sciences, 2016, , 155-172.	0.4	0
104	Biotechnologie schnellwachsender Baumarten. , 2018, , 147-168.		0