

Helge KÃ¼ster

List of Publications by Year in descending order

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83
papers

5,624
citations

66343
42
h-index

76900
74
g-index

83
all docs

83
docs citations

83
times ranked

5171
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Medicago truncatula</i> Transcriptome Database MtExpress: Genome-Wide Expression Profiles at Your Fingertips. <i>Plant and Cell Physiology</i> , 2021, 62, 1359-1361.	3.1	2
2	The gene space of European mistletoe (<i>Viscum album</i>). <i>Plant Journal</i> , 2021, , .	5.7	9
3	Insights into the complex role of GRAS transcription factors in the arbuscular mycorrhiza symbiosis. <i>Scientific Reports</i> , 2019, 9, 3360.	3.3	14
4	Molecular Background of Pi Deficiency-Induced Root Hair Growth in <i>Brassica carinata</i> – A Fasciclin-Like Arabinogalactan Protein Is Involved. <i>Frontiers in Plant Science</i> , 2018, 9, 1372.	3.6	13
5	The mycorrhiza-dependent defensin MtDefMd1 of <i>Medicago truncatula</i> acts during the late restructuring stages of arbuscule-containing cells. <i>PLoS ONE</i> , 2018, 13, e0191841.	2.5	9
6	Pre-announcement of symbiotic guests: transcriptional reprogramming by mycorrhizal lipochitooligosaccharides shows a strict co-dependency on the GRAS transcription factors NSP1 and RAM1. <i>BMC Genomics</i> , 2015, 16, 994.	2.8	36
7	Spatial gene expression analysis in tomato hypocotyls suggests cysteine as key precursor of vascular sulfur accumulation implicated in <i>Verticillium dahliae</i> defense. <i>Physiologia Plantarum</i> , 2015, 153, 253-268.	5.2	7
8	Plant Defense Responses in <i>Medicago truncatula</i> Unveiled by Microarray Analysis. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 569-583.	1.8	8
9	Through the doors of perception to function in arbuscular mycorrhizal symbioses. <i>New Phytologist</i> , 2014, 204, 833-840.	7.3	105
10	A roadmap of cell-type specific gene expression during sequential stages of the arbuscular mycorrhiza symbiosis. <i>BMC Genomics</i> , 2013, 14, 306.	2.8	93
11	Gene expression profiles of seed coats and biochemical properties of seed coats and cotyledons of two field pea (<i>Pisum sativum</i>) cultivars contrasting in green cotyledon bleaching resistance. <i>Euphytica</i> , 2013, 193, 49-65.	1.2	6
12	Transcriptome-Wide Mapping of Pea Seed Ageing Reveals a Pivotal Role for Genes Related to Oxidative Stress and Programmed Cell Death. <i>PLoS ONE</i> , 2013, 8, e78471.	2.5	74
13	Cell- and Tissue-Specific Transcriptome Analyses of <i>Medicago truncatula</i> Root Nodules. <i>PLoS ONE</i> , 2013, 8, e64377.	2.5	86
14	Transcriptional Responses toward Diffusible Signals from Symbiotic Microbes Reveal <i>MtNFP</i> - and <i>MtDMI3</i> -Dependent Reprogramming of Host Gene Expression by Arbuscular Mycorrhizal Fungal Lipochitooligosaccharides A. <i>Plant Physiology</i> , 2012, 159, 1671-1685.	4.8	126
15	Plant Genes Related to Gibberellin Biosynthesis and Signaling Are Differentially Regulated during the Early Stages of AM Fungal Interactions. <i>Molecular Plant</i> , 2012, 5, 951-954.	8.3	40
16	Involvement of bacterial TonB-dependent signaling in the generation of an oligogalacturonide damage-associated molecular pattern from plant cell walls exposed to <i>Xanthomonas campestris</i> pv. <i>campestris</i> pectate lyases. <i>BMC Microbiology</i> , 2012, 12, 239.	3.3	33
17	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. <i>New Phytologist</i> , 2012, 193, 755-769.	7.3	305
18	<i>Phoma medicaginis</i> stimulates the induction of the octadecanoid and phenylpropanoid pathways in <i>Medicago truncatula</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 593-603.	4.2	25

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19	Identification of genes differentially expressed in a resistant reaction to <i>Mycosphaerella pinodes</i> in pea using microarray technology. <i>BMC Genomics</i> , 2011, 12, 28.	2.8	77
20	Laser Microdissection Unravels Cell-Type-Specific Transcription in Arbuscular Mycorrhizal Roots, Including CAAT-Box Transcription Factor Gene Expression Correlating with Fungal Contact and Spread Å. <i>Plant Physiology</i> , 2011, 157, 2023-2043.	4.8	195
21	The 2-oxoglutarate/malate translocator mediates amino acid and storage protein biosynthesis in pea embryos. <i>Plant Journal</i> , 2010, 61, 350-363.	5.7	22
22	MediPIEx - a tool to combine in silico & experimental gene expression profiles of the model legume <i>Medicago truncatula</i> . <i>BMC Research Notes</i> , 2010, 3, 262.	1.4	1
23	Membrane steroid-binding protein 1 induced by a diffusible fungal signal is critical for mycorrhization in <i>Medicago truncatula</i> . <i>New Phytologist</i> , 2010, 185, 716-733.	7.3	115
24	Absciscic acid deficiency of developing pea embryos achieved by immunomodulation attenuates developmental phase transition and storage metabolism. <i>Plant Journal</i> , 2010, 64, 715-730.	5.7	21
25	Knockdown of the Symbiotic Sucrose Synthase MtSucS1 Affects Arbuscule Maturation and Maintenance in Mycorrhizal Roots of <i>Medicago truncatula</i> Å Å. <i>Plant Physiology</i> , 2010, 152, 1000-1014.	4.8	77
26	Communication and Signaling in the Plant-Fungus Symbiosis: The Mycorrhiza. <i>Signaling and Communication in Plants</i> , 2009, , 45-71.	0.7	10
27	Composite <i>Medicago truncatula</i> plants harbouring <i>Agrobacterium rhizogenes</i> -transformed roots reveal normal mycorrhization by <i>Glomus intraradices</i> . <i>Journal of Experimental Botany</i> , 2009, 60, 3797-3807.	4.8	25
28	EMMA 2 Å A MAGE-compliant system for the collaborative analysis and integration of microarray data. <i>BMC Bioinformatics</i> , 2009, 10, 50.	2.6	68
29	TRUNCATULIX - a data warehouse for the legume community. <i>BMC Plant Biology</i> , 2009, 9, 19.	3.6	11
30	Overlapping expression patterns and differential transcript levels of phosphate transporter genes in arbuscular mycorrhizal, Pi-fertilised and phytohormone-treated <i>Medicago truncatula</i> roots. <i>Planta</i> , 2009, 229, 1023-1034.	3.2	112
31	Gene expression profiling of <i>Medicago truncatula</i> roots in response to the parasitic plant <i>Orobancha crenata</i> . <i>Weed Research</i> , 2009, 49, 66-80.	1.7	26
32	The Sequence Analysis and Management System Å SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12.	3.8	37
33	ADP-Glucose Pyrophosphorylase-Deficient Pea Embryos Reveal Specific Transcriptional and Metabolic Changes of Carbon-Nitrogen Metabolism and Stress Responses Å. <i>Plant Physiology</i> , 2009, 149, 395-411.	4.8	78
34	The Signal Peptide of the <i>Medicago truncatula</i> Modular Nodulin MtNOD25 Operates as an Address Label for the Specific Targeting of Proteins to Nitrogen-Fixing Symbiosomes. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 63-72.	2.6	22
35	Increasing amino acid supply in pea embryos reveals specific interactions of N and C metabolism, and highlights the importance of mitochondrial metabolism. <i>Plant Journal</i> , 2008, 55, 909-926.	5.7	110
36	Exploring the nuclear proteome of <i>Medicago truncatula</i> at the switch towards seed filling. <i>Plant Journal</i> , 2008, 56, 398-410.	5.7	60

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37	Knockdown of the MEP pathway isogene <i>1-deoxyxylulose 5-phosphate synthase2</i> inhibits formation of arbuscular mycorrhiza-induced apocarotenoids, and abolishes normal expression of mycorrhiza-specific plant marker genes. <i>Plant Journal</i> , 2008, 56, 86-100.	5.7	135
38	Identification of a multigene family encoding putative β -glucan-binding proteins in <i>Medicago truncatula</i> . <i>Journal of Plant Physiology</i> , 2008, 165, 766-776.	3.5	6
39	Evidence for Transcriptional and Post-Translational Regulation of Sucrose Synthase in Pea Nodules by the Cellular Redox State. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 622-630.	2.6	33
40	Evidence for the Involvement in Nodulation of the Two Small Putative Regulatory Peptide-Encoding Genes <i>MtRALFL1</i> and <i>MtDVL1</i> . <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 1118-1127.	2.6	68
41	Host Genes Involved in Nodulation Preference in Common Bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 587 Td (v Molecular Plant-Microbe Interactions, 2008, 21, 459-468.	2.6	41
42	A Combined Proteome and Transcriptome Analysis of Developing <i>Medicago truncatula</i> Seeds. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 2165-2179.	3.8	237
43	The Lipopolysaccharide of <i>Sinorhizobium meliloti</i> Suppresses Defense-Associated Gene Expression in Cell Cultures of the Host Plant <i>Medicago truncatula</i> Å. <i>Plant Physiology</i> , 2007, 143, 825-837.	4.8	100
44	Antisense Repression of the <i>Medicago truncatula</i> Nodule-Enhanced Sucrose Synthase Leads to a Handicapped Nitrogen Fixation Mirrored by Specific Alterations in the Symbiotic Transcriptome and Metabolome. <i>Plant Physiology</i> , 2007, 145, 1600-1618.	4.8	90
45	Suppression of the pathogen-inducible <i>Medicago truncatula</i> putative protease-inhibitor MtTi2 does not influence root infection by <i>Aphanomyces euteiches</i> but results in transcriptional changes from wildtype roots. <i>Plant Science</i> , 2007, 173, 84-95.	3.6	8
46	Development of bioinformatic tools to support EST-sequencing, in silico- and microarray-based transcriptome profiling in mycorrhizal symbioses. <i>Phytochemistry</i> , 2007, 68, 19-32.	2.9	49
47	Identification and expression regulation of symbiotically activated legume genes. <i>Phytochemistry</i> , 2007, 68, 8-18.	2.9	64
48	Sugar for my honey: Carbohydrate partitioning in ectomycorrhizal symbiosis. <i>Phytochemistry</i> , 2007, 68, 82-91.	2.9	107
49	Metabolite Profiles of Nodulated Alfalfa Plants Indicate That Distinct Stages of Nodule Organogenesis Are Accompanied by Global Physiological Adaptations. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 998-1013.	2.6	50
50	Transcriptome profiling uncovers metabolic and regulatory processes occurring during the transition from desiccation-sensitive to desiccation-tolerant stages in <i>Medicago truncatula</i> seeds. <i>Plant Journal</i> , 2006, 47, 735-750.	5.7	142
51	Genetic and genomic analysis of legume flowers and seeds. <i>Current Opinion in Plant Biology</i> , 2006, 9, 133-141.	7.1	35
52	Transcriptional snapshots provide insights into the molecular basis of arbuscular mycorrhiza in the model legume <i>Medicago truncatula</i> . <i>Functional Plant Biology</i> , 2006, 33, 737.	2.1	29
53	Combined Transcriptome Profiling Reveals a Novel Family of Arbuscular Mycorrhizal-Specific <i>Medicago truncatula</i> Lectin Genes. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 771-782.	2.6	63
54	Two genes encoding different truncated hemoglobins are regulated during root nodule and arbuscular mycorrhiza symbioses of <i>Medicago truncatula</i> . <i>Planta</i> , 2005, 220, 757-766.	3.2	88

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55	EST sequencing and time course microarray hybridizations identify more than 700 <i>Medicago truncatula</i> genes with developmental expression regulation in flowers and pods. <i>Planta</i> , 2005, 222, 269-283.	3.2	35
56	The promoter of the leghaemoglobin gene <i>VfLb29</i> : functional analysis and identification of modules necessary for its activation in the infected cells of root nodules and in the arbuscule-containing cells of mycorrhizal roots. <i>Journal of Experimental Botany</i> , 2005, 56, 799-806.	4.8	67
57	Overlaps in the Transcriptional Profiles of <i>Medicago truncatula</i> Roots Inoculated with Two Different <i>Glomus</i> Fungi Provide Insights into the Genetic Program Activated during Arbuscular Mycorrhiza. <i>Plant Physiology</i> , 2005, 137, 1283-1301.	4.8	322
58	Global Changes in Gene Expression in <i>Sinorhizobium meliloti</i> 1021 under Microoxic and Symbiotic Conditions. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 292-303.	2.6	230
59	Expression Profiling in <i>Medicago truncatula</i> Identifies More Than 750 Genes Differentially Expressed during Nodulation, Including Many Potential Regulators of the Symbiotic Program. <i>Plant Physiology</i> , 2004, 136, 3159-3176.	4.8	269
60	Transcriptome Profiling in Root Nodules and Arbuscular Mycorrhiza Identifies a Collection of Novel Genes Induced During <i>Medicago truncatula</i> Root Endosymbioses. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1063-1077.	2.6	152
61	Construction and validation of cDNA-based Mt6k-RIT macro- and microarrays to explore root endosymbioses in the model legume <i>Medicago truncatula</i> . <i>Journal of Biotechnology</i> , 2004, 108, 95-113.	3.8	103
62	The Promoter of the <i>Vicia faba</i> L. Leghemoglobin Gene <i>VfLb29</i> Is Specifically Activated in the Infected Cells of Root Nodules and in the Arbuscule-Containing Cells of Mycorrhizal Roots from Different Legume and Nonlegume Plants. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 62-69.	2.6	122
63	Genomics insights into symbiotic nitrogen fixation. <i>Current Opinion in Biotechnology</i> , 2003, 14, 200-205.	6.6	43
64	Transcriptional profiling of <i>Medicago truncatula</i> roots after infection with <i>Aphanomyces euteiches</i> (oomycota) identifies novel genes upregulated during this pathogenic interaction. <i>Physiological and Molecular Plant Pathology</i> , 2003, 63, 17-26.	2.5	50
65	Syntenic Relationships between <i>Medicago truncatula</i> and <i>Arabidopsis</i> Reveal Extensive Divergence of Genome Organization. <i>Plant Physiology</i> , 2003, 131, 1018-1026.	4.8	67
66	Transcriptional Changes in Response to Arbuscular Mycorrhiza Development in the Model Plant <i>Medicago truncatula</i> . <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 306-314.	2.6	134
67	The <i>Medicago truncatula</i> Sucrose Synthase Gene <i>MtSucS1</i> Is Activated Both in the Infected Region of Root Nodules and in the Cortex of Roots Colonized by Arbuscular Mycorrhizal Fungi. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 903-915.	2.6	106
68	The broad bean nodulin <i>VfENOD18</i> is a member of a novel family of plant proteins with homologies to the bacterial MJ0577 superfamily. <i>Molecular Genetics and Genomics</i> , 2000, 264, 241-250.	2.1	25
69	Genomic organization and expression properties of the <i>VfENOD5</i> gene from broad bean (<i>Vicia faba</i> L.). <i>Plant Science</i> , 2000, 155, 169-178.	3.6	20
70	The promoter of the <i>Vicia faba</i> L. gene <i>VfEnod12</i> encoding an early nodulin is active in cortical cells and nodule primordia of transgenic hairy roots of <i>Vicia hirsuta</i> as well as in the prefixing zone II of mature transgenic <i>V. hirsuta</i> root nodules. <i>Plant Science</i> , 2000, 160, 67-75.	3.6	19
71	Genomic organization and expression properties of the <i>MtSucS1</i> gene, which encodes a nodule-enhanced sucrose synthase in the model legume <i>Medicago truncatula</i> . <i>Molecular Genetics and Genomics</i> , 1999, 261, 514-522.	2.4	42
72	Analysis of genes encoding modular nodulins from <i>Vicia hirsuta</i> and <i>Vicia faba</i> . <i>Plant Science</i> , 1999, 149, 1-11.	3.6	2

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73	The asparagine synthetase gene <i>VfAS1</i> is strongly expressed in the nitrogen-fixing zone of broad bean (<i>Vicia faba</i> L.) root nodules. <i>Plant Science</i> , 1997, 124, 89-95.	3.6	11
74	The 32-kilobase exp gene cluster of <i>Rhizobium meliloti</i> directing the biosynthesis of galactoglucan: genetic organization and properties of the encoded gene products. <i>Journal of Bacteriology</i> , 1997, 179, 1375-1384.	2.2	139
75	Analysis of genes expressed in root nodules of broad bean (<i>Vicia faba</i> L.) . , 1997, , 91-94.		2
76	The <i>Vicia faba</i> Lipoygenase Gene <i>VfLOXI</i> Is Expressed in the Root Nodule Parenchyma. <i>Molecular Plant-Microbe Interactions</i> , 1996, 9, 860.	2.6	17
77	The nodule-specific <i>VfENOD-GRP3</i> gene encoding a glycine-rich early nodulin is located on chromosome I of <i>Vicia faba</i> L. and is predominantly expressed in the interzone II-III of root nodules. <i>Plant Molecular Biology</i> , 1995, 28, 405-421.	3.9	29
78	The promoter of the <i>Vicia faba</i> L. <i>VfENOD-GRP3</i> gene encoding a glycine-rich early nodulin mediates a predominant gene expression in the interzone II-III region of transgenic <i>Vicia hirsuta</i> root nodules. <i>Plant Molecular Biology</i> , 1995, 29, 759-772.	3.9	25
79	Extension of the <i>Rhizobium meliloti</i> succinoglycan biosynthesis gene cluster: identification of the <i>exsA</i> gene encoding an ABC transporter protein, and the <i>exsB</i> gene which probably codes for a regulator of succinoglycan biosynthesis. <i>Molecular Genetics and Genomics</i> , 1995, 249, 487-497.	2.4	70
80	Members of a broadbean nodulin family with partial homologies to the alfalfa nodulin 25 are composed of two types of amino acid repeats flanked by unique amino acid sequence termini. <i>Plant Molecular Biology</i> , 1994, 24, 143-157.	3.9	13
81	The Sucrose Synthase Gene Is Predominantly Expressed in the Root Nodule Tissue of <i>Vicia faba</i> . <i>Molecular Plant-Microbe Interactions</i> , 1993, 6, 507.	2.6	33
82	Analysis of the <i>Rhizobium meliloti</i> Genes <i>exoU</i> , <i>exoV</i> , <i>exoW</i> , <i>exoT</i> , and <i>exoI</i> Involved in Exopolysaccharide Biosynthesis and Nodule Invasion: <i>exoU</i> and <i>exoW</i> Probably Encode Glucosyltransferases. <i>Molecular Plant-Microbe Interactions</i> , 1993, 6, 735.	2.6	74
83	Microarrays as Tools to Decipher Transcriptomes in Symbiotic Interactions. , 0, , 137-162.		0