

JÃ¼rgen Ehling

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

3,083
citations

201674

27
h-index

302126

39
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41
all docs

41
docs citations

41
times ranked

4687
citing authors

#	ARTICLE	IF	CITATIONS
1	Three 4-coumarate:coenzyme A ligases in <i>Arabidopsis thaliana</i> represent two evolutionarily divergent classes in angiosperms. <i>Plant Journal</i> , 1999, 19, 9-20.	5.7	402
2	Global transcript profiling of primary stems from <i>Arabidopsis thaliana</i> identifies candidate genes for missing links in lignin biosynthesis and transcriptional regulators of fiber differentiation. <i>Plant Journal</i> , 2005, 42, 618-640.	5.7	254
3	Genome-wide association implicates numerous genes underlying ecological trait variation in natural populations of <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2014, 203, 535-553.	7.3	171
4	Genome-wide association mapping for wood characteristics in <i>Populus</i> identifies an array of candidate single nucleotide polymorphisms. <i>New Phytologist</i> , 2013, 200, 710-726.	7.3	158
5	A phenol-enriched cuticle is ancestral to lignin evolution in land plants. <i>Nature Communications</i> , 2017, 8, 14713.	12.8	157
6	Evolution of a Novel Phenolic Pathway for Pollen Development. <i>Science</i> , 2009, 325, 1688-1692.	12.6	148
7	A coumaroyl-ester-3-hydroxylase Insertion Mutant Reveals the Existence of Nonredundant meta-Hydroxylation Pathways and Essential Roles for Phenolic Precursors in Cell Expansion and Plant Growth. <i>Plant Physiology</i> , 2006, 140, 30-48.	4.8	139
8	Evolutionary classification of ammonium, nitrate, and peptide transporters in land plants. <i>BMC Evolutionary Biology</i> , 2014, 14, 11.	3.2	127
9	An extensive (co-)expression analysis tool for the cytochrome P450 superfamily in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2008, 8, 47.	3.6	108
10	Gene Coexpression Analysis Reveals Complex Metabolism of the Monoterpene Alcohol Linalool in <i>Arabidopsis</i> Flowers. <i>Plant Cell</i> , 2013, 25, 4640-4657.	6.6	104
11	Cloning, Functional Expression, and Subcellular Localization of Multiple NADPH-Cytochrome P450 Reductases from Hybrid Poplar. <i>Plant Physiology</i> , 2002, 130, 1837-1851.	4.8	102
12	Mutational analysis of 4-coumarate:CoA ligase identifies functionally important amino acids and verifies its close relationship to other adenylate-forming enzymes. <i>FEBS Letters</i> , 2000, 467, 117-122.	2.8	99
13	Structure and Evolution of 4-Coumarate:Coenzyme A Ligase (4CL) Gene Families. <i>Biological Chemistry</i> , 2001, 382, 645-54.	2.5	97
14	Cytochromes P450 in phenolic metabolism. <i>Phytochemistry Reviews</i> , 2006, 5, 239-270.	6.5	93
15	Comparative transcriptome analysis of <i>Arabidopsis thaliana</i> infested by diamond back moth (<i>Plutella</i>) Tj ETQq1 1 0.784314 rgBT /Ove Genomics, 2008, 9, 154.	2.8	90
16	Multiple cis-regulatory elements regulate distinct and complex patterns of developmental and wound-induced expression of <i>Arabidopsis thaliana</i> 4CL gene family members. <i>Planta</i> , 2006, 224, 1226-1238.	3.2	79
17	<i>Arabidopsis thaliana</i> CYP77A4 is the first cytochrome P450 able to catalyze the epoxidation of free fatty acids in plants. <i>FEBS Journal</i> , 2009, 276, 719-735.	4.7	73
18	Identification of 4-coumarate:coenzyme A ligase (4CL) substrate recognition domains. <i>Plant Journal</i> , 2001, 27, 455-465.	5.7	61

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19	Transcriptional responses of <i>Arabidopsis thaliana</i> to chewing and sucking insect herbivores. <i>Frontiers in Plant Science</i> , 2014, 5, 565.	3.6	61
20	Microarray expression profiling and functional characterization of AtTPS genes: Duplicated <i>Arabidopsis thaliana</i> sesquiterpene synthase genes At4g13280 and At4g13300 encode root-specific and wound-inducible (Z)- β -bisabolene synthases. <i>Archives of Biochemistry and Biophysics</i> , 2006, 448, 104-116.	3.0	60
21	Molecular Characterization of Quinate and Shikimate Metabolism in <i>Populus trichocarpa</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 23846-23858.	3.4	55
22	The Reductase Activity of the <i>Arabidopsis</i> Caleosin RESPONSIVE TO DESSICATION20 Mediates Gibberellin-Dependent Flowering Time, Abscisic Acid Sensitivity, and Tolerance to Oxidative Stress. <i>Plant Physiology</i> , 2014, 166, 109-124.	4.8	53
23	Evolution of a secondary metabolic pathway from primary metabolism: shikimate and quinate biosynthesis in plants. <i>Plant Journal</i> , 2018, 95, 823-833.	5.7	44
24	The regulatory role of shikimate in plant phenylalanine metabolism. <i>Journal of Theoretical Biology</i> , 2019, 462, 158-170.	1.7	42
25	Network analysis reveals the relationship among wood properties, gene expression levels and genotypes of natural <i>Populus trichocarpa</i> accessions. <i>New Phytologist</i> , 2013, 200, 727-742.	7.3	37
26	Actin Coding Regions: Gene Family Evolution and Use as a Phylogenetic Marker. <i>Archiv für Protistenkunde</i> , 1995, 145, 155-164.	0.8	33
27	Evolution of coumaroyl conjugate 3-hydroxylases in land plants: lignin biosynthesis and defense. <i>Plant Journal</i> , 2019, 99, 924-936.	5.7	32
28	Evolutionary Quantitative Genomics of <i>Populus trichocarpa</i> . <i>PLoS ONE</i> , 2015, 10, e0142864.	2.5	31
29	Discovery of salicyl benzoate UDP-glycosyltransferase, a central enzyme in poplar salicinoid phenolic glycoside biosynthesis. <i>Plant Journal</i> , 2020, 102, 99-115.	5.7	31
30	A role for <i>SPEECHLESS</i> in the integration of leaf stomatal patterning with the growth vs disease trade-off in poplar. <i>New Phytologist</i> , 2019, 223, 1888-1903.	7.3	25
31	<i>Arabidopsis thaliana</i> Full Genome Longmer Microarrays: A Powerful Gene Discovery Tool for Agriculture and Forestry. <i>Transgenic Research</i> , 2005, 14, 551-561.	2.4	19
32	Net NH ₄ ⁺ and NO ₃ ⁻ flux, and expression of NH ₄ ⁺ and NO ₃ ⁻ transporters in roots of <i>Picea glauca</i> . <i>Trees - Structure and Function</i> , 2012, 26, 1403-1411.	1.9	17
33	Extensive Functional Pleiotropy of REVOLUTA Substantiated through Forward Genetics. <i>Plant Physiology</i> , 2014, 164, 548-554.	4.8	17
34	Cytochrome P450s in Lignin Biosynthesis. <i>Advances in Botanical Research</i> , 2012, , 113-143.	1.1	13
35	Transcriptome analysis provides insight into venom evolution in a seed-parasitic wasp, <i>Megastigmus spermotrophus</i> . <i>Insect Molecular Biology</i> , 2016, 25, 604-616.	2.0	13
36	Comparative Genomics of The Shikimate Pathway in <i>Arabidopsis</i> , <i>Populus Trichocarpa</i> and <i>Oryza Sativa</i> : Shikimate Pathway Gene Family Structure and Identification of Candidates for Missing Links in Phenylalanine Biosynthesis. <i>Recent Advances in Phytochemistry</i> , 2006, , 85-113.	0.5	12

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37	Genetic analysis and epigenetic silencing of At4CL1 and At4CL2 expression in transgenic Arabidopsis. <i>Biotechnology Journal</i> , 2006, 1, 1124-1136.	3.5	8
38	A transcriptomic resource for Douglas-fir seed development and analysis of transcription during late megagametophyte development. <i>Plant Reproduction</i> , 2016, 29, 273-286.	2.2	8
39	Phenylpropanoid and Phenolic Metabolism in <i>Populus</i> . , 2011, , 304-326.		4
40	Genome Wide Approaches in Natural Product Research. , 2009, , 475-503.		0