

Evolutionary conservation of the transcriptional network biosynthesis

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Gene expression in developing fibres of Upland cotton (<i>Gossypium hirsutum</i> L.) was massively altered by domestication. <i>BMC Biology</i> , 2010, 8, 139.	1.7	87
2	Senescence-associated Barley NAC (NAM, ATAF1,2, CUC) Transcription Factor Interacts with Radical-induced Cell Death 1 through a Disordered Regulatory Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 35418-35429.	1.6	84
3	Overexpression of constitutively active <i>Arabidopsis</i> RabG3b promotes xylem development in transgenic poplars. <i>Plant, Cell and Environment</i> , 2011, 34, 2212-2224.	2.8	24
4	A NAC domain protein family contributing to the regulation of wood formation in poplar. <i>Plant Journal</i> , 2011, 67, 499-512.	2.8	182
5	NAC domain function and transcriptional control of a secondary cell wall master switch. <i>Plant Journal</i> , 2011, 68, 1104-1114.	2.8	112
6	SND2, a NAC transcription factor gene, regulates genes involved in secondary cell wall development in <i>Arabidopsis</i> fibres and increases fibre cell area in <i>Eucalyptus</i> . <i>BMC Plant Biology</i> , 2011, 11, 173.	1.6	164
7	Biotechnological improvement of lignocellulosic feedstock for enhanced biofuel productivity and processing. <i>Plant Biotechnology Reports</i> , 2011, 5, 1-7.	0.9	13
8	Dissection of the Transcriptional Program Regulating Secondary Wall Biosynthesis during Wood Formation in Poplar. <i>Plant Physiology</i> , 2011, 157, 1452-1468.	2.3	220
9	Transcriptional Activation of Secondary Wall Biosynthesis by Rice and Maize NAC and MYB Transcription Factors. <i>Plant and Cell Physiology</i> , 2011, 52, 1856-1871.	1.5	270
10	Secondary wall NAC binding element (SNBE), a key cis-acting element required for target gene activation by secondary wall NAC master switches. <i>Plant Signaling and Behavior</i> , 2011, 6, 1282-1285.	1.2	37
11	Cotton fiber: a powerful single-cell model for cell wall and cellulose research. <i>Frontiers in Plant Science</i> , 2012, 3, 104.	1.7	286
12	Xylem cell death: emerging understanding of regulation and function. <i>Journal of Experimental Botany</i> , 2012, 63, 1081-1094.	2.4	179
13	Transcription Factors of Lotus: Regulation of Isoflavonoid Biosynthesis Requires Coordinated Changes in Transcription Factor Activity. <i>Plant Physiology</i> , 2012, 159, 531-547.	2.3	64
14	MYB46 and MYB83 Bind to the SMRE Sites and Directly Activate a Suite of Transcription Factors and Secondary Wall Biosynthetic Genes. <i>Plant and Cell Physiology</i> , 2012, 53, 368-380.	1.5	325
15	Transcriptional Regulation of the Lignin Biosynthetic Pathway Revisited: New Players and Insights. <i>Advances in Botanical Research</i> , 2012, 61, 173-218.	0.5	28
16	On "Off Switches for Secondary Cell Wall Biosynthesis. <i>Molecular Plant</i> , 2012, 5, 297-303.	3.9	186
17	The promoter region of the <i>Zinnia elegans</i> basic peroxidase isoenzyme gene contains cis-elements responsive to nitric oxide and hydrogen peroxide. <i>Planta</i> , 2012, 236, 327-342.	1.6	15
18	Role of recently evolved miRNA regulation of sunflower <i>HaWRKY6</i> in response to temperature damage. <i>New Phytologist</i> , 2012, 195, 766-773.	3.5	118

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19	Engineering of plants with improved properties as biofuels feedstocks by vessel-specific complementation of xylan biosynthesis mutants. <i>Biotechnology for Biofuels</i> , 2012, 5, 84.	6.2	97
20	Progress in the biological synthesis of the plant cell wall: new ideas for improving biomass for bioenergy. <i>Current Opinion in Biotechnology</i> , 2012, 23, 330-337.	3.3	79
21	Natural Hypolignification Is Associated with Extensive Oligolignol Accumulation in Flax Stems. <i>Plant Physiology</i> , 2012, 158, 1893-1915.	2.3	82
22	Deep EST profiling of developing fenugreek endosperm to investigate galactomannan biosynthesis and its regulation. <i>Plant Molecular Biology</i> , 2012, 79, 243-258.	2.0	32
23	Functional characterization of the switchgrass (<i>Panicum virgatum</i>) R2R3MYB transcription factor PvMYB4 for improvement of lignocellulosic feedstocks. <i>New Phytologist</i> , 2012, 193, 121-136.	3.5	264
24	The Class II KNOX gene KNAT7 negatively regulates secondary wall formation in <i>Arabidopsis</i> and is functionally conserved in <i>Populus</i> . <i>New Phytologist</i> , 2012, 194, 102-115.	3.5	186
25	Isolation and Partial Characterization of an R2R3MYB Transcription Factor from the Bamboo Species <i>Fargesia fungosa</i> . <i>Plant Molecular Biology Reporter</i> , 2012, 30, 131-138.	1.0	4
26	The developing xylem transcriptome and genome-wide analysis of alternative splicing in <i>Populus trichocarpa</i> (black cottonwood) populations. <i>BMC Genomics</i> , 2013, 14, 359.	1.2	76
27	Identification of molecular processes needed for vascular formation through transcriptome analysis of different vascular systems. <i>BMC Genomics</i> , 2013, 14, 217.	1.2	21
28	Characterization of expressed sequence tags from developing fibers of <i>Gossypium barbadense</i> and evaluation of insertion-deletion variation in tetraploid cultivated cotton species. <i>BMC Genomics</i> , 2013, 14, 170.	1.2	8
29	The interacting MYB75 and KNAT7 transcription factors modulate secondary cell wall deposition both in stems and seed coat in <i>Arabidopsis</i> . <i>Planta</i> , 2013, 237, 1199-1211.	1.6	78
30	Induced somatic sector analysis of cellulose synthase (CesA) promoter regions in woody stem tissues. <i>Planta</i> , 2013, 237, 799-812.	1.6	14
31	The PmNAC1 gene is induced by auxin and expressed in differentiating vascular cells in callus cultures of <i>Passiflora</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 115, 275-283.	1.2	8
32	Diversity and cis-element architecture of the promoter regions of cellulose synthase genes in <i>Eucalyptus</i> . <i>Tree Genetics and Genomes</i> , 2013, 9, 989-1004.	0.6	3
33	Cellular Aspects of Wood Formation. <i>Plant Cell Monographs</i> , 2013, , .	0.4	32
34	The R2R3-MYB-Like Regulatory Factor EOBI, Acting Downstream of EOBI, Regulates Scent Production by Activating ODO1 and Structural Scent-Related Genes in <i>Petunia</i> . <i>Plant Cell</i> , 2013, 24, 5089-5105.	3.1	114
35	Polar Auxin Transport. <i>Signaling and Communication in Plants</i> , 2013, , .	0.5	18
36	Xylem tissue specification, patterning, and differentiation mechanisms. <i>Journal of Experimental Botany</i> , 2013, 64, 11-31.	2.4	197

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37	Functions of rice NAC transcriptional factors, ONAC122 and ONAC131, in defense responses against <i>Magnaporthe grisea</i> . <i>Plant Molecular Biology</i> , 2013, 81, 41-56.	2.0	113
38	Hormone interactions in xylem development: a matter of signals. <i>Plant Cell Reports</i> , 2013, 32, 867-883.	2.8	48
39	Transcriptional Regulation of Wood Formation in Tree Species. <i>Plant Cell Monographs</i> , 2013, , 141-158.	0.4	7
40	Post mortem function of <i>AtMYC9</i> in xylem vessel elements. <i>New Phytologist</i> , 2013, 200, 498-510.	3.5	117
41	Phytohormones in Japanese Mugwort Gall Induction by a Gall-Inducing Gall Midge. <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 1942-1948.	0.6	58
42	Phloem parenchyma transfer cells in <i>Arabidopsis</i> – an experimental system to identify transcriptional regulators of wall ingrowth formation. <i>Frontiers in Plant Science</i> , 2013, 4, 102.	1.7	24
43	Navigating the transcriptional roadmap regulating plant secondary cell wall deposition. <i>Frontiers in Plant Science</i> , 2013, 4, 325.	1.7	124
44	Regulation of secondary wall synthesis and cell death by NAC transcription factors in the monocot <i>Brachypodium distachyon</i> . <i>Journal of Experimental Botany</i> , 2013, 64, 1333-1343.	2.4	78
45	Neighboring Parenchyma Cells Contribute to <i>Arabidopsis</i> Xylem Lignification, while Lignification of Interfascicular Fibers Is Cell Autonomous. <i>Plant Cell</i> , 2013, 25, 3988-3999.	3.1	138
46	The Transcriptomics of Secondary Growth and Wood Formation in Conifers. <i>Molecular Biology International</i> , 2013, 2013, 1-12.	1.7	22
47	Functional characterization of the orthologs of <i>AtNST1/2</i> in <i>Glycine soja</i> (<i>Fabaceae</i>) and the evolutionary implications. <i>Journal of Systematics and Evolution</i> , 2013, 51, 693-703.	1.6	10
48	The Poplar MYB Master Switches Bind to the SMRE Site and Activate the Secondary Wall Biosynthetic Program during Wood Formation. <i>PLoS ONE</i> , 2013, 8, e9219.	1.1	130
49	Identification of novel transcription factors regulating secondary cell wall formation in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 189.	1.7	106
50	Transcriptomic Analysis of Fiber Strength in Upland Cotton Chromosome Introgression Lines Carrying Different <i>Gossypium barbadense</i> Chromosomal Segments. <i>PLoS ONE</i> , 2014, 9, e94642.	1.1	14
52	Plant biotechnology for lignocellulosic biofuel production. <i>Plant Biotechnology Journal</i> , 2014, 12, 1174-1192.	4.1	96
53	Databases for Bioenergy-Related Enzymes. , 2014, , 95-107.		2
54	Cellulose Synthesis and Its Regulation. <i>The Arabidopsis Book</i> , 2014, 12, e0169.	0.5	119
55	Genetic Determinants for Enzymatic Digestion of Lignocellulosic Biomass Are Independent of Those for Lignin Abundance in a Maize Recombinant Inbred Population. <i>Plant Physiology</i> , 2014, 165, 1475-1487.	2.3	51

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57	PtrKOR1 is required for secondary cell wall cellulose biosynthesis in <i>Populus</i> . <i>Tree Physiology</i> , 2014, 34, 1289-1300.	1.4	43
58	Intron-Mediated Alternative Splicing of WOOD-ASSOCIATED NAC TRANSCRIPTION FACTOR1B Regulates Cell Wall Thickening during Fiber Development in <i>Populus</i> Species <i>A</i> . <i>Plant Physiology</i> , 2014, 164, 765-776.	2.3	123
59	Spatial gradients in cell wall composition and transcriptional profiles along elongating maize internodes. <i>BMC Plant Biology</i> , 2014, 14, 27.	1.6	50
60	The MYB46/MYB83-mediated transcriptional regulatory programme is a gatekeeper of secondary wall biosynthesis. <i>Annals of Botany</i> , 2014, 114, 1099-1107.	1.4	152
61	Opposite action of R2R3-MYBs from different subgroups on key genes of the shikimate and monolignol pathways in spruce. <i>Journal of Experimental Botany</i> , 2014, 65, 495-508.	2.4	34
62	Systems and synthetic biology approaches to alter plant cell walls and reduce biomass recalcitrance. <i>Plant Biotechnology Journal</i> , 2014, 12, 1207-1216.	4.1	46
63	Aberrant phenotype and transcriptome expression during fiber cell wall thickening caused by the mutation of the <i>Im</i> gene in immature fiber (<i>im</i>) mutant in <i>Gossypium hirsutum</i> L. <i>BMC Genomics</i> , 2014, 15, 94.	1.2	25
64	Large-scale screening of transcription factor-promoter interactions in spruce reveals a transcriptional network involved in vascular development. <i>Journal of Experimental Botany</i> , 2014, 65, 2319-2333.	2.4	59
65	Pod shattering resistance associated with domestication is mediated by a NAC gene in soybean. <i>Nature Communications</i> , 2014, 5, 3352.	5.8	177
66	Lignin bioengineering. <i>Current Opinion in Biotechnology</i> , 2014, 26, 189-198.	3.3	126
67	Xylan biosynthesis. <i>Current Opinion in Biotechnology</i> , 2014, 26, 100-107.	3.3	249
68	The formation of wood and its control. <i>Current Opinion in Plant Biology</i> , 2014, 17, 56-63.	3.5	126
69	AtMYB41 activates ectopic suberin synthesis and assembly in multiple plant species and cell types. <i>Plant Journal</i> , 2014, 80, 216-229.	2.8	172
70	<i>Arabidopsis</i> VASCULAR-RELATED UNKNOWN PROTEIN1 Regulates Xylem Development and Growth by a Conserved Mechanism That Modulates Hormone Signaling <i>A</i> . <i>Plant Physiology</i> , 2014, 164, 1991-2010.	2.3	5
71	Regulation of galactomannan biosynthesis in coffee seeds. <i>Journal of Experimental Botany</i> , 2014, 65, 323-337.	2.4	27
72	Complexity of the transcriptional network controlling secondary wall biosynthesis. <i>Plant Science</i> , 2014, 229, 193-207.	1.7	124
73	Molecular cloning, characterization, and expression analysis of LeMYB1 from <i>Lithospermum erythrorhizon</i> . <i>Biologia Plantarum</i> , 2014, 58, 436-444.	1.9	11

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75	A survey of plant and algal genomes and transcriptomes reveals new insights into the evolution and function of the cellulose synthase superfamily. <i>BMC Genomics</i> , 2014, 15, 260.	1.2	63
76	Comparative genomic analysis of the R2R3 MYB secondary cell wall regulators of Arabidopsis, poplar, rice, maize, and switchgrass. <i>BMC Plant Biology</i> , 2014, 14, 135.	1.6	74
77	Programmes of cell death and autolysis in tracheary elements: when a suicidal cell arranges its own corpse removal. <i>Journal of Experimental Botany</i> , 2014, 65, 1313-1321.	2.4	96
79	The NAC transcription factor family in maritime pine (<i>Pinus Pinaster</i>): molecular regulation of two genes involved in stress responses. <i>BMC Plant Biology</i> , 2015, 15, 254.	1.6	54
80	Exogenous GA3 Application Enhances Xylem Development and Induces the Expression of Secondary Wall Biosynthesis Related Genes in <i>Betula platyphylla</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 22960-22975.	1.8	34
81	Functional Characterization of NAC and MYB Transcription Factors Involved in Regulation of Biomass Production in Switchgrass (<i>Panicum virgatum</i>). <i>PLoS ONE</i> , 2015, 10, e0134611.	1.1	68
82	NAC-MYB-based transcriptional regulation of secondary cell wall biosynthesis in land plants. <i>Frontiers in Plant Science</i> , 2015, 6, 288.	1.7	344
83	Seed shattering: from models to crops. <i>Frontiers in Plant Science</i> , 2015, 6, 476.	1.7	114
84	Short day transcriptomic programming during induction of dormancy in grapevine. <i>Frontiers in Plant Science</i> , 2015, 6, 834.	1.7	48
85	Comparative proteomic analysis of <i>Populus trichocarpa</i> early stem from primary to secondary growth. <i>Journal of Proteomics</i> , 2015, 126, 94-108.	1.2	22
86	Metabolomic and transcriptomic insights into how cotton fiber transitions to secondary wall synthesis, represses lignification, and prolongs elongation. <i>BMC Genomics</i> , 2015, 16, 477.	1.2	72
87	Cellulose-hemicellulose interaction in wood secondary cell-wall. <i>Modelling and Simulation in Materials Science and Engineering</i> , 2015, 23, 085010.	0.8	71
88	A R2R3-MYB transcription factor that is specifically expressed in cotton (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Over <i>Arabidopsis</i> . <i>Physiologia Plantarum</i> , 2015, 154, 420-432.	2.6	51
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90	Molecular control of wood formation in trees. <i>Journal of Experimental Botany</i> , 2015, 66, 4119-4131.	2.4	148
91	Comprehensive Analysis Suggests Overlapping Expression of Rice ONAC Transcription Factors in Abiotic and Biotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2015, 16, 4306-4326.	1.8	67
92	A role for OVATE FAMILY PROTEIN1 (OFP1) and OFP4 in a BLH6-KNAT7 multi-protein complex regulating secondary cell wall formation in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2015, 10, e1033126.	1.2	50

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94	Poplar PdMYB221 is involved in the direct and indirect regulation of secondary wall biosynthesis during wood formation. Scientific Reports, 2015, 5, 12240.	1.6	52
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97	Transcript profiling of <i>Populus tomentosa</i> genes in normal, tension, and opposite wood by RNA-seq. BMC Genomics, 2015, 16, 164.	1.2	58
98	The <i>Arabidopsis</i> NAC transcription factor NST2 functions together with SND1 and NST1 to regulate secondary wall biosynthesis in fibers of inflorescence stems. Plant Signaling and Behavior, 2015, 10, e989746.	1.2	53
99	Genome-wide analysis reveals dynamic changes in expression of microRNAs during vascular cambium development in Chinese fir, <i>Cunninghamia lanceolata</i> . Journal of Experimental Botany, 2015, 66, 3041-3054.	2.4	37
100	Regulation of secondary cell wall biosynthesis by poplar R2R3 MYB transcription factor PtrMYB152 in <i>Arabidopsis</i> . Scientific Reports, 2014, 4, 5054.	1.6	106
101	Editorial: An Emerging View of Plant Cell Walls as an Apoplastic Intelligent System. Plant and Cell Physiology, 2015, 56, 177-179.	1.5	18
102	<i>Brachypodium distachyon</i> as a Model Species to Understand Grass Cell Walls. Plant Genetics and Genomics: Crops and Models, 2015, , 197-217.	0.3	2
103	Modular organization of the white spruce (<i>Picea glauca</i>) transcriptome reveals functional organization and evolutionary signatures. New Phytologist, 2015, 207, 172-187.	3.5	35
104	BEL1-LIKE HOMEODOMAIN6 and KNOTTED ARABIDOPSIS THALIANA7 Interact and Regulate Secondary Cell Wall Formation via Repression of <i>REVOLUTA</i> . Plant Cell, 2015, 26, 4843-4861.	3.1	124
105	Structural, evolutionary and functional analysis of the NAC domain protein family in <i>Eucalyptus</i> . New Phytologist, 2015, 206, 1337-1350.	3.5	69
106	Bioethanol from maize cell walls: genes, molecular tools, and breeding prospects. GCB Bioenergy, 2015, 7, 591-607.	2.5	19
107	Secondary Cell Walls: Biosynthesis, Patterned Deposition and Transcriptional Regulation. Plant and Cell Physiology, 2015, 56, 195-214.	1.5	360
108	The <i>Eucalyptus grandis</i> R2R3MYB transcription factor family: evidence for woody growth-related evolution and function. New Phytologist, 2015, 206, 1364-1377.	3.5	107
109	Designer Plants for Biofuels: A Review. Current Metabolomics, 2016, 4, 49-55.	0.5	10
110	Genetic Engineering for Secondary Xylem Modification: Unraveling the Genetic Regulation of Wood Formation. , 2016, , 193-211.		1

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111	Identification of Candidate Transcriptional Regulators of Epidermal Transfer Cell Development in <i>Vicia faba</i> Cotyledons. <i>Frontiers in Plant Science</i> , 2016, 7, 717.	1.7	6
112	Biosynthesis and Metabolic Fate of Phenylalanine in Conifers. <i>Frontiers in Plant Science</i> , 2016, 7, 1030.	1.7	98
113	Genetic variations and miRNA–target interactions contribute to natural phenotypic variations in <i>Populus</i> . <i>New Phytologist</i> , 2016, 212, 150-160.	3.5	17
114	Co-localization of QTLs for pod fiber content and pod shattering in F2 and backcross populations between yardlong bean and wild cowpea. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	45
115	Transcriptome analyses of seed development in grape hybrids reveals a possible mechanism influencing seed size. <i>BMC Genomics</i> , 2016, 17, 898.	1.2	39
116	Genetic architecture of wood properties based on association analysis and co-expression networks in white spruce. <i>New Phytologist</i> , 2016, 210, 240-255.	3.5	43
117	<i>Eucalyptus</i> hairy roots, a fast, efficient and versatile tool to explore function and expression of genes involved in wood formation. <i>Plant Biotechnology Journal</i> , 2016, 14, 1381-1393.	4.1	54
118	Conifer genomics and adaptation: at the crossroads of genetic diversity and genome function. <i>New Phytologist</i> , 2016, 209, 44-62.	3.5	73
119	To Have and to Hold. <i>Current Topics in Developmental Biology</i> , 2016, 119, 63-109.	1.0	53
120	Regulation of plant secondary metabolism and associated specialized cell development by MYBs and bHLHs. <i>Phytochemistry</i> , 2016, 131, 26-43.	1.4	143
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123	Evolutionary and Expression Analysis Provides Evidence for the Plant Glutamate-like Receptors Family is Involved in Woody Growth-related Function. <i>Scientific Reports</i> , 2016, 6, 32013.	1.6	16
124	Cotton Fiber Biotechnology: Potential Controls and Transgenic Improvement of Elongation and Cell Wall Thickening. <i>Sustainable Development and Biodiversity</i> , 2016, , 127-153.	1.4	5
125	Fiber Plants. <i>Sustainable Development and Biodiversity</i> , 2016, , .	1.4	6
126	A stress-associated <i>NAC</i> transcription factor (<i>SINAC35</i>) from tomato plays a positive role in biotic and abiotic stresses. <i>Physiologia Plantarum</i> , 2016, 158, 45-64.	2.6	92
127	Transcriptional regulation of vascular cambium activity during the transition from juvenile to mature stages in <i>Cunninghamia lanceolata</i> . <i>Journal of Plant Physiology</i> , 2016, 200, 7-17.	1.6	19
128	Functional Analysis of Cellulose and Xyloglucan in the Walls of Stomatal Guard Cells of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2016, 170, 1398-1419.	2.3	75
129	Development of functional modules based on co-expression patterns for cell-wall biosynthesis related genes in rice. <i>Journal of Plant Biology</i> , 2016, 59, 1-15.	0.9	18

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130	Spatially and temporally restricted expression of PtrMYB021 regulates secondary cell wall formation in Arabidopsis. <i>Journal of Plant Biology</i> , 2016, 59, 16-23.	0.9	9
131	Genetics and Genomics of Brachypodium. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , .	0.3	22
132	Resistance of Plants to Cu Stress. , 2016, , 69-114.		7
133	Changes in cell wall polysaccharide composition, gene transcription and alternative splicing in germinating barley embryos. <i>Journal of Plant Physiology</i> , 2016, 191, 127-139.	1.6	11
134	SIMYB1 and SIMYB2 , two new MYB genes from tomato, transcriptionally regulate cellulose biosynthesis in tobacco. <i>Journal of Integrative Agriculture</i> , 2017, 16, 65-75.	1.7	13
135	Beyond Genomics: Studying Evolution with Gene Coexpression Networks. <i>Trends in Plant Science</i> , 2017, 22, 298-307.	4.3	96
136	EliteTreeâ„¢: an advanced biomass tree crop technology that features greater wood density and accelerated stem growth. <i>Biofuels, Bioproducts and Biorefining</i> , 2017, 11, 521-533.	1.9	7
137	Identifying gene coexpression networks underlying the dynamic regulation of woodâ€™forming tissues in <i>Populus</i> under diverse environmental conditions. <i>New Phytologist</i> , 2017, 214, 1464-1478.	3.5	56
138	PtoMYB156 is involved in negative regulation of phenylpropanoid metabolism and secondary cell wall biosynthesis during wood formation in poplar. <i>Scientific Reports</i> , 2017, 7, 41209.	1.6	87
139	BLISS: A Bioorthogonal Dual-Labeling Strategy to Unravel Lignification Dynamics in Plants. <i>Cell Chemical Biology</i> , 2017, 24, 326-338.	2.5	41
140	Digital gene expression profiling of flax (<i>Linum usitatissimum</i> L.) stem peel identifies genes enriched in fiber-bearing phloem tissue. <i>Gene</i> , 2017, 626, 32-40.	1.0	23
141	Transcriptomics and proteomics reveal genetic and biological basis of superior biomass crop <i>Miscanthus</i> . <i>Scientific Reports</i> , 2017, 7, 13777.	1.6	13
142	Genetic connection between cell-wall composition and grain yield via parallel QTL analysis in indica and japonica subspecies. <i>Scientific Reports</i> , 2017, 7, 12561.	1.6	11
143	Regulation of secondary cell wall biosynthesis by a <i>NAC</i> transcription factor from <i>Miscanthus</i> . <i>Plant Direct</i> , 2017, 1, e00024.	0.8	19
144	QTL analysis of four main stem bark traits using a GBS-SNP-based high-density genetic map in ramie. <i>Scientific Reports</i> , 2017, 7, 13458.	1.6	34
145	SmMYB36, a Novel R2R3-MYB Transcription Factor, Enhances Tanshinone Accumulation and Decreases Phenolic Acid Content in <i>Salvia miltiorrhiza</i> Hairy Roots. <i>Scientific Reports</i> , 2017, 7, 5104.	1.6	97
146	Functional Characterization of <i>Populus</i> PsnSHN2 in Coordinated Regulation of Secondary Wall Components in Tobacco. <i>Scientific Reports</i> , 2017, 7, 42.	1.6	52
147	Mediator Complex Subunits MED2, MED5, MED16, and MED23 Genetically Interact in the Regulation of Phenylpropanoid Biosynthesis. <i>Plant Cell</i> , 2017, 29, 3269-3285.	3.1	46

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148	The essence of NAC gene family to the cultivation of drought-resistant soybean (<i>Glycine max</i> L. Merr.) cultivars. <i>BMC Plant Biology</i> , 2017, 17, 55.	1.6	74
149	A Combined Comparative Transcriptomic, Metabolomic, and Anatomical Analyses of Two Key Domestication Traits: Pod Dehiscence and Seed Dormancy in Pea (<i>Pisum</i> sp.). <i>Frontiers in Plant Science</i> , 2017, 8, 542.	1.7	53
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151	Transcriptome analysis provides insights into xylogenesis formation in Moso bamboo (<i>Phyllostachys Tj ETQq1 1 0.784314 rgBT /Over</i>	1.6	36
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