Michael K Udvardi

List of Publications by Year
in descending order

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185 papers	24,086 citations	7551 77 h-index	7931 149 g-index
198 all docs	198 docs citations	198 times ranked	21347 citing authors

#	Article	IF	Citations
1	Physiological and biochemical adaptive traits support the specific breeding of alfalfa (<scp><i>Medicago sativa</i></scp>) for severely droughtâ€stressed or moistureâ€favourable environments. Journal of Agronomy and Crop Science, 2023, 209, 132-143.	1.7	8
2	Microscopic and Transcriptomic Analyses of Dalbergoid Legume Peanut Reveal a Divergent Evolution Leading to Nod-Factor-Dependent Epidermal Crack-Entry and Terminal Bacteroid Differentiation. Molecular Plant-Microbe Interactions, 2022, 35, 131-145.	1.4	11
3	Spectroscopic analysis reveals that soil phosphorus availability and plant allocation strategies impact feedstock quality of nutrient-limited switchgrass. Communications Biology, 2022, 5, 227.	2.0	1
4	Transcriptional Programs and Regulators Underlying Age-Dependent and Dark-Induced Senescence in Medicago truncatula. Cells, 2022, 11, 1570.	1.8	2
5	Nitrogen Fertilization Reduces Nitrogen Fixation Activity of Diverse Diazotrophs in Switchgrass Roots. Phytobiomes Journal, 2021, 5, 80-87.	1.4	33
6	Transcriptional, metabolic, physiological and developmental responses of switchgrass to phosphorus limitation. Plant, Cell and Environment, 2021, 44, 186-202.	2.8	27
7	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. Nature, 2021, 590, 438-444.	13.7	144
8	Draft Genome Sequences of Switchgrass Diazotrophs. Microbiology Resource Announcements, 2021, 10, e0028421.	0.3	1
9	A Research Road Map for Responsible Use of Agricultural Nitrogen. Frontiers in Sustainable Food Systems, 2021, 5, .	1.8	48
10	Increased Ascorbate Biosynthesis Does Not Improve Nitrogen Fixation Nor Alleviate the Effect of Drought Stress in Nodulated Medicago truncatula Plants. Frontiers in Plant Science, 2021, 12, 686075.	1.7	0
11	Three Common Symbiotic ABC Subfamily B Transporters in<i>Medicago truncatula</i>Are Regulated by a NIN-Independent Branch of the Symbiosis Signaling Pathway. Molecular Plant-Microbe Interactions, 2021, 34, 939-951.	1.4	12
12	PHO1 family members transport phosphate from infected nodule cells to bacteroids in Medicago truncatula. Plant Physiology, 2021, 185, 196-209.	2.3	11
13	Dissection of physiological, transcriptional, and metabolic traits in two tall fescue genotypes with contrasting drought tolerance. Plant-Environment Interactions, 2021, 2, 277.	0.7	1
14	Application of Synthetic Peptide CEP1 Increases Nutrient Uptake Rates Along Plant Roots. Frontiers in Plant Science, 2021, 12, 793145.	1.7	9
15	Celebrating 20 Years of Genetic Discoveries in Legume Nodulation and Symbiotic Nitrogen Fixation. Plant Cell, 2020, 32, 15-41.	3.1	416
16	A Plant Gene Encoding One-Heme and Two-Heme Hemoglobins With Extreme Reactivities Toward Diatomic Gases and Nitrite. Frontiers in Plant Science, 2020, 11, 600336.	1.7	8
17	MtSSPdb: The <i>Medicago truncatula</i> Small Secreted Peptide Database. Plant Physiology, 2020, 183, 399-413.	2.3	40
18	GmVTL1a is an iron transporter on the symbiosome membrane of soybean with an important role in nitrogen fixation. New Phytologist, 2020, 228, 667-681.	3.5	36

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19	Silencing Folylpolyglutamate Synthetase1 (FPGS1) in Switchgrass (Panicum virgatum L.) Improves Lignocellulosic Biofuel Production. Frontiers in Plant Science, 2020, 11, 843.	1.7	6
20	Lotus japonicus karrikin receptors display divergent ligand-binding specificities and organ-dependent redundancy. PLoS Genetics, 2020, 16, e1009249.	1.5	26
21	A protein complex required for polar growth of rhizobial infection threads. Nature Communications, 2019, 10, 2848.	5.8	72
22	The Nodule-Specific PLAT Domain Protein NPD1 Is Required for Nitrogen-Fixing Symbiosis. Plant Physiology, 2019, 180, 1480-1497.	2.3	20
23	Genomeâ€wide analysis of flanking sequences reveals thatÂ<i>Tnt1</i> insertion is positively correlated with gene methylation in <i>Medicago truncatula</i>. Plant Journal, 2019, 98, 1106-1119.	2.8	25
24	The future of legume genetic data resources: Challenges, opportunities, and priorities. , 2019, 1, e16.		30
25	Genomeâ€wide association analysis of salinity responsive traits in Medicago truncatula. Plant, Cell and Environment, 2019, 42, 1513-1531.	2.8	26
26	GWASpro: a high-performance genome-wide association analysis server. Bioinformatics, 2019, 35, 2512-2514.	1.8	18
27	Sugar release and growth of biofuel crops are improved by downregulation of pectin biosynthesis. Nature Biotechnology, 2018, 36, 249-257.	9.4	136
28	<i>Medicago truncatula</i> copper transporter 1 (Mt<scp>COPT</scp>1) delivers copper for symbiotic nitrogen fixation. New Phytologist, 2018, 218, 696-709.	3.5	42
29	An Iron-Activated Citrate Transporter, MtMATE67, Is Required for Symbiotic Nitrogen Fixation. Plant Physiology, 2018, 176, 2315-2329.	2.3	55
30	Senescence and nitrogen use efficiency in perennial grasses for forage and biofuel production. Journal of Experimental Botany, 2018, 69, 855-865.	2.4	53
31	MtMTP2-Facilitated Zinc Transport Into Intracellular Compartments Is Essential for Nodule Development in Medicago truncatula. Frontiers in Plant Science, 2018, 9, 990.	1.7	23
32	Revealing the transcriptomic complexity of switchgrass by PacBio long-read sequencing. Biotechnology for Biofuels, 2018, 11, 170.	6.2	30
33	Functional Analysis of Cellulose Synthase CesA4 and CesA6 Genes in Switchgrass (Panicum virgatum) by Overexpression and RNAi-Mediated Gene Silencing. Frontiers in Plant Science, 2018, 9, 1114.	1.7	34
34	Enabling Reverse Genetics in Medicago truncatula Using High-Throughput Sequencing for Tnt1 Flanking Sequence Recovery. Methods in Molecular Biology, 2017, 1610, 25-37.	0.4	12
35	Genome-Wide Identification of <i>Medicago</i> Peptides Involved in Macronutrient Responses and Nodulation. Plant Physiology, 2017, 175, 1669-1689.	2.3	101
36	Development and use of a switchgrass (Panicum virgatum L.) transformation pipeline by the BioEnergy Science Center to evaluate plants for reduced cell wall recalcitrance. Biotechnology for Biofuels, 2017, 10, 309.	6.2	26

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37	Identification and Overexpression of a Knotted1-Like Transcription Factor in Switchgrass (Panicum) Tj ETQq1 1 0.784314 rgBT /Overlo	1.7	39
38	Downregulation of a UDP-Arabinomutase Gene in Switchgrass (Panicum virgatum L.) Results in Increased Cell Wall Lignin While Reducing Arabinose-Glycans. Frontiers in Plant Science, 2016, 7, 1580.	1.7	20
39	Analysis of Large Seeds from Three Different Medicago truncatula Ecotypes Reveals a Potential Role of Hormonal Balance in Final Size Determination of Legume Grains. International Journal of Molecular Sciences, 2016, 17, 1472.	1.8	7
40	<i>Lotus japonicus</i> NF-YA1 Plays an Essential Role During Nodule Differentiation and Targets Members of the <i>SHI/STY</i> Gene Family. Molecular Plant-Microbe Interactions, 2016, 29, 950-964.	1.4	44
41	Nitrogen remobilization and conservation, and underlying senescenceâ€associated gene expression in the perennial switchgrass <i>Panicum virgatum</i>. New Phytologist, 2016, 211, 75-89.	3.5	37
42	Symbiotic Nitrogen Fixation and the Challenges to Its Extension to Nonlegumes. Applied and Environmental Microbiology, 2016, 82, 3698-3710.	1.4	443
43	MtSWEET11, a Nodule-Specific Sucrose Transporter of <i>Medicago truncatula</i>. Plant Physiology, 2016, 171, 554-565.	2.3	101
44	The <i>Vigna unguiculata</i> Gene Expression Atlas (Vu<scp>GEA</scp>) from <i>de novo</i> assembly and quantification of <scp>RNA</scp>â€seq data provides insights into seed maturation mechanisms. Plant Journal, 2016, 88, 318-327.	2.8	64
45	A <i>Medicago truncatula</i> Cystathionine-Î²-Synthase-like Domain-Containing Protein Is Required for Rhizobial Infection and Symbiotic Nitrogen Fixation. Plant Physiology, 2016, 170, 2204-2217.	2.3	55
46	Targeted Switchgrass BAC Library Screening and Sequence Analysis Identifies Predicted Biomass and Stress Response-Related Genes. Bioenergy Research, 2016, 9, 109-122.	2.2	10
47	Standards for plant synthetic biology: a common syntax for exchange of <scp>DNA</scp> parts. New Phytologist, 2015, 208, 13-19.	3.5	263
48	<i>Medicago truncatula</i> Natural Resistance-Associated Macrophage Protein1 Is Required for Iron Uptake by Rhizobia-Infected Nodule Cells Â. Plant Physiology, 2015, 168, 258-272.	2.3	85
49	Control of Vegetative to Reproductive Phase Transition Improves Biomass Yield and Simultaneously Reduces Lignin Content in Medicago truncatula. Bioenergy Research, 2015, 8, 857-867.	2.2	23
50	Global gene expression profiling of two switchgrass cultivars following inoculation with<i>Burkholderia phytofirmans</i>strain PsJN. Journal of Experimental Botany, 2015, 66, 4337-4350.	2.4	21
51	DASH transcription factor impacts Medicago truncatula seed size by its action on embryo morphogenesis and auxin homeostasis. Plant Journal, 2015, 81, 453-466.	2.8	31
52	PvNAC1 and PvNAC2 Are Associated with Leaf Senescence and Nitrogen Use Efficiency in Switchgrass. Bioenergy Research, 2015, 8, 868-880.	2.2	21
53	Suppression of Arbuscule Degeneration in <i>Medicago truncatula phosphate transporter4</i> Mutants Is Dependent on the Ammonium Transporter 2 Family Protein AMT2;3. Plant Cell, 2015, 27, 1352-1366.	3.1	180
54	Genomeâ€wide association of droughtâ€related and biomass traits with HapMap SNPs in <i>Medicago truncatula</i>. Plant, Cell and Environment, 2015, 38, 1997-2011.	2.8	69

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55	Loss of the nodule-specific cysteine rich peptide, NCR169, abolishes symbiotic nitrogen fixation in the <i>Medicago truncatula dnf7</i> mutant. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15232-15237.	3.3	154
56	Nitrogen-Fixing Nodules Are an Important Source of Reduced Sulfur, Which Triggers Global Changes in Sulfur Metabolism in <i>Lotus japonicus</i>. Plant Cell, 2015, 27, 2384-2400.	3.1	23
57	Identification and overexpression of <i>gibberellin 2â€oxidase</i> (<i><scp>GA</scp>2ox</i>) in switchgrass (<i><scp>P</scp>anicum virgatum</i> L.) for improved plant architecture and reduced biomass recalcitrance. Plant Biotechnology Journal, 2015, 13, 636-647.	4.1	117
58	A High-Throughput RNA Interference (RNAi)-Based Approach Using Hairy Roots for the Study of Plantâ€“Rhizobia Interactions. Methods in Molecular Biology, 2015, 1287, 159-178.	0.4	11
59	The H+-ATPase HA1 of <i>Medicago truncatula</i> Is Essential for Phosphate Transport and Plant Growth during Arbuscular Mycorrhizal Symbiosis Â Â. Plant Cell, 2014, 26, 1808-1817.	3.1	118
60	Extreme specificity of NCR gene expression in Medicago truncatula. BMC Genomics, 2014, 15, 712.	1.2	70
61	Lignin Modification Leads to Increased Nodule Numbers in Alfalfa Â Â Â. Plant Physiology, 2014, 164, 1139-1150.	2.3	40
62	A NAP-AAO3 Regulatory Module Promotes Chlorophyll Degradation via ABA Biosynthesis in <i>Arabidopsis</i> Leaves. Plant Cell, 2014, 26, 4862-4874.	3.1	221
63	Diversity of Nitrogen-Fixing Bacteria Associated with Switchgrass in the Native Tallgrass Prairie of Northern Oklahoma. Applied and Environmental Microbiology, 2014, 80, 5636-5643.	1.4	77
64	Keel petal incision: a simple and efficient method for genetic crossing in Medicago truncatula. Plant Methods, 2014, 10, 11.	1.9	21
65	An efficient reverse genetics platform in the model legume <i><scp>M</scp>edicago truncatula</i>. New Phytologist, 2014, 201, 1065-1076.	3.5	113
66	Global reprogramming of transcription and metabolism in <scp><i>M</i></scp><i>edicago truncatula</i> during progressive drought and after rewatering. Plant, Cell and Environment, 2014, 37, 2553-2576.	2.8	138
67	A Tutorial on Lotus japonicus Transcriptomic Tools. Compendium of Plant Genomes, 2014, , 183-199.	0.3	0
68	Transcriptomic and Metabolic Changes Associated with Photorespiratory Ammonium Accumulation in the Model Legume Lotus japonicus Â Â. Plant Physiology, 2013, 162, 1834-1848.	2.3	26
69	Cessation of photosynthesis in Lotus japonicus leaves leads to reprogramming of nodule metabolism. Journal of Experimental Botany, 2013, 64, 1317-1332.	2.4	18
70	<i>Medicago truncatula </i><scp>DNF</scp>2 is a <scp>PI</scp>â€<scp>PLC</scp>â€<scp>XD</scp>â€containing protein required for bacteroid persistence and prevention of nodule early senescence and defenseâ€like reactions. New Phytologist, 2013, 197, 1250-1261.	3.5	128
71	Establishment of the <i><scp>L</scp>otus japonicus</i> Gene Expression Atlas (<scp>L</scp>j<scp>GEA</scp>) and its use to explore legume seed maturation. Plant Journal, 2013, 74, 351-362.	2.8	134
72	Transport and Metabolism in Legume-Rhizobia Symbioses. Annual Review of Plant Biology, 2013, 64, 781-805.	8.6	683

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73	A Regulatory Network-Based Approach Dissects Late Maturation Processes Related to the Acquisition of Desiccation Tolerance and Longevity of Medicago truncatula Seeds. Plant Physiology, 2013, 163, 757-774.	2.3	155
74	The C₂H₂ Transcription Factor REGULATOR OF SYMBIOSOME DIFFERENTIATION Represses Transcription of the Secretory Pathway Gene <i>VAMP721a</i> and Promotes Symbiosome Development in <i>Medicago truncatula</i>. Plant Cell, 2013, 25, 3584-3601.	3.1	109
75	Rhizobial Infection Is Associated with the Development of Peripheral Vasculature in Nodules of<i>Medicago truncatula</i>Â Â Â. Plant Physiology, 2013, 162, 107-115.	2.3	92
76	PlantTFcat: an online plant transcription factor and transcriptional regulator categorization and analysis tool. BMC Bioinformatics, 2013, 14, 321.	1.2	119
77	Development of an integrated transcript sequence database and a gene expression atlas for gene discovery and analysis in switchgrass (<i>Panicum virgatum</i> L.). Plant Journal, 2013, 74, 160-173.	2.8	70
78	LegumeGRN: A Gene Regulatory Network Prediction Server for Functional and Comparative Studies. PLoS ONE, 2013, 8, e67434.	1.1	37
79	The Integral Membrane Protein SEN1 is Required for Symbiotic Nitrogen Fixation in Lotus japonicus Nodules. Plant and Cell Physiology, 2012, 53, 225-236.	1.5	95
80	Global regulation of reactive oxygen species scavenging genes in alfalfa root and shoot under gradual drought stress and recovery. Plant Signaling and Behavior, 2012, 7, 539-543.	1.2	32
81	MtPAR MYB transcription factor acts as an on switch for proanthocyanidin biosynthesis in <i>Medicago truncatula</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1766-1771.	3.3	135
82	The Medicago truncatula Gene Expression Atlas (MtGEA): A Tool for Legume Seed Biology and Biotechnology. , 2012, , 111-127.		2
83	A <i>Medicago truncatula</i> Tobacco Retrotransposon Insertion Mutant Collection with Defects in Nodule Development and Symbiotic Nitrogen Fixation Â Â. Plant Physiology, 2012, 159, 1686-1699.	2.3	109
84	Ascorbate oxidase: The unexpected involvement of a â€˜wasteful enzymeâ€™ in the symbioses with nitrogen-fixing bacteria and arbuscular mycorrhizal fungi. Plant Physiology and Biochemistry, 2012, 59, 71-79.	2.8	26
85	Comparative metabolomics of drought acclimation in model and forage legumes. Plant, Cell and Environment, 2012, 35, 136-149.	2.8	128
86	Overexpression of AtLOV1 in Switchgrass Alters Plant Architecture, Lignin Content, and Flowering Time. PLoS ONE, 2012, 7, e47399.	1.1	48
87	Cloning and functional characterization of<i>Lj</i>PLT4, a plasma membrane xylitol H⁺-symporter from<i>Lotus japonicus</i>. Molecular Membrane Biology, 2011, 28, 1-13.	2.0	10
88	The Medicago genome provides insight into the evolution of rhizobial symbioses. Nature, 2011, 480, 520-524.	13.7	1,166
89	Comparative ionomics and metabolomics in extremophile and glycophytic <i>Lotus</i> species under salt stress challenge the metabolic preâ€adaptation hypothesis. Plant, Cell and Environment, 2011, 34, 605-617.	2.8	122
90	System responses to longâ€term drought and reâ€watering of two contrasting alfalfa varieties. Plant Journal, 2011, 68, 871-889.	2.8	127

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91	<i>Vapyrin</i>, a gene essential for intracellular progression of arbuscular mycorrhizal symbiosis, is also essential for infection by rhizobia in the nodule symbiosis of <i>Medicago truncatula</i>. Plant Journal, 2011, 65, 244-252.	2.8	211
92	Genome-wide SNP discovery in tetraploid alfalfa using 454 sequencing and high resolution melting analysis. BMC Genomics, 2011, 12, 1-11.	1.2	353
93	Characterization of two novel nodule-enhanced Î±-type carbonic anhydrases from Lotus japonicus. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 496-504.	1.1	9
94	From Model to Crop: Functional Analysis of a <i>STAY-GREEN</i> Gene in the Model Legume <i>Medicago truncatula</i> and Effective Use of the Gene for Alfalfa Improvement Â Â. Plant Physiology, 2011, 157, 1483-1496.	2.3	124
95	Nodulation enhances dark CO2 fixation and recycling in the model legume Lotus japonicus. Journal of Experimental Botany, 2011, 62, 2959-2971.	2.4	19
96	Comparative Functional Genomics of Salt Stress in Related Model and Cultivated Plants Identifies and Overcomes Limitations to Translational Genomics. PLoS ONE, 2011, 6, e17094.	1.1	119
97	Identification of potential early regulators of aphid resistance in <i>Medicago truncatula</i> via transcription factor expression profiling. New Phytologist, 2010, 186, 980-994.	3.5	36
98	Deficiency in plastidic glutamine synthetase alters proline metabolism and transcriptomic response in <i>Lotus japonicus</i> under drought stress. New Phytologist, 2010, 188, 1001-1013.	3.5	98
99	Recent insights into antioxidant defenses of legume root nodules. New Phytologist, 2010, 188, 960-976.	3.5	147
100	Mining for robust transcriptional and metabolic responses to longâ€term salt stress: a case study on the model legume <i>Lotus japonicus</i>. Plant, Cell and Environment, 2010, 33, 468-480.	2.8	57
101	Gene expression profiling identifies two regulatory genes controlling dormancy and ABA sensitivity in Arabidopsis seeds. Plant Journal, 2010, 61, 611-622.	2.8	95
102	Genomic Inventory and Transcriptional Analysis of <i>Medicago truncatula</i> Transporters. Plant Physiology, 2010, 152, 1716-1730.	2.3	73
103	A remorin protein interacts with symbiotic receptors and regulates bacterial infection. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2343-2348.	3.3	316
104	Inferring large-scale gene regulatory networks using a low-order constraint-based algorithm. Molecular BioSystems, 2010, 6, 988.	2.9	13
105	Plant Transcription Factors as Novel Molecular Markers for Legumes. , 2010, , 421-425.		2
106	Dissection of Symbiosis and Organ Development by Integrated Transcriptome Analysis of Lotus japonicus Mutant and Wild-Type Plants. PLoS ONE, 2009, 4, e6556.	1.1	134
107	AtMyb41 Regulates Transcriptional and Metabolic Responses to Osmotic Stress in Arabidopsis Â. Plant Physiology, 2009, 149, 1761-1772.	2.3	176
108	Legume Transcription Factor Genes: What Makes Legumes So Special? Â. Plant Physiology, 2009, 151, 991-1001.	2.3	87

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109	Global Changes in the Transcript and Metabolic Profiles during Symbiotic Nitrogen Fixation in Phosphorus-Stressed Common Bean Plants Â Â. Plant Physiology, 2009, 151, 1221-1238.	2.3	163
110	Molecular and Biochemical Characterization of the Parvulin-Type PPIases in <i>Lotus japonicus</i> Â Â Â Â. Plant Physiology, 2009, 150, 1160-1173.	2.3	16
111	Translating Medicago truncatula genomics to crop legumes. Current Opinion in Plant Biology, 2009, 12, 193-201.	3.5	171
112	TransportTP: A two-phase classification approach for membrane transporter prediction and characterization. BMC Bioinformatics, 2009, 10, 418.	1.2	53
113	The Medicago truncatula gene expression atlas web server. BMC Bioinformatics, 2009, 10, 441.	1.2	175
114	Medicago truncatula and Glomus intraradices gene expression in cortical cells harboring arbuscules in the arbuscular mycorrhizal symbiosis. BMC Plant Biology, 2009, 9, 10.	1.6	277
115	Identification of transcription factors involved in root apex responses to salt stress in Medicago truncatula. Molecular Genetics and Genomics, 2009, 281, 55-66.	1.0	76
116	Natural Variation for Nutrient Use and Remobilization Efficiencies in Switchgrass. Bioenergy Research, 2009, 2, 257-266.	2.2	82
117	Genomeâ€wide reprogramming of regulatory networks, transport, cell wall and membrane biogenesis during arbuscular mycorrhizal symbiosis in <i>Lotus japonicus</i>. New Phytologist, 2009, 182, 200-212.	3.5	318
118	Priming of plant innate immunity by rhizobacteria and Î²â€aminobutyric acid: differences and similarities in regulation. New Phytologist, 2009, 183, 419-431.	3.5	192
119	Presymbiotic factors released by the arbuscular mycorrhizal fungus <i>Gigaspora margarita</i> induce starch accumulation in <i>Lotus japonicus</i> roots. New Phytologist, 2009, 183, 53-61.	3.5	72
120	Absence of Symbiotic Leghemoglobins Alters Bacteroid and Plant Cell Differentiation During Development of <i>Lotus japonicus</i> Root Nodules. Molecular Plant-Microbe Interactions, 2009, 22, 800-808.	1.4	55
121	Plant metabolomics reveals conserved and divergent metabolic responses to salinity. Physiologia Plantarum, 2008, 132, 209-219.	2.6	290
122	Integrative functional genomics of salt acclimatization in the model legume <i>Lotus japonicus</i>. Plant Journal, 2008, 53, 973-987.	2.8	199
123	Gene expression profiling of M. truncatula transcription factors identifies putative regulators of grain legume seed filling. Plant Molecular Biology, 2008, 67, 567-580.	2.0	85
124	Tissue-specific down-regulation of LjAMT1;1 compromises nodule function and enhances nodulation in Lotus japonicus. Plant Molecular Biology, 2008, 68, 585-595.	2.0	22
125	A gene expression atlas of the model legume <i>Medicago truncatula</i>. Plant Journal, 2008, 55, 504-513.	2.8	668
126	A community resource for high-throughput quantitative RT-PCR analysis of transcription factor gene expression in Medicago truncatula. Plant Methods, 2008, 4, 18.	1.9	120

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127	Eleven Golden Rules of Quantitative RT-PCR. Plant Cell, 2008, 20, 1736-1737.	3.1	580
128	Metabolome-ionome-biomass interactions. Plant Signaling and Behavior, 2008, 3, 598-600.	1.2	26
129	AffyTrees: Facilitating Comparative Analysis of Affymetrix Plant Microarray Chips. Plant Physiology, 2008, 146, 377-386.	2.3	10
130	Systemic Signaling of the Plant Nitrogen Status Triggers Specific Transcriptome Responses Depending on the Nitrogen Source in <i>Medicago truncatula</i> Â Â. Plant Physiology, 2008, 146, 2020-2035.	2.3	136
131	Defects in Rhizobial Cyclic Glucan and Lipopolysaccharide Synthesis Alter Legume Gene Expression During Nodule Development. Molecular Plant-Microbe Interactions, 2008, 21, 50-60.	1.4	21
132	Phosphorus Stress in Common Bean: Root Transcript and Metabolic Responses. Plant Physiology, 2007, 144, 752-767.	2.3	300
133	Legume Transcription Factors: Global Regulators of Plant Development and Response to the Environment. Plant Physiology, 2007, 144, 538-549.	2.3	244
134	Metabolism of Reactive Oxygen Species Is Attenuated in Leghemoglobin-Deficient Nodules of Lotus japonicus. Molecular Plant-Microbe Interactions, 2007, 20, 1596-1603.	1.4	53
135	Identification of 118 <i>Arabidopsis</i> Transcription Factor and 30 Ubiquitin-Ligase Genes Responding to Chitin, a Plant-Defense Elicitor. Molecular Plant-Microbe Interactions, 2007, 20, 900-911.	1.4	254
136	Genome-wide reprogramming of metabolism and regulatory networks of Arabidopsis in response to phosphorus. Plant, Cell and Environment, 2007, 30, 85-112.	2.8	533
137	Mechanisms of ammonium transport, accumulation, and retention in ooyctes and yeast cells expressingArabidopsisAtAMT1;1. FEBS Letters, 2006, 580, 3931-3936.	1.3	48
138	Functional genomics of plant transporters in legume nodules. Functional Plant Biology, 2006, 33, 731.	1.1	12
139	Over-expression of the rice OsAMT1-1 gene increases ammonium uptake and content, but impairs growth and development of plants under high ammonium nutrition. Functional Plant Biology, 2006, 33, 153.	1.1	77
140	Spatial and Temporal Organization of Sucrose Metabolism in Lotus japonicus Nitrogen-Fixing Nodules Suggests a Role for the Elusive Alkaline/Neutral Invertase. Plant Molecular Biology, 2006, 62, 53-69.	2.0	40
141	Genetic and genomic analysis of legume flowers and seeds. Current Opinion in Plant Biology, 2006, 9, 133-141.	3.5	35
142	Symbiotic Leghemoglobins Are Crucial for Nitrogen Fixation in Legume Root Nodules but Not for General Plant Growth and Development. Current Biology, 2005, 15, 531-535.	1.8	350
143	Peace Talks and Trade Deals. Keys to Long-Term Harmony in Legume-Microbe Symbioses: Figure 1.. Plant Physiology, 2005, 137, 1205-1210.	2.3	99
144	PLANT SCIENCE: GRAS Genes and the Symbiotic Green Revolution. Science, 2005, 308, 1749-1750.	6.0	20

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145	Repressor- and Activator-Type Ethylene Response Factors Functioning in Jasmonate Signaling and Disease Resistance Identified via a Genome-Wide Screen of Arabidopsis Transcription Factor Gene Expression. Plant Physiology, 2005, 139, 949-959.	2.3	540
146	The Sulfate Transporter SST1 Is Crucial for Symbiotic Nitrogen Fixation in Lotus japonicus Root Nodules. Plant Cell, 2005, 17, 1625-1636.	3.1	227
147	Genome-Wide Identification and Testing of Superior Reference Genes for Transcript Normalization in Arabidopsis. Plant Physiology, 2005, 139, 5-17.	2.3	2,835
148	Lotus japonicus Metabolic Profiling. Development of Gas Chromatography-Mass Spectrometry Resources for the Study of Plant-Microbe Interactions. Plant Physiology, 2005, 137, 1302-1318.	2.3	196
149	Lotus japonicus: legume research in the fast lane. Trends in Plant Science, 2005, 10, 222-228.	4.3	123
150	Metabolome analysis using GC-MS. , 2005, , 165-174.		5
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